

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 8.93784 Seconds  
(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-20  
Perfect score: 8527  
Sequence: 1 ADECADEGGPQRCMPFV.....EDIKTLPTGCFNTSPSIEKP 1572

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8460	99.2	1607	1 LMG1_MOUSE	P02468 mus musculus
2	8034	94.2	1609	1 LMG1_HUMAN	P11047 homo sapien
3	3586	42.1	1587	1 LMG3_HUMAN	Q9Y6N6 homo sapien
4	3486.5	40.9	1581	1 LMG3_MOUSE	Q9Y6N6 mus musculus
5	3476	40.8	1639	1 LMG1_DROME	P15215 drosophila
6	3176	37.2	1535	1 LML1_CAEBL	Q18823 caenorhabdi
7	2592	30.4	1193	1 LMG2_HUMAN	Q13753 homo sapien
8	2475	29.0	1191	1 LMG2_MOUSE	Q61092 mus musculus
9	1812.5	21.3	3106	1 LMA2_MOUSE	Q60675 mus musculus
10	1790.5	21.0	3110	1 LMA2_HUMAN	P24043 homo sapien
11	1780.5	20.9	3084	1 LMA1_MOUSE	P19137 mus musculus
12	1735	20.3	3075	1 LMA1_HUMAN	P25391 homo sapien
13	1677	19.7	1786	1 LMB1_HUMAN	P07942 homo sapien
14	1661.5	19.5	1786	1 LMB1_MOUSE	P02469 mus musculus
15	1656.5	19.4	1790	1 LMB1_DROME	P11046 drosophila
16	1569	18.4	1801	1 LMB2_RAT	P15800 rattus norv
17	1541.5	18.1	1798	1 LMB2_HUMAN	P55268 homo sapien
18	1526	17.9	1799	1 LMB2_MOUSE	Q61292 mus musculus
19	1454	17.1	3712	1 LMA_DROME	Q00174 drosophila
20	1384	16.2	3672	1 LML2_CAEBL	Q21313 caenorhabdi
21	1376	16.1	3718	1 LMA5_MOUSE	Q61001 mus musculus
22	1330.5	15.6	3695	1 LMA5_HUMAN	Q15230 homo sapien
23	1300.5	13.6	3333	1 LMA3_MOUSE	Q61789 mus musculus
24	1162.5	13.6	606	1 NET1_CHICK	Q0C922 gallus gall
25	1145.5	13.4	604	1 NET1_MOUSE	O09118 mus musculus
26	1137	13.3	604	1 NET1_HUMAN	Q95631 homo sapien
27	1044.5	12.2	581	1 NET2_CHICK	Q90923 gallus gall
28	986.5	11.6	612	1 UNC6_CAEBL	P34710 caenorhabdi
29	948	11.1	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	903.5	10.6	4391	1 PGBM_HUMAN	P98160 homo sapien
31	902	10.6	1168	1 LMB3_MOUSE	Q61087 mus musculus
32	883	10.4	727	1 NETA_DROME	Q24567 drosophila
33	877.5	10.3	3707	1 PGBM_MOUSE	Q05793 mus musculus

34	841.5	9.9	793	1 NETB_DROME	Q24568 drosophila
35	637.5	7.5	3375	1 UNS2_CAEBL	Q06561 caenorhabdi
36	623.5	7.3	539	1 NTG1_MOUSE	Q82490 mus musculus
37	585	6.9	1816	1 LMA4_HUMAN	Q16363 homo sapien
38	574.5	6.7	1816	1 LMA4_MOUSE	P97927 mus musculus
39	560.5	6.6	530	1 NTG2_HUMAN	Q96C99 homo sapien
40	532	6.2	589	1 NTG2_MOUSE	Q84411 mus musculus
41	514	6.0	1713	1 LMA3_HUMAN	Q16787 homo sapien
42	479	5.6	2470	1 NTG2_MOUSE	Q35516 mus musculus
43	477	5.6	2471	1 NTG2_RAT	Q9GW30 rattus norv
44	471	5.5	303	1 LMB1_CHICK	Q01635 gallus gall
45	469.5	5.5	2703	1 NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1

LMG1\_MOUSE

ID LMG1\_MOUSE STANDARD; PRT; 1607 AA.

AC P02468;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Laminin gamma-1 chain precursor (Laminin B2 chain).

GN LAMC1 OR LAMC-1 OR LAMB-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88059118; PubMed=3680290;

RA Sasaki M., Yamada Y.;

RT "The laminin B2 chain has a multidomain structure homologous to the B1 chain."

RL J. Biol. Chem. 262:17111-17117(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=89000737; PubMed=3167041;

RA Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;

RT "Primary structure of the mouse laminin B2 chain and comparison with laminin B1."

RL Biochemistry 27:5198-5204(1988).

RN [3]

RP SEQUENCE OF 1-239 FROM N.A.

RX MEDLINE=8828071; PubMed=2836421;

RA Ogawa K., Furubelo P.D., Sasaki M., Yamada Y.;

RT "The laminin B2 chain promoter contains unique repeat sequences and is active in transient transfection."

RL J. Biol. Chem. 263:8384-8389(1988).

RN [4]

RP SEQUENCE OF 1391-1607 FROM N.A.

RX MEDLINE=85051302; PubMed=6209134;

RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;

RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil alpha-helix."

RL EMBO J. 3:2355-2362(1984).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.

RX MEDLINE=96196434; PubMed=8648630;

RA Stetefeld J., Mayer U., Timpi R., Huber R.;

RT "Crystal structure of three consecutive laminin-type epidermal growth factor-like (LE) modules of laminin gamma1 chain harboring the nidogen binding site."

RL J. Mol. Biol. 257:644-657(1996).

RN [6]

RP STRUCTURE BY NMR OF 824-881.

RX MEDLINE=96196435; PubMed=8648631;

RA Baumgartner R., Csisch M., Mayer U., Poeschl E., Huber R.;

RA Timpi R., Holak T.A.;

RT "Structure of the nidogen binding LE module of the laminin gamma1 chain in solution."

J. Mol. Biol. 257:658-668(1996).

-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin), laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin), laminin-6 (K-laminin) and laminin-7 (KS-laminin).

-!- SUBCELLULAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: Found in the basement membranes (major component).

-!- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.

-!- DOMAIN: Domains VI and IV are globular.

-!- SIMILARITY: Contains 1 laminin N-terminal domain.

-!- SIMILARITY: Contains 11 laminin EGF-like domains.

-!- SIMILARITY: Contains 1 laminin IV domain.

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EMBL; X05211; ARA28838.1; -  
DR EMBL; J03484; ARA39405.1; -  
DR EMBL; J02930; ARA39408.1; -  
DR EMBL; J03749; ARA39409.1; -  
DR F01; A28469; MMSB2.  
DR PDB; 1KLO; 20-AUG-97.  
DR PDB; 1TLE; 12-FEB-97.  
DR MGD; MGI:99914; Lamc1.  
DR GO; GO:0005604; C:basement membrane; IDA.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR008212; Lam\_N2.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin\_B; 1.  
DR Pfam; PF00053; laminin\_EGF; 9.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PRODOM; PRO02082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 8.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 10.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.  
FT SIGNAL 1 33  
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.  
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.  
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.  
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.  
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.  
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 503 687 LAMININ DOMAIN IV.  
FT DOMAIN 688 721 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 722 770 LAMININ EGF-LIKE 6.  
FT DOMAIN 771 825 LAMININ EGF-LIKE 7.  
FT DOMAIN 826 881 LAMININ EGF-LIKE 8 (NIDOGEN-BINDING).  
FT DOMAIN 882 932 LAMININ EGF-LIKE 9.  
FT DOMAIN 933 980 LAMININ EGF-LIKE 10.  
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.

FT	DOMAIN	1029	1607	DOMAIN II AND I.
FT	DISULFID	1034	1594	COILED COIL (POTENTIAL).
FT	DISULFID	340	349	BY SIMILARITY.
FT	DISULFID	342	365	BY SIMILARITY.
FT	DISULFID	368	377	BY SIMILARITY.
FT	DISULFID	380	393	BY SIMILARITY.
FT	DISULFID	396	408	BY SIMILARITY.
FT	DISULFID	398	414	BY SIMILARITY.
FT	DISULFID	416	425	BY SIMILARITY.
FT	DISULFID	428	440	BY SIMILARITY.
FT	DISULFID	443	454	BY SIMILARITY.
FT	DISULFID	445	461	BY SIMILARITY.
FT	DISULFID	463	472	BY SIMILARITY.
FT	DISULFID	475	490	BY SIMILARITY.
FT	DISULFID	722	731	BY SIMILARITY.
FT	DISULFID	724	738	BY SIMILARITY.
FT	DISULFID	740	749	BY SIMILARITY.
FT	DISULFID	752	768	BY SIMILARITY.
FT	DISULFID	771	779	BY SIMILARITY.
FT	DISULFID	773	790	BY SIMILARITY.
FT	DISULFID	793	802	BY SIMILARITY.
FT	DISULFID	805	823	BY SIMILARITY.
FT	DISULFID	826	840	BY SIMILARITY.
FT	DISULFID	828	847	BY SIMILARITY.
FT	DISULFID	850	859	BY SIMILARITY.
FT	DISULFID	862	879	BY SIMILARITY.
FT	DISULFID	882	896	BY SIMILARITY.
FT	DISULFID	884	903	BY SIMILARITY.
FT	DISULFID	905	914	BY SIMILARITY.
FT	DISULFID	917	930	BY SIMILARITY.
FT	DISULFID	933	945	BY SIMILARITY.
FT	DISULFID	935	952	BY SIMILARITY.
FT	DISULFID	954	963	BY SIMILARITY.
FT	DISULFID	966	978	BY SIMILARITY.
FT	DISULFID	981	993	BY SIMILARITY.
FT	DISULFID	983	999	BY SIMILARITY.
FT	DISULFID	1001	1010	BY SIMILARITY.
FT	DISULFID	1033	1026	BY SIMILARITY.
FT	DISULFID	1039	1029	INTERCHAIN (PROBABLE).
FT	DISULFID	1032	1032	INTERCHAIN (PROBABLE).
FT	DISULFID	1598	1598	INTERCHAIN (WITH BETA-1 CHAIN).
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	648	648	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1020	1020	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1105	1105	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1159	1159	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1173	1173	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1203	1203	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1221	1221	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1239	1239	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1437	1437	N-LINKED (GLCNAC. . .)
FT	CONFLICT	216	216	G -> A (IN REF. 3).
FT	CONFLICT	260	260	E -> D (IN REF. 2).
FT	CONFLICT	337	337	S -> C (IN REF. 2).
FT	CONFLICT	447	448	LR -> PS (IN REF. 2).
FT	CONFLICT	544	544	D -> Y (IN REF. 2).
FT	CONFLICT	662	662	T -> S (IN REF. 2).
FT	CONFLICT	886	886	MISSING (IN REF. 2).
FT	CONFLICT	1158	1158	MISSING (IN REF. 2).
FT	CONFLICT	1434	1434	V -> A (IN REF. 2).
FT	CONFLICT	1475	1475	R -> K (IN REF. 4).
FT	CONFLICT	1576	1576	D -> N (IN REF. 4).
FT	TURN	775	776	
FT	STRAND	781	781	
FT	STRAND	788	790	
FT	TURN	795	796	
FT	STRAND	797	798	
FT	TURN	800	801	
FT	STRAND	804	805	



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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 42.6441 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-20

Perfect score: 8527

Sequence: 1 AMDECADEGRPCRCMPEFV.....EDIKKTLPTGCFNTSIEKP 1572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6145	72.1	1593	13 Q8JHV8	Q8jvh8 brachydanio
2	4704	55.2	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3535.5	41.5	1623	5 Q9U3U7	Q9u3u7 anopheles g
4	2583.5	30.3	1196	6 Q867A2	Q867a2 canis famil
5	2579.5	30.3	1190	6 Q84ZL9	Q84zl9 equus caball
6	1715	20.1	1785	13 Q8JHV7	Q8jvh7 brachydanio
7	1687	19.8	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1655	19.4	1792	13 Q57484	Q57484 gallus gall
9	1638	19.2	351	11 P97552	P97552 rattus norv
10	1632	19.1	3102	5 Q45614	Q45614 caenorhabdi
11	1630	19.1	1761	4 Q86XN2	Q86xn2 homo sapien
12	1523	17.9	1799	11 Q8R0Y0	Q8r0y0 mus musculu
13	1502.5	17.6	2731	5 Q9VJTS	Q9vjt5 drosophila
14	1502.5	17.6	3367	5 Q9XZC9	Q9xzc9 drosophila
15	1502.5	17.6	3375	5 Q81P51	Q81p51 drosophila
16	1478	17.3	1827	13 Q8JHV6	Q8jvh6 brachydanio

#### ALIGNMENTS

#### RESULT 1

Q8JHV8  
ID Q8JHV8  
AC Q8JHV8  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Laminin gamma 1.  
GN LAMC1.  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22065263; PubMed=12070089;  
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,  
RA Hirst E.M., Stemple D.L.;  
RT "Zebrafish mutants identify an essential role for laminins in  
RT notochord formation."  
RL Development 129:3137-3146(2002).  
DR EMBL; AF468048; AAM61766.1; -.  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPRO06209; EGF like.  
DR InterPro; IPRO00034; Laminin B.  
DR InterPro; IPRO02049; Laminin\_EGF.  
DR InterPro; IPRO08211; LamNT.  
DR InterPro; IPRO08212; Lam\_N2.  
DR Pfam; PF00052; laminin B; 1.  
DR Pfam; PF00052; laminin\_EGF; 10.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR SMART; SMO0180; EGF\_Lam; 11.  
DR SMART; SMO0281; LamB; 1.  
DR SMART; SMO0136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 7.

Q9Y6U6 homo sapien  
Q9VRW0 drosophila  
Q96BH6 homo sapien  
P91904 caenorhabdi  
Q8TDF8 homo sapien  
Q967S8 schistocerc  
Q42140 brachydanio  
Q92429 rattus norv  
O57339 xenopus lae  
Q42203 brachydanio  
Q8SWY0 drosophila  
Q61965 mus musculu  
Q9P822 bombyx mori  
Q8TAS6 homo sapien  
Q4565 caenorhabdi  
Q9NFW6 branchiosto  
Q9NS27 homo sapien  
Q75445 homo sapien  
O96659 hirudo medi  
Q9JLP3 mus musculu  
Q8K271 mus musculu  
Q8K3K1 rattus norv  
O14637 homo sapien  
Q8C9J2 mus musculu  
Q91V90 mus musculu  
Q9CRX6 mus musculu  
Q9VY25 drosophila  
Q00634 homo sapien  
Q9RIA3 mus musculu

DR	PROSITE; PS01186; EGF 2; 2.
DR	PROSITE; PS01248; LAMININ_Type_EGF; 10.
KW	Laminin EGF-like domain.
SQ	SEQUENCE 1593 AA; 176218 MW; A501F3A8884AA411 CRC64;
	Query Match 72.1%; Score 6145; DB 13; Length 1593;
	Best local similarity 69.3%; Pred. No. 5.7e-258;
	Matches 1091; Conservative 213; Mismatches 268; Indels 2; Gaps 2
QY	1 AMDECADEGGRPQRCKPEFFVNAANPVVAITNCTGPPPEBYCYQTGTGVTVKSHCLDAG 60
DB	20 AMDECIDBDDRPQRCEPFVNAATVAITNTCGSPPEEFCVQTGTGVTVKSHCINAA 79
QY	61 QQHLOHGAFLTDYNNQADTTWMSQTMLAGOVQNSINTLHLKAFOITVRLKFHTS 120
DB	80 DPLRHGAFLTDYNQPQPTWMSQTMLAGIYPNSINTLHLGKSFOITVRLKFHTS 139
QY	121 RESFAIKRYEEDEGPWTPIYOYSGSCENTYSKANRGFIPTGDGOALCTDERSDISPL 180
DB	140 RESFAIKRSESDGPWTPIYIYSGSEKIYSKNRGFIPTGDBBOALCTDERSDISPL 199
QY	181 TGGNVAFSTLEGRPSAYNFDSNPVLOBKVATDTRIVTLNLNTFTGEVFNDPKVKSYYY 240
DB	200 YGGNVAFSTLEGRPSAYNFDSNPVLQDWVTATDIRVTLNLNTFGDEVENDPKVKSYYY 259
QY	241 AISDFAVGGRCKNGHASECVKNEFDKLMCNKHNTYGVDCXCLPFENDRPWRRATAES 300
DB	260 AISDFAVGGRCKNGHASECVKNEYSKLVCNKENTEGADCNCKFYNDPRWRSAATEN 319
QY	301 ASECLUPCDONGRSQBCYFDPELYNSTGHGHCTWCNRDNTDGAKCERCRNPFELGNWEAC 360
DB	320 PNECILPCNCHGASACYDPDLRYATGTHGGHCRCADNTDGPKECRCLANYREASGORC 379
QY	361 SPCHSGPVGSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRCPCSDPGSGTDE 420
DB	380 LSQGCNPVGSLSLTQCDNTGRCSCKPGVMGDKDCRCQPGYHSLSEAGRCPCSNPAGSTOE 439
QY	421 CNVETGRVCVKDNVEGFNERCKGFGFNLESSPKGTCPCFCGHSSVCTNAVGYSVVDI 480
DB	440 CNYTGRCCKENVDFNCDCRKLGYFLNDPQNPGTCTPCFQHSTVCSADGYSVHKI 499
QY	481 SSTFQIDEDGWREVORDSEASLESSMDROQVIAYSISYPRIFYAPVKFLGNQLVSYGQ 540
DB	500 TSFTFRDDEGWKGKORDDSSVPVQWSPSSGISLIISEDYFPPIYFVADPADFLNQLLSXGQ 559
QY	541 NLSFSFVRDRRTLSASLDLLEGAGLRVSVPELLAOGNSYPSSTTKVYIFRLHEATDTPW 600
DB	560 NLTLNPRIOHRPARLSADVWLBSGLAVVFLLAQNSYPGETQTQTFVFLRDITDTPW 619
QY	601 RPALSPEFKLLNKLNTSIKIRGYSESAGYLDDVTLOSARGPGVPATWVESCTCPVG 660
DB	620 RPTIKHADPKQLLYNLTSIMTIGTYSAGSYLDNLSLVTAARRGPGTPARWKEKTCPOG 679
QY	661 YGQCFCECTLPGYRRETSLGIPSPCVLCTCNHGSETCDPETGVCCRNONTAGPHCEKS 720
DB	680 YLGHCCEQCDQGFRSRRELRFSTFCERCNCNGHSDDTCDETCMNCQHTAGLSERCCK 739
QY	721 DGYVGDSTLGTSSDQPCPCPGGSSCAIVPKTKEVVCTHCTGTAGKRCELDDGYFGDP 780
DB	740 DGYVGDSTVGGSSDCKACPAGATCAVVPKTNEVWCTNCTPTGTTGKRCLELDDGDFGDP 799
QY	781 LGSNGPVLRLCPQCNDINDPNVAGNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNLPA 840
DB	800 LGEKGPVRAACRACSNNNIEPNVAGNCNRESGECLKCIYNTAGVCFDRCQKQPYGDARA 859
QY	841 NPADKKCAACN-YGTVOQQSSCPVPTGCCOCLPHVSGRBCGCTCDGYNYLMSGQCERC 899
DB	860 NVADKKCKCKSPGYTVDRTAKSQVTQCQPCFLPHVINRCGACELGYFMYLQSGKCERC 919
QY	900 DCHALGSTGQCDIRTGQCECOQGITGQRCERCETNHFGPGPGCKPCDCDHGSLSLQOC 959
DB	920 NCNPIGSTNGQCDIYVGQCECOQPGVTGQRCERCENFVFGSSGCKPCDCDPEGSESAOC 979

Qy	960	KDGRCECRGFGVGNRCDCQCEENYFNRSWPGCQCPACPYLVKDKAAEHRVKLOBLES	101
Db	980	KEDGRGCRGFGVGNRCDCQCEENYFNRSWPGCQCPACPYLVKDKAAEHRVKLOBLES	1039
Qy	1020	IANLGTGDMVYTQCAFEDRLKEAREVITDILLREAEQKVDQNLMDRLQRVNSLSHSQIS	1079
Db	1040	IDSLSNTTETVSDKAFEDRLKEAREVITDILLREAEQKVDQNLMDRLQRVNSLSHSQIS	1099
Qy	1080	RLQIRNTIETGTLAERARSRYESTEQLIETASLEKAKMA-ANYSITQPESTGEPNN	1138
Db	1100	RLQIRNTIETGTLAERARSRYESTEQLIETASLEKAKMA-ANYSITQPESTGEPNN	1159
Qy	1139	MTLAEARRLAEHKKQEAADDIVRVAKTANETSASAYNLLRLTLAGENCTALBTEELNRK	1198
Db	1160	MTLAEARRLAEHKKQEAADDIVRVAKTANETSASAYNLLRLTLAGENCTALBTEELNRK	1219
Qy	1199	YEQAKNISQDLEKQARVHEPEAKRAGDKAVETIYASVAQLTPVDSEALNEANKIKGEAAD	1258
Db	1220	YLEAKDLAKNLEKQARVHEPEAKRAGDKAVETIYASVAQLTPVDSEALNEANKIKGEAAD	1279
Qy	1259	LDRLLDQKLDYEDLREDMGKEHYKNLLKKGKAEQOQTADQOLLARADAALKAAEAAKK	1318
Db	1280	LDKLIDKTEKYNDLREDLGKETEYVKLLDKGKTEQQTADQOLLARADAALKAAEAAKK	1339
Qy	1319	GRESTLOEANDILNLLKDFRRVNDNKTAAEALRIPAINRTIAFANEKTEAQALAGNA	1378
Db	1340	GKSTFQEAQDTILNLRDFDKRVNDNKTAAEALRIPAINRTIAFANEKTEAQALAGNA	1399
Qy	1379	AADAEAKKKAHEAERTIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLQLEAEANEL	1438
Db	1400	AADAKAKAKAEAEAKIANDVQKSGAKTKADAERKAFEDTMKLDKQVDKMDQMTAAKSEL	1459
Qy	1439	KEKODDADDMMWAGMASQAQAEALNASKAKNSVSSLLSOLNLLDLQGLDTPVDLKL	1498
Db	1460	EKKAEADTDMMASVMSDNKADAEGRNARKASAREVINTINALLGQGLGWIDKVDLSKL	1519
Qy	1499	NEIEGSLNAKDEMKASDLDRKVSVDLESARKQEAAMIDYVDRDTABIIKIHNLIEDIKKT	1558
Db	1520	NQIDNALKQAKXWAGSELDKRLKELNDIAKSCQDMISDYDRQIQE-RADIANDINDIKNT	1579
Qy	1559	LPTGCGFNTPTSEIKP	1572
Db	1580	LPEGCGFNTPSLRP	1593

RESULT 2

Q90ZN3 PRELIMINARY; PRT; 1007 AA.

AC Q90ZN3;

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Laminin gamma 1 (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI\_TaxID=9031;

[1]

SEQUENCE FROM N.A.

RP Halfter W., Dong S., Balasubramani M., Bier M.E.;

RT "Aberrant histogenesis after temporary disruption of the retinal basal

RL lamina.;"

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF373841; AKX55397.1;

DR GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR000034; Laminin\_B.

DR InterPro; IPR002049; Laminin\_EGF.

DR InterPro; IPR008211; LamNT.

DR Pfam; PF00052; laminin\_B; 1.

DR Pfam; PF00053; laminin\_EGF; 9.

QY 1259 LRLDIDOKLYEDLREDMRGKEHEVKNLLEKGAFOOTADOLLARADAAKALAEAAKK 1318  
 Db 1294 LRLDIDOKLYEDLREDMRGKEHEVKNLLEKGAFOOTADOLLARADAAKALAEAAKK 1353  
 QY 1319 GRSTLQFANDIILNNKDFRRVNDKNTAAEALRRIPAINRTTAAEANEKTRTQAALAGNA 1378  
 Db 1354 GRSTLQFANDIILNNKDFRRVNDKNTAAEALRRIPAINRTTAAEANEKTRTQAALAGNA 1413  
 QY 1379 ADATAEAKKAHEAEERIASAAQKATSTTADAEFTFGEVTDLDNEVNGMLRQLEAEANEL 1438  
 Db 1414 ADATAEAKKAHEAEERIASAAQKATSTTADAEFTFGEVTDLDNEVNGMLRQLEAEANEL 1473  
 QY 1439 KRQDDADQDMWAGWASQAQAEALNARKKNSVSSLLSQNLNLLDQLGQDITVDLNLK 1498  
 Db 1474 KRQDDADQDMWAGWASQAQAEALNARKKNSVSSLLSQNLNLLDQLGQDITVDLNLK 1533  
 QY 1499 NIEGSLNKADEMKAASDLDRKVSJLSEAPKQEAIAIMDYNRDIABIIKDIHNLDEIKKT 1558  
 Db 1534 NIEGSLNKADEMKAASDLDRKVSJLSEAPKQEAIAIMDYNRDIABIIKDIHNLDEIKKT 1593  
 QY 1559 LPTGCFNTSIEKP 1572  
 Db 1594 LPTGCFNTSIEKP 1607

RESULT 2  
 MMHUB2  
 N:Alternate names: laminin chain B2  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1991 #sequence, revision 30-Jun-1991 #text, change 10-Dec-1999  
 C:Accession: S13548; A28158; S13549; B34961; S14664; S23567  
 R:Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.  
 J. Biol. Chem. 266, 221-228, 1991  
 A:Title: Structure of the human laminin B2 chain gene reveals extensive divergence from  
 A:Reference number: S13548; MUID:91093128; PMID:1985895  
 A:Accession: S13548  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1609 <KAL>  
 A:Cross-references: GB:M55217; NID:G186937  
 A>Note: the nucleotide sequence was submitted to GenBank, February 1991  
 R:Pikkarainen, T.; Kallunki, T.; Tryggvason, K.  
 J. Biol. Chem. 267, 6751-6758, 1992  
 A:Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the  
 A:Reference number: A28158; MUID:88198245; PMID:3360804  
 A:Accession: A28158  
 A:Molecule type: mRNA  
 A:Residues: 1-211, I', 213-1609 <PIK>  
 A:Cross-references: EMBL:J03202; NID:G186916; PIDN:AAA59488.1; PID:G307107  
 R:Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He  
 Cyogenet. Cell Genet. 48, 137-141, 1988  
 A:Title: Isolation of a human laminin B2 (IAMB2) cDNA clone and assignment of the gene t  
 A:Reference number: S13549; MUID:89169663; PMID:3234037  
 A:Accession: S13549  
 A:Molecule type: mRNA  
 A:Residues: 1393-1609 <FUK>  
 A:Cross-references: EMBL:M27654; NID:G186923; PIDN:AAA59489.1; PID:G186924  
 R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
 Lab. Invest. 60, 772-782, 1989  
 A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
 A:Reference number: A34961; MUID:89280632; PMID:2733383  
 A:Accession: B34961  
 A:Molecule type: mRNA  
 A:Residues: 868-1551, N', 1553-1609 <OLS>  
 R:Santos, C.L.S.; Sabbaga, J.; Brentani, R.  
 DNA Seq. 1, 275-277, 1991  
 A:Title: Differences in human laminin B2 sequences.  
 A:Reference number: S14664; MUID:92216129; PMID:1806043  
 A:Accession: S14664  
 A:Molecule type: mRNA  
 A:Residues: 1282-1609 <SAN>  
 A:Cross-references: EMBL:X13939; NID:G34237; PIDN:CAA32122.1; PID:G34238

R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.  
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P.  
 A:Title: Genes for the human laminin B1 and B2 chains.  
 A:Reference number: S23566  
 A:Accession: S23567  
 A:Molecule type: DNA  
 A:Residues: 801-1481, R', 1483-1609 <VUO>  
 A>Note: mRNA was also sequenced  
 C:Genetics:  
 A:Gene: GDB:LAMC1; LAMB2  
 A:Cross-references: GDB:120136; OMIM:150290  
 A:Map position: 1q31-1q31  
 A:Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;  
 /3; 1525/1  
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C:Function:  
 A:Description: interact with cells and with other basement membrane proteins to promote  
 C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:34-1609/Product: laminin gamma-1 chain #status predicted <MAT>  
 F:34-285/Domain: VI <DOM6>  
 F:286-504/Domain: V <DOM5>  
 F:286-339/Domain: laminin-type EGF-like homology <LE01>  
 F:342-395/Domain: laminin-type EGF-like homology <LE02>  
 F:398-442/Domain: laminin-type EGF-like homology <LE03>  
 F:445-492/Domain: laminin-type EGF-like homology <LE04>  
 F:495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:505-689/Domain: IV <DOM4>  
 F:690-1034/Domain: III <DOM3>  
 F:690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>  
 F:724-770/Domain: laminin-type EGF-like homology <LE07>  
 F:773-825/Domain: laminin-type EGF-like homology <LE08>  
 F:828-881/Domain: laminin-type EGF-like homology <LE09>  
 F:884-932/Domain: laminin-type EGF-like homology <LE10>  
 F:935-980/Domain: laminin-type EGF-like homology <LE11>  
 F:983-1028/Domain: laminin-type EGF-like homology <LE12>  
 F:1035-1609/Domain: II/I <DOM1>  
 F:1035-1609/Region: heptad repeats  
 F:40-50/Disulfide bonds: #status predicted  
 F:60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbonyl  
 F:1031,1034,1600/Disulfide bonds: interchain #status predicted

Query Match 94.2%; Score 8034; DB 1; Length 1609;  
 Best Local Similarity 93.3%; Pred. No. 3,1e-297;  
 Matches 1466; Conservative 56; Mismatches 48; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPORCMPEFVNAAFNTVATNTCGTPPEYCVQTGVTGTSCHLCDAG 60  
 Db 36 AMDECTDEGGRPORCMPEFVNAAFNTVATNTCGTPPEYCVQTGVTGTSCHLCDAG 95  
 QY 61 QQHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITYVRLKFHTS 120  
 Db 96 QPHLQHGAFLTDYNNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITYVRLKFHTS 155  
 QY 121 RPSEFATYKRETDGPKWIPYQYSGSCENTYSKANEGFTRTGGDEQOALCTDFSDISPL 180  
 Db 156 RPSEFATYKRETDGPKWIPYQYSGSCENTYSKANEGFTRTGGDEQOALCTDFSDISPL 215  
 QY 181 TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240  
 Db 216 TGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 275  
 QY 241 AISDPVAGGRCKCNHASECVKNEFKLMCNCKNTYGVDCCKLPFFNDPRPWRATAES 300  
 Db 276 AISDPVAGGRCKCNHASECMKNEFKLMCNCKNTYGVDCCKLPFFNDPRPWRATAES 335  
 QY 301 ASECLPCDCNCRSQECVFPPELYRSTGHGHCTNCRDNTDGAKECRENFFPLGNTEAC 360  
 Db 336 ASECLPCDCNCRSQECVFPPELYRSTGHGHCTNCRDNTDGAKECRENFFPLGNTEAC 395  
 QY 361 SPCHSPVGSLSLTCQDSYGRCSCKPQVMGKDCRQCPGPHSLTEACRPSCDPSGSTDB 420

396 SSSHCSPPVGSISTQCDSDSYGRCSCKPGVNGDKDCRCQPGFHSHTBAGCRPCSCDPSGSD 455  
421 CNVETGRVCVKDNVEGFNCERCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGYSYDI 480  
456 CNVETGRVCVKDNVEGFNCERCKPGFFNLESNPGRCTPCFCFGHSSVCTNAVGYSYSI 515  
481 SSTSQIDEDGHRVORDGSEASLWSRDQVIATISDSYPRYFIAPVKELGNOVLSYQ 540  
516 SSTSQIDEDGHRVORDGSEASLWSRDQVIATISDSYPRYFIAPVKELGNOVLSYQ 575  
541 NLSFSFRVDRDTRLASDLVLEGAGLRVSVPLIAQNSYSESTTVKYIFRLHEATDYPW 600  
576 NLSFSFRVDRDTRLASDLVLEGAGLRVSVPLIAQNSYSESTTVKYVFLHEATDYPW 635  
601 RPALSPFPFOKLNNLTISKIRGYISERSAGYLDVTLQSRPGPGVPATWVESCCTPVG 660  
636 RPAITPFPFOKLNNLTISKIRGYISERSAGYLDVTLQSRPGPGVPATWVESCCTPVG 695  
661 YGGQFCETCLPGYRRETSGLPGYSPVLCNCGHSETCDPTGTGVCNCRDNTAGPHCKCS 720  
696 YGGQFCETCLPGYRRETSGLPGYSPVLCNCGHSETCDPTGTGVCNCRDNTAGPHCKCS 755  
721 DGYGDSSTLGTSSDCQPCPCPGGSSCAIVPTKKEVWVTHCTPTGTAGKRCCLCDGYPGDP 780  
756 DGYGDSSTLGTSSDCQPCPCPGGSSCAIVPTKKEVWVTHCTPTGTAGKRCCLCDGYPGDP 815  
781 LGSNGFVRLCRPCQCNNDIDNAGVNCNRLTGECLKCIYNTAGVFCRCKEGRFGNPLAP 840  
816 LGRNGFVRLCRPCQCNNDIDNAGVNCNRLTGECLKCIYNTAGVFCRCKEGRFGNPLAP 875  
841 NPADCKKACACN-YGTVOQQSSCNPTVTCQCLPHVSGDCGTCDPGYNN-OSQGGCERC 899  
876 NPADCKKACACNPTVTCQCLPHVSGDCGTCDPGYNN-OSQGGCERC 935  
900 DCHALGSTNGQCDITGTGCEQCPGTTGHCERCETNHFGPEGCKPCDCHHESLSLQC 959  
936 DCHALGSTNGQCDITGTGCEQCPGTTGHCERCETNHFGPEGCKPCDCHHESLSLQC 995  
960 KDDGCECREGFGVNRKQCEBENFYNRSPGQCPCACRYLRVLDKAAEHKVLQLESL 1019  
996 KDDGCECREGFGVNRKQCEBENFYNRSPGQCPCACRYLRVLDKAAEHKVLQLESL 1055  
1020 IANLGTGDDVTDQAFEDRLKAEAEVTDLLRAEQEVKDVQDNLDRLQVNNLSHQSIS 1079  
1056 IANLGTGDDVTDQAFEDRLKAEAEVTDLLRAEQEVKDVQDNLDRLQVNNLSHQSIS 1115  
1080 RLQNTIRNTIETGILAEARSRVSTEOLEIASRELEKAKV-AANVSITOPESGEPNN 1138  
1116 RLQNTIRNTIETGILAEARSRVSTEOLEIASRELEKAKV-AANVSITOPESGEPNN 1175  
1139 MTLAEAEARLAEHKKQADDIRVAKTANETSAEAYNLLRTLAGENQTALEIELNRK 1198  
1176 MTLAEAEARLAEHKKQADDIRVAKTANETSAEAYNLLRTLAGENQTALEIELNRK 1235  
1199 YEQAKNISDLEKQARVHEEAKRAGDKAVETIYASVAQLTPVDSALENEANKIKKEAD 1258  
1236 YEQAKNISDLEKQARVHEEAKRAGDKAVETIYASVAQLTPVDSALENEANKIKKEAD 1295  
1259 LDRIDQKLKDYEDLREDNRGHEHYKNLLEKGAEQQTADQLLARAADAALAEAAKK 1318  
1296 LDRIDQKLKDYEDLREDNRGHEHYKNLLEKGAEQQTADQLLARAADAALAEAAKK 1355  
1319 GRSTIQEANDIINLLKDFRRVNDNKTAAEBALRIPAINRTIABENKTEAQLAGNA 1378  
1356 GRSTIQEANDIINLLKDFRRVNDNKTAAEBALRIPAINRTIABENKTEAQLAGNA 1415  
1379 ADATAEKNAKAEAEARISAAQKATSTKADARTFGEVTDLDNENVMGLRLEAEANEL 1438  
1416 ADATAEKNAKAEAEARISAAQKATSTKADARTFGEVTDLDNENVMGLRLEAEANEL 1475  
1439 KRQDDADQDDMMVAGNASQAQAEAEINARKAKNSVSLLSQNNLLDQLGQDITVDLNL 1498  
1476 KRQDDADQDDMMVAGNASQAQAEAEINARKAKNSVSLLSQNNLLDQLGQDITVDLNL 1535

## RESULT 3

## MMFFB2

laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)

N;Alternate names: laminin chain B2

C;Species: Drosophila melanogaster

C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000

C;Accession: A31483; A33737; S01733; A40502

R;Chi, H.C.; Hui, C.F.

J. Biol. Chem. 264, 1543-1550, 1989

A;Title: Primary structure of the Drosophila laminin B2 chain and comparison with human, R;Chi, H.C.; Hui, C.F.

A;Reference number: A31483; MUID:89109164; PMID:2912972

A;Accession: A31483

A;Molecule type: mRNA

A;Residues: 1-1639 <CHI>

A;Cross-references: EMBL:M25063; NID:g157803; PIDN:AAA28664.1; PID:g157804

R;Montell, D.J.; Goodman, C.S.

J. Cell Biol. 109, 2441-2453, 1989

A;Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits A;Reference number: A33737; MUID:90037237; PMID:2808533

A;Accession: A33737

A;Molecule type: mRNA

A;Residues: 1-39, 'T', 'L', '893-1106, 'T', '1108-1459, 'HV', '1462-1581, 'G', '1583-1639 <M> R;Chi, H.C.; Hui, C.F.

Nucleic Acids Res. 16, 7205-7206, 1988

A;Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.

A;Reference number: S01733; MUID:88303364; PMID:3405777

A;Accession: S01733

A;Molecule type: mRNA

A;Residues: 344-1639 <CH2>

A;Cross-references: EMBL:X07806; NID:g8179; PIDN:CAA30665.1; PID:g135618 A;Note: the authors translated the codon GGC for residue 409 as Phe

R;Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.

DNA Cell Biol. 10, 451-466, 1991

A;Title: Structure of the Drosophila gene for the laminin B2 chain.

A;Reference number: A40502; MUID:91299161; PMID:1840513

A;Accession: A40502

A;Molecule type: DNA

A;Residues: 1-891, 'L', '893-1639 <CH3>

A;Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806

C;Genetics:

A;Gene: lamB2

A;Cross-references: FlyBase:FBgn0002528

A;Map position: 3L 67C

A;Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1

C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin C;Function:

A;Description: interact with cells and with other basement membrane proteins to promote C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C;Keywords: Basement membrane; calcium binding; cell binding; coiled coil; extracellular F;1-33/Domain: signal sequence #status predicted <SIG>

F;34-1639/Product: laminin gamma-1 chain #status predicted <MAT>

F;34-297/Domain: VI <DOM6>

F;298-528/Domain: V <DOM5>

F;299-356/Domain: laminin-type EGF-like homology <LE01>

F;359-411/Domain: laminin-type EGF-like homology <LE02>

F;414-458/Domain: laminin-type EGF-like homology <LE03>

F;461-511/Domain: laminin-type EGF-like homology <LE04>

F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;529-705/Domain: IV <DOM4>

F;706-1057/Domain: III <DOM3>

F;710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>

F;744-790/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.4672 Seconds  
(without alignments)

10452.141 Million cell updates/sec

Title: US-10-037-182-20

Perfect score: 8527  
Sequence: 1 ANDECADEGGRFCRCMPFV.....EDIKTKLPTGCTNPTSIKPK 1572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*\*

- 1: PIR1:\*\*
- 2: PIR2:\*\*
- 3: PIR3:\*\*
- 4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	8460	99.2	1607	1 MMHUB2	laminin gamma-1 ch
2	8034	94.2	1609	1 MMHUB2	laminin gamma-1 ch
3	3439	40.7	1839	1 MMHUB2	laminin gamma-1 ch
4	3193	37.4	1557	2 T28811	hypothetical prote
5	2591	30.4	1193	2 A44018	laminin B2t chain
6	2400.5	28.2	1192	2 S69000	laminin gamma 2 ch
7	1812.5	21.3	3106	1 S53868	laminin alpha-2 ch
8	1780.5	20.9	3084	1 MMHSA	laminin alpha-1 ch
9	1735	20.3	3075	2 S14458	laminin alpha-1 ch
10	1677	19.7	1786	1 MMHUB1	laminin beta-1 cha
11	1661.5	19.5	1786	1 MMHUB1	laminin beta-1 cha
12	1655.5	19.4	1790	1 MMHUB1	laminin beta-1 cha
13	1632	19.1	2823	2 T23064	hypothetical prote
14	1632	19.1	2823	2 F87908	protein T22A3.8 li
15	1632	19.1	3102	2 T43291	laminin alpha chai
16	1620.5	19.0	1808	2 T15099	hypothetical prote
17	1569	18.4	1801	1 MMHUB1	laminin beta-2 cha
18	1547.5	18.1	1798	2 S53869	laminin beta-2 cha
19	1457	17.1	1797	2 A55677	laminin beta-2 cha
20	1454	17.1	3712	2 S18253	laminin alpha-1 ch
21	1384	16.2	3672	2 T23433	hypothetical prote
22	1384	16.2	3704	2 T37316	probable laminin a
23	1347.5	15.8	3635	2 T10053	laminin alpha 5 ch
24	1155.5	13.6	606	2 A54665	netrin-1 precursor
25	1044.5	12.2	581	2 S45665	netrin-2 precursor
26	986.5	11.6	612	2 JH0799	laminin-related pr
27	938	11.0	1170	2 A53612	laminin B1k chain
28	903.5	10.6	4391	2 A38096	perlecan precursor
29	903	10.6	1168	2 I55985	kalinin B1 - mouse

30	877.5	10.3	3707	2	S18252	heparan sulfate pr
31	637.5	7.5	1160	2	P88369	protein unc-52 (im
32	637.5	7.5	2295	2	C88359	protein unc-52 (im
33	637.5	7.5	3375	2	T19821	hypothetical prote
34	619	7.3	1751	1	MMHUMH	laminin alpha-2 ch
35	588	6.9	1620	2	T27283	hypothetical prote
36	586	6.9	1816	1	S68960	hypothetical prote
37	555.5	6.5	1574	2	T13954	laminin alpha-4 ch
38	551	6.5	1111	2	T26972	hypothetical prote
39	514	6.0	1713	2	A55347	adhesive ligand ep
40	490	5.7	400	2	T46383	hypothetical prote
41	477	5.6	2471	2	A49128	cell-fate determin
42	471	5.5	303	2	B45067	laminin B1 chain -
43	466.5	5.5	2703	1	A24420	notch protein - fr
44	466	5.5	2318	2	S45306	notch 3 protein -
45	459.5	5.4	2352	2	T30201	Notch homolog prot

ALIGNMENTS

RESULT 1

MMHUB2  
laminin gamma-1 chain precursor - mouse  
N:Alternate names: laminin chain B2  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Feb-1986 #sequence-revision 30-Jun-1991 #text change 10-Dec-1999  
C:Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552  
R:Sasaki, M.; Yamada, Y.  
J. Biol. Chem. 262, 17111-17117, 1987  
A:Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.  
A:Reference number: A28469; MUID:88059118; PMID:3680290  
A:Accession: A28469  
A:Molecule type: mRNA  
A:Residues: 1-1607 <SAS>  
A:Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G293688  
R:Dutkin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.  
Biochemistry 27, 5198-5204, 1988  
A:Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.  
A:Reference number: A27729; MUID:89000737; PMID:3167041  
A:Accession: A27729  
A:Molecule type: mRNA  
A:Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'  
A:Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G293691  
A:Note: The authors translated the codon TAT for residue 544 as Asp and GCG for residue 1  
R:Ogawa, K.; Burhelo, P.D.; Sasaki, M.; Yamada, Y.  
J. Biol. Chem. 263, 8384-8389, 1988  
A:Title: The laminin B2 chain promoter contains unique repeat sequences and is active in  
A:Reference number: A28082; MUID:88228071; PMID:2836421  
A:Accession: A28082  
A:Molecule type: DNA  
A:Residues: 1-215, 'A', 217-239 <OGA>  
A:Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184  
R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Tampl, R.  
Biochem. J. 252, 453-461, 1988  
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02680  
A:Molecule type: protein  
A:Residues: 227-238 <FUS>  
R:Hartl, L.; Oberbaumer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A:Title: The N terminus of laminin A chain is homologous to the B chains.  
A:Reference number: S00624; MUID:88225080; PMID:3267223  
A:Accession: S05327  
A:Molecule type: protein  
A:Residues: 227-238, 387-393, 'P', 395-405, 881-912, 1022-1034 <HAR>  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.  
Eur. J. Biochem. 177, 33-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter  
A:Reference number: S01790; MUID:89030693; PMID:3181157  
A:Accession: S02037  
A:Molecule type: protein

A:Residues: 1362-1377, 'X', 1379-1392, 'X', 1394-1406 <DEU>  
 R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.  
 EMBO J. 3, 2355-2362, 1984  
 A:Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a  
 A:Reference number: A02870; MUID:85051302; PMID:629134  
 A:Accession: A02870  
 A:Molecule type: mRNA  
 A:Residues: 1391-1474, 'K', 1476-1575, 'N', 1577-1607 <BAR>  
 A:Cross-references: EMBL:X05211; NID:952862; PIDN:CAA28838.1; PID:9817975  
 R:Paulsson, M.; Deutmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
 EMBO J. 4, 309-316, 1985  
 A:Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
 A:Reference number: S13543; MUID:85257455; PMID:3848400  
 A:Accession: S13544  
 A:Molecule type: protein  
 A:Residues: 1506-1523, 'X', 1525 <PAU>  
 R:Olson, D.; Nagayoshi, T.; Pazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, Lab. Invest. 60, 772-782, 1989  
 A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
 A:Reference number: A34961; MUID:89280632; PMID:2733383  
 A:Accession: S14552  
 A:Molecule type: protein  
 A:Residues: 881-912, 1022-1034, 1364-1377, 1379-1392, 1394-1409, 1506-1525, 1593-1606 <OLS>  
 C:Genetics:  
 A:Gene: Lamb-2  
 A:Map position: 1  
 A:Introns: 138/1; 239/3  
 A:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C:Function:  
 A:Description: interact with cells and with other basement membrane proteins to promote  
 C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:34-1607/Product: laminin gamma-1 chain #status predicted <MAT>  
 F:34-283/Domain: VI <DOM6>  
 F:284-502/Domain: V <DOM5>  
 F:284-337/Domain: laminin-type EGF-like homology #status atypical <LE01>  
 F:340-393/Domain: laminin-type EGF-like homology <LE02>  
 F:396-440/Domain: laminin-type EGF-like homology <LE03>  
 F:443-490/Domain: laminin-type EGF-like homology <LE04>  
 F:493-502/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:503-687/Domain: laminin-type EGF-like homology IV <DOM4>  
 F:688-1032/Domain: III <DOM3>  
 F:688-719/Domain: laminin-type EGF-like homology #status atypical <LE06>  
 F:722-768/Domain: laminin-type EGF-like homology <LE07>  
 F:771-823/Domain: laminin-type EGF-like homology <LE08>  
 F:826-879/Domain: laminin-type EGF-like homology <LE09>  
 F:882-930/Domain: laminin-type EGF-like homology <LE10>  
 F:933-978/Domain: laminin-type EGF-like homology <LE11>  
 F:981-1026/Domain: laminin-type EGF-like homology <LE12>  
 F:1033-1607/Domain: II/I <DOM2>  
 F:1033-1607/Region: heptad repeats  
 F:38-48/Disulfide bonds: #status predicted  
 F:58,132,574,648,1020,1105,1159,1173,1203,1221,1239,1437/Binding site: carbohydrate (Asn  
 F:1029,1032/Disulfide bonds: interchain #status predicted  
 F:1378,1393/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:1598/Disulfide bonds: interchain (to chain B1) #status experimental

Query Match 99.2%; Score 8460; DB 1; Length 1607;

Best Local Similarity 99.4%; Pred No. 2.2e-313;

Matches 1565; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPQRCMPFVNAFNVVATNTCTTPPEYCVQGTGVTGKSHLCDAG 60

DB 34 AMDECADEGGRPQRCMPFVNAFNVVATNTCTTPPEYCVQGTGVTGKSHLCDAG 93

QY 61 QOHLQHGAAFLDYNNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITVRLKPHTS 120

DB 94 QOHLQHGAAFLDYNNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITVRLKPHTS 153

QY 121 RPESFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDQQAALCTDFSDISPL 180

DB 154 RPESFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDQQAALCTDFSDISPL 213

QY 181 TCGNVAFTLEGRPSAYNFDNSPVLQEWVTATDITVTLNRLNTFGDEVNPKVLKSYYY 240  
 DB 214 TCGNVAFTLEGRPSAYNFDNSPVLQEWVTATDITVTLNRLNTFGDEVNPKVLKSYYY 273  
 QY 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKNTYGVDCBCKLPFFNDRPWRATAES 300  
 DB 274 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKNTYGVDCBCKLPFFNDRPWRATAES 333  
 QY 301 ASECLPCDCNGRSQBYCFDPPELYRSTGHGHCNCRDNTDGAKCRCRCRNFRLGNTAC 360  
 DB 334 ASESLPCDCNGRSQBYCFDPPELYRSTGHGHCNCRDNTDGAKCRCRCRNFRLGNTAC 393  
 QY 361 SPCHSPVGLSTQCDSSYGRCSCKPGVMDKCDRCQPGFHSJTEAGCRPCSCDLSGSTDE 420  
 DB 394 SPCHSPVGLSTQCDSSYGRCSCKPGVMDKCDRCQPGFHSJTEAGCRPCSCDLSGSTDE 453  
 QY 421 CNVETGRVCCKNVGFCNRCRCKPGFFNLESSNPKGTCPCFCGHSSVCTNAVGSVYDI 480  
 DB 454 CNVETGRVCCKNVGFCNRCRCKPGFFNLESSNPKGTCPCFCGHSSVCTNAVGSVYDI 513  
 QY 481 SSTFQIDEDGWRVEQDGSSEASLEWSSDRQYTAVIDSDSYFPRYFTAPVKFLGNQVLSYGO 540  
 DB 514 SSTFQIDEDGWRVEQDGSSEASLEWSSDRQYTAVIDSDSYFPRYFTAPVKFLGNQVLSYGO 573  
 QY 541 NLSFSPVRDRDRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLHEATDYPW 600  
 DB 574 NLSFSPVRDRDRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLHEATDYPW 633  
 QY 601 RPALSPFEQKLLNLTSTIKRGTVSERSAGYLDVTLQSPARPGVATWVESCPCVG 660  
 DB 634 RPALSPFEQKLLNLTSTIKRGTVSERTAGYLDVTLQSPARPGVATWVESCPCVG 693  
 QY 661 YGQFCETCLPGVRETPLSLGYSVPCVLTGNGHSETCDPETGVCDRCNTAGPCEKCS 720  
 DB 694 YGQFCETCLPGVRETPLSLGYSVPCVLTGNGHSETCDPETGVCDRCNTAGPCEKCS 753  
 QY 721 DGYGDSLTGTSDDQPCPCPGSSCAIYVPTKVVWVCHTCTGTGTAGKRCCLCDDGYFGDP 780  
 DB 754 DGYGDSLTGTSDDQPCPCPGSSCAIYVPTKVVWVCHTCTGTGTAGKRCCLCDDGYFGDP 813  
 QY 781 LGSNGVRLRCQCNNDNDPNAVNCNRLTGCECLKCIYNTAGFYCDRCCKEFGFNGLAP 840  
 DB 814 LGSNGVRLRCQCNNDNDPNAVNCNRLTGCECLKCIYNTAGFYCDRCCKEFGFNGLAP 873  
 QY 841 NPADKCKACACN-YGTVQQQSSCNVPTGQCCLPHVSGRDCGTCDPGYYNLSGGGCERC 899  
 DB 874 NPADKCKACACNYPYGTVQQQSSCNVPTGQCCLPHVSGRDCGTCDPGYYNLSGGGCERC 933  
 QY 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERTNHFGEFGCKPCDCHEGSLSLQC 959  
 DB 934 DCHALGSTNGQCDIRTGQCECQPGITGQHCERTNHFGEFGCKPCDCHEGSLSLQC 993  
 QY 960 KDDGRCECEGFGVGNRCDCENYFYNRSWPGQCEPCACRYLVKOKAAHRYVLOLESL 1019  
 DB 994 KDDGRCECEGFGVGNRCDCENYFYNRSWPGQCEPCACRYLVKOKAAHRYVLOLESL 1053  
 QY 1020 IANLGTGDDVTDQAFEDRLKEAREVTDLLREAEVKDQNDLMDRLQVNSLSHQSLS 1079  
 DB 1054 IANLGTGDDVTDQAFEDRLKEAREVTDLLREAEVKDQNDLMDRLQVNSLSHQSLS 1113  
 QY 1080 RLQNIQNTTIEETGILAEARARSVESTEQLEIETASRELEKAKM-AANVSTIQESTGEPNN 1138  
 DB 1114 RLQNIQNTTIEETGILAEARARSVESTEQLEIETASRELEKAKMAANVSTIQESTGEPNN 1173  
 QY 1139 MTLLAEARRLAEHRHKEADDDIVRVAKTANETSAAEYNNLLRTLAGENOTALIEELNRK 1198  
 DB 1174 MTLLAEARRLAEHRHKEADDDIVRVAKTANETSAAEYNNLLRTLAGENOTALIEELNRK 1233  
 QY 1199 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIVASVAQLTPVDSEALENEANKIKKEAAD 1258  
 DB 1234 YEQAKNISQDLEKQAARVHEEAKRAGDKAVEIVASVAQLTPVDSEALENEANKIKKEAAD 1293

Query Match				99.2%; Score 8460; DB 1; Length 1607;			
Best Local Similarity				99.4%; Pred. No. 2,1e-310;			
Matches 1565; Conservative				2; Mismatches 5; Indels 2; Gaps 2;			
QY	1	AMDECADEGRPORCMPEFNAAFTVATNTCGTPPEEYCVQGTGVTAKSCHLCOAG	60	QY	1020	IANLGTGDDMWTDQAFEDRLKEAREVTDLLREAEQVKVDONLMDRLQVNSSLSHSQIS	1079
DB	34	AMDECADEGRPORCMPEFNAAFTVATNTCGTPPEEYCVQGTGVTAKSCHLCOAG	93	DB	1054	IANLGTGDDMWTDQAFEDRLKEAREVTDLLREAEQVKVDONLMDRLQVNSSLSHSQIS	1113
QY	61	QOHLQHGAAFLTDYNNQADTTWQSQTLAGVQYPSINLTLHLGKAFDITTVRLKFTS	120	QY	1080	RLOMIRNTIBETGLAERARSVESTQLEIASRELEKAKM-AANVSIITQPESTGSPNN	1138
DB	94	QOHLQHGAAFLTDYNNQADTTWQSQTLAGVQYPSINLTLHLGKAFDITTVRLKFTS	153	DB	1114	RLOMIRNTIBETGLAERARSVESTQLEIASRELEKAKM-AANVSIITQPESTGSPNN	1173
QY	121	RPESFAIYKTRTDGFWIPYQYSGSCENTYKANKGFRTGGDEQOALCTDFESDISPL	180	QY	1139	MTLAEARLAEHKKQADIVRVAKTANETSAAENLLRLTAGENQTALEIEELNRK	1198
DB	154	RPESFAIYKTRTDGFWIPYQYSGSCENTYKANKGFRTGGDEQOALCTDFESDISPL	213	DB	1174	MTLAEARLAEHKKQADIVRVAKTANETSAAENLLRLTAGENQTALEIEELNRK	1233
QY	181	TGNVAFSTLEGRPSAYNFDNSVLEQWVATDITVTLNRLNTFGDEVNDPKVLKSYYY	240	QY	1199	YEQAKNISQDLKEAARVHEEAKKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD	1258
DB	214	TGNVAFSTLEGRPSAYNFDNSVLEQWVATDITVTLNRLNTFGDEVNDPKVLKSYYY	273	DB	1234	YEQAKNISQDLKEAARVHEEAKKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD	1293
QY	241	AISDFAVGRCCKNGHASECVKNEFVKLMCNCHKNTYGVDCCKLPFFNDRPWRATABS	300	QY	1259	LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADADAALAEBAKK	1318
DB	274	AISDFAVGRCCKNGHASECVKNEFVKLMCNCHKNTYGVDCCKLPFFNDRPWRATABS	333	DB	1294	LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADADAALAEBAKK	1353
QY	301	ASECLPCDNGRSOBCVDFPELVRSTGHGHCNTCRDNDTGAKCERENFRLGNTEAC	360	QY	1319	GRSTLQEAANDILNNLKDFDRRVNDKNTAAEEALRIPAINRTIAEANEKTRAEQALQNA	1378
DB	334	ASECLPCDNGRSOBCVDFPELVRSTGHGHCNTCRDNDTGAKCERENFRLGNTEAC	393	DB	1354	GRSTLQEAANDILNNLKDFDRRVNDKNTAAEEALRIPAINRTIAEANEKTRAEQALQNA	1413
QY	361	SPCHSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSCDPSGSTD	420	QY	1379	AADATEAKNAHEAERIASAAQKNATSTKADAERTFGVTDLDNEVNGMLRQLEEAENEL	1438
DB	394	SPCHSPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSCDPSGSTD	453	DB	1414	AADATEAKNAHEAERIASAAQKNATSTKADAERTFGVTDLDNEVNGMLRQLEEAENEL	1473
QY	421	CNVETGRVCCKDNVEGNCERCKPGFNLESNNPKGCTCFPGHSSVCTNAGVSVYDI	480	QY	1439	KRQDDADQDMMAGMASQAQAEALNARKAKNSVSSLLSQANLLDQLGOLDTVDLNLK	1498
DB	454	CNVETGRVCCKDNVEGNCERCKPGFNLESNNPKGCTCFPGHSSVCTNAGVSVYDI	513	DB	1474	KRQDDADQDMMAGMASQAQAEALNARKAKNSVSSLLSQANLLDQLGOLDTVDLNLK	1533
QY	481	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNVLSYQ	540	QY	1499	NEISGSLNKAKDEMKAQSDLRKVDLSEARKQBAAMNDYNDIAEIIKDIHNLEDIKKT	1558
DB	514	SSTFQIDEDGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNVLSYQ	573	DB	1534	NEISGSLNKAKDEMKAQSDLRKVDLSEARKQBAAMNDYNDIAEIIKDIHNLEDIKKT	1593
QY	541	NLSFSPVDRDRRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYLFRLEHATDYPW	600	RESULT 2			
DB	574	NLSFSPVDRDRRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYLFRLEHATDYPW	633	ID	LMGI_HUMAN	STANDARD;	PRT; 1609 AA.
QY	601	RPALSPPEFQKLNNTSIKIRGTYSERSAGYLDVTLQASRPGVPAATWESCTCPVG	660	AC	P11047;		
DB	634	RPALSPPEFQKLNNTSIKIRGTYSERSAGYLDVTLQASRPGVPAATWESCTCPVG	693	DT	01-JUL-1989 (Rel. 11, Created)		
QY	661	YGGQFCETCLPGVRRTPSLGYPSPCVLCTCNHSETCDPETGVCDCRNTAGPHCEKCS	720	DT	01-JUL-1989 (Rel. 11, Created)		
DB	694	YGGQFCETCLPGVRRTPSLGYPSPCVLCTCNHSETCDPETGVCDCRNTAGPHCEKCS	753	DT	15-NOV-1991 (Rel. 20, Last sequence update)		
QY	721	DGYVGSSTLTSDDQPCPCPGSSCAIVPKTEVVCTHCTGTAGKCELDGDFGDP	780	DT	15-NOV-2004 (Rel. 43, Last annotation update)		
DB	754	DGYVGSSTLTSDDQPCPCPGSSCAIVPKTEVVCTHCTGTAGKCELDGDFGDP	813	DE	Laminin gamma-1 chain precursor (Laminin B2 chain).		
QY	781	LGSGNPVRLRCPQCNDNDPNAVGNRLTGELCKIYNTAGFYCDRCGEFFGNPLAP	840	GN	LAMC1 OR LAMB2.		
DB	814	LGSGNPVRLRCPQCNDNDPNAVGNRLTGELCKIYNTAGFYCDRCGEFFGNPLAP	873	OS	Homo sapiens (Human).		
QY	841	NPADKCKACACN-YGTVQOQSSCNVPTGQOCLPHVSGRDCGTCDPGYNLQSGQCERC	899	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DB	874	NPADKCKACACN-YGTVQOQSSCNVPTGQOCLPHVSGRDCGTCDPGYNLQSGQCERC	933	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
QY	900	DCHALGSTNGQCDIRTCQCEQPGITGQHCHERCETHNFGPGGCKPCDCHHEGSLQ	959	OX	NCBI_TaxID=9606;		
DB	934	DCHALGSTNGQCDIRTCQCEQPGITGQHCHERCETHNFGPGGCKPCDCHHEGSLQ	993	RN	[1]		
QY	960	KDGRCEGRCFGVGNRCDCQCEENFYNNRSPGQCECPACVRLVKDAAEHRVKLBESL	1019	RP	SEQUENCE FROM N.A. PubMed=1985895;		
DB	994	KDGRCEGRCFGVGNRCDCQCEENFYNNRSPGQCECPACVRLVKDAAEHRVKLBESL	1053	RX	MEDLINE=91093128; PubMed=3360804;		

RA Kallunki T., Tryggvason K.;  
"Human laminin B2 chain. Comparison of the complete amino acid  
sequence with the B1 chain reveals variability in sequence homology  
between different structural domains";  
J. Biol. Chem. 263:6751-6758 (1988).  
[3]  
SEQUENCE OF 1393-1609 FROM N.A.  
RP MEDLINE=89169663; PubMed=3234037;  
Fukushima Y., Pikkariainen T., Kallunki T., Eddy R.L., Byers M.G.,



HALEY L.L., Henry W.M., Tryggvason K., Shows T.B.;  
"Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of  
the gene to chromosome region 1q25-->q31";  
Cytogenet. Cell Genet. 48:137-141(1988).  
[4]  
SEQUENCE OF 1282-1609 FROM N.A.  
RC TISSUE-Endothelial cells;  
MEDLINE=22660472; PubMed=12754519;  
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;  
"Identification and quantification of N-linked glycoproteins using  
hydrazone chemistry, stable isotope labeling and mass spectrometry.";  
Nat. Biotechnol. 21:660-666(2003).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end. The gamma-1 chain is a subunit of laminin-1 (EHS laminin),  
laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),  
laminin-6 (K-laminin) and laminin-7 (KS-laminin).  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major  
component).  
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact  
with other laminin chains to form a coiled coil structure.  
CC -!- DOMAIN: Domains VI and IV are globular.  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 1 laminin IV domain.  
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DR EMBL; M55210; AAA59492.1; -;  
DR EMBL; M55217; AAA59492.1; JOINED.  
DR EMBL; M55201; AAA59492.1; JOINED.  
DR EMBL; M55211; AAA59492.1; JOINED.  
DR EMBL; M55212; AAA59492.1; JOINED.  
DR EMBL; M55213; AAA59492.1; JOINED.  
DR EMBL; M55214; AAA59492.1; JOINED.  
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DR EMBL; M55193; AAA59492.1; JOINED.  
DR EMBL; M55194; AAA59492.1; JOINED.  
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DR EMBL; M55208; AAA59492.1; JOINED.  
DR EMBL; M55209; AAA59492.1; JOINED.  
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DR EMBL; X13939; CAA32122.1; -;  
DR PIR; S13548; MHUB2.  
DR HSSP; P02468; 1TLE.  
DR Genew; HGNC:6492; LAMC1.  
DR MIM; 150290; -;  
DR GO; GO:0005604; C:basement membrane; TAS.  
DR GO; GO:0007492; P:embryonic development; TAS.  
DR GO; GO:0006461; P:protein complex assembly; TAS.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR008212; Lam\_N2.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin\_B; 1.  
DR Pfam; PF00053; laminin\_EGF; 9.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 8.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.  
FT SIGNAL 1 33  
FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.  
FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 286 341 LAMININ EGF-LIKE 1.  
FT DOMAIN 342 397 LAMININ EGF-LIKE 2.  
FT DOMAIN 398 444 LAMININ EGF-LIKE 3.  
FT DOMAIN 445 494 LAMININ EGF-LIKE 4.  
FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 505 689 LAMININ DOMAIN IV.  
FT DOMAIN 690 723 LAMININ EGF-LIKE 6.  
FT DOMAIN 724 772 LAMININ EGF-LIKE 7.  
FT DOMAIN 773 827 LAMININ EGF-LIKE 8.  
FT DOMAIN 828 834 LAMININ EGF-LIKE 9.  
FT DOMAIN 835 932 LAMININ EGF-LIKE 10.  
FT DOMAIN 933 1030 LAMININ EGF-LIKE 11.  
FT DOMAIN 1030 1609 DOMAIN II AND I.  
FT DOMAIN 1038 1609 COILED COIL (POTENTIAL).  
FT DISULFID 286 295 BY SIMILARITY.  
FT DISULFID 298 305 BY SIMILARITY.  
FT DISULFID 307 316 BY SIMILARITY.  
FT DISULFID 319 339 BY SIMILARITY.  
FT DISULFID 342 351 BY SIMILARITY.  
FT DISULFID 344 367 BY SIMILARITY.  
FT DISULFID 370 379 BY SIMILARITY.  
FT DISULFID 382 395 BY SIMILARITY.  
FT DISULFID 398 410 BY SIMILARITY.  
FT DISULFID 400 416 BY SIMILARITY.  
FT DISULFID 418 427 BY SIMILARITY.  
FT DISULFID 430 442 BY SIMILARITY.  
FT DISULFID 445 456 BY SIMILARITY.  
FT DISULFID 447 463 BY SIMILARITY.  
FT DISULFID 465 474 BY SIMILARITY.  
FT DISULFID 477 492 BY SIMILARITY.  
FT DISULFID 724 733 BY SIMILARITY.  
FT DISULFID 726 740 BY SIMILARITY.  
FT DISULFID 742 751 BY SIMILARITY.  
FT DISULFID 754 770 BY SIMILARITY.  
FT DISULFID 773 781 BY SIMILARITY.  
FT DISULFID 775 792 BY SIMILARITY.  
FT DISULFID 795 804 BY SIMILARITY.  
FT DISULFID 807 825 BY SIMILARITY.  
FT DISULFID 828 842 BY SIMILARITY.  
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FT DISULFID 852 861 BY SIMILARITY.



FT	DISULFID	864	881	BY SIMILARITY.	
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FT	DISULFID	886	905	BY SIMILARITY.	
FT	DISULFID	907	916	BY SIMILARITY.	
FT	DISULFID	919	932	BY SIMILARITY.	
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FT	DISULFID	956	965	BY SIMILARITY.	
FT	DISULFID	968	980	BY SIMILARITY.	
FT	DISULFID	983	995	BY SIMILARITY.	
FT	DISULFID	985	1001	BY SIMILARITY.	
FT	DISULFID	1003	1012	BY SIMILARITY.	
FT	DISULFID	1015	1028	BY SIMILARITY.	
FT	DISULFID	1031	1031	INTERCHAIN (PROBABLE).	
FT	DISULFID	1034	1034	INTERCHAIN (PROBABLE).	
FT	DISULFID	1600	1600	INTERCHAIN (PROBABLE).	
FT	CARBOHYD	60	60	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	576	576	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	650	650	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1175	1175	N-LINKED (GLCNAC. . .)	(POTENTIAL).
Query Match					94.2%; Score 8034; DB 1; Length 1609;
Best Local Similarity					93.3%; Pred. No. 2e-294;
Matches 1468; Conservative 56; Mismatches 48; Indels 2; Gaps 2;					
Qy	1	AMDECADEGGRPORCHPEFVNAAFNVTWATNTCGTPPEYCVQGTGVTGKSCHLCDAG	60		
Db	36	AMDECTDEGGRPORCHPEFVNAAFNVTWATNTCGTPPEYCVQGTGVTGKSCHLCDAG	95		
Qy	61	QOHLQGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDITVYRLKFTS	120		
Db	96	QPHLOHGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDITVYRLKFTS	155		
Qy	121	RPSFALYKKTREDGPMIPQYVSGSCENTYSKANRGFTRTGGDEQQAALCTDEFSDISPL	180		
Db	156	RPSFALYKKTREDGPMIPQYVSGSCENTYSKANRGFTRTGGDEQQAALCTDEFSDISPL	215		
Qy	181	TGNVAFSTLEGRPSAYFNDSVPLQEWATDITVTLNRLNTPFGDEVNDPKVLKSYIY	240		
Db	216	TGNVAFSTLEGRPSAYFNDSVPLQEWATDITVTLNRLNTPFGDEVNDPKVLKSYIY	275		
Qy	241	AISDFAVGGRCKNGHASECVKNEFKLMCNCKHNTYGVDCCKLPFFNDRPWRATAS	300		
Db	276	AISDFAVGGRCKNGHASECVKNEFKLMCNCKHNTYGVDCCKLPFFNDRPWRATAS	335		
Qy	301	ASECLPCDCNGRSGQCYFDPPELYRSTGHGHCNTNCRDNTDGAKECRNFRPLGNTEAC	360		
Db	336	ASECLPCDCNGRSGQCYFDPPELYRSTGHGHCNTNCRDNTDGAKECRNFRPLGNTEAC	395		
Qy	361	SPCHSPVGLSTQCDYSGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGSTDB	420		
Db	396	SSCHSPVGLSTQCDYSGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGSTDB	455		
Qy	421	CNVETGRVCVKDVEGFCNCRKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI	480		
Db	456	CNVETGRVCVKDVEGFCNCRKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSVYDI	515		
Qy	481	SSTFQIDEDGWRVEQRDGSASLEWSSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYQ	540		
Db	516	SSTFQIDEDGWRVEQRDGSASLEWSSDRQYIAVISDSYPPRYFIAPVKFLGNQVLSYQ	575		
Qy	541	NLSFSPVRDRDRLSADLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEADYDPW	600		
Db	576	NLSFSPVRDRDRLSADLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEADYDPW	635		
Qy	601	RPALSPFEQKLLNNLTSIKIRGYTSRSAGYLDVTLQSRPQGPVATWBSCTCPVG	660		
Db	636	RPALTPEFQKLLNNLTSIKIRGYTSRSAGYLDVTLQSRPQGPVATWBSCTCPVG	695		

RESULT 3  
LMG3 HUMAN  
ID LMG3 HUMAN STANDARD; PRT; 1587 AA.  
AC Q9Y5N6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, last sequence update)  
DT 15-MAR-2004 (Rel. 43, last annotation update)  
DE Laminin gamma-3 chain precursor (laminin 12 gamma 3).

GN LAMC3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=9242614; PubMed=1025960;  
RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,  
Burgeson R.E., Champlaud M.F.;  
RT "Characterization and expression of the laminin gamma3 chain: a novel,  
non-basement membrane-associated, laminin chain.";  
RL J. Cell Biol. 145:605-618(1999).  
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end. The gamma-3 chain is a subunit of laminin-12.  
CC -1- SUBCELLULAR LOCATION: Extracellular.  
CC -1- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and  
the reproductive tracts.  
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact  
with other laminin chains to form a coiled coil structure.  
CC -1- DOMAIN: Domain IV is globular.  
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -1- SIMILARITY: Contains 11 laminin EGF-like domains.  
CC -1- SIMILARITY: Contains 1 laminin IV domain.

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DR EMBL: AF041835; AAD36991.1; .  
DR HSP: P02468; ITLE.  
DR Genew; HGNC:6494; LAMC3.  
DR MIM; 604349; .  
DR GO; GO:0005578; C:extracellular matrix; TAS.  
DR GO; GO:0016020; C:membrane; TAS.  
DR GO; GO:0005198; F:structural molecule activity; TAS.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR008212; Lam\_N2.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin B; 1.  
DR Pfam; PF00053; laminin\_EGF; 9.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR SMART; SM00136; LamNT; 1.  
DR SMART; SM00180; EGF\_Lam; 9.  
DR PROSITE; PS00022; EGF\_1; 7.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ TYPE EGF; 10.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 1587 LAMININ GAMMA-3 CHAIN.  
FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 271 326 LAMININ EGF-LIKE 1.  
FT DOMAIN 327 382 LAMININ EGF-LIKE 2.  
FT DOMAIN 383 429 LAMININ EGF-LIKE 3.  
FT DOMAIN 430 479 LAMININ EGF-LIKE 4.  
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 42.1%; Score 3586; DB 1; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 1.3e-127;  
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;

QY	2	MEECADEGRPORCMPEFVNAAFVTVATVTCGTPPEYCVQGTGVTGKSHLCAQ	61
DB	22	MGACVDGGRPORCLPVFENAAFGLAQASHTCGSPEDFCFHVGAAGAGAHQCRDAAD	81
QY	62	QHLQGAAPLTDDYNNQADTTWQSQTMLAGVQVYNSINLTLHKGAFDITVRLKFTSR	121
DB	82	PQRHNASYLTDFHQSDSTWQSPSMAFGVQVPTSVNITLKGAYEITVRLKFTSR	141
QY	122	PSPFALYKTRDGDGWIYQYVYSGSCENTYKANGFIRTCGDEQQAALCTDFSDISPLT	181
DB	142	PSPFALYKRSRAGDGEWYQVYFASQCKYPRGQVLRPGEDSERVAFCTSEFSDISPLS	201
QY	182	GGNVAFTLEGPSAYNFDSNPVLQEWYATDITVTLNRLNTDFGVNPKVLKSYIA	241
DB	202	GGNVAFTLEGPSAYNFDSNPVLQEWYATDITVTLNRLNTDFGVNPKVLKSYIA	261
QY	242	ISDFAVGRCCKNGHASECVKNEFDKLMCNKNTYGVDEKCLPFNDRWRRAESEA	301
DB	262	VSDFSVGRCKNGHASECGPDVAGQACRQCHNTTGTDCERCCLPFFQDRPWARGTAA	321
QY	302	SECLPCDCNGRSQECYFDPFLYRSTGHGHCNCRDNTDGAACRCRCNFRRLGNTBACS	361
DB	322	HECLPCNGSRSECTFDRFLRSTGHGRCRCRDHTAGHCRCRCNFRVHMDRMPQC	381
QY	362	PCHSPVGLSTQDCSYGRCSCKPGVMDKDCRCQPGFHSITRAGRCPCSDPSGSDDEC	421
DB	382	PCDSAGSLHLQCDTGTCAKPTVTGKCDRCCLPGFHSLSGEGRCPCNPGASLDTC	441
QY	422	NVETGRVCYKDNVSGFNCRCCKPGFNLSSNPKGCTPCFCFGHSSVCTNAVGVVYDIS	481
DB	442	DPRSGRCPCKNVEGNLDCRCRCPTGNLPHNPAGCSCFCYGHSKVCASTAQFQVHHIL	501
QY	482	STFQIDEDGWRVQRDQSEASLEWSSDROYIAVSDSYFFRYFIAPVKFICGNQVLSQON	541
DB	502	SDFHGAGGWARVSGGSEHSPQWSPN----GVLLSPDEDEELTAPGKFGDORFSGQP	557
QY	542	LSFSPVRDRDRLASDLVLEGAGLRVSVPLIAQGNYSPESTTVKYIFRLH---EATDY	598
DB	558	LITLTFVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGGPDARASQGGRAQVPLQETSE	614
QY	599	PWRPALSPEFQKLNILNITSIKRGTYSERASG--YLDVDTLOSARRPGVGVATVWESCT	656
DB	615	DVAPLPFPFHFORLLANLTLRLRVSPGSPAGVFLTVRLTSARPLSPASWWEICIS	674

Sequence 390, App  
Sequence 1269, Ap  
Sequence 147, App  
Sequence 13, Appl  
Sequence 26, Appl  
Sequence 28, Appl  
Sequence 30, Appl  
Sequence 2, Appl  
Sequence 32, Appl  
Sequence 15, Appl  
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Sequence 34, Appl  
Sequence 7, Appl  
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Sequence 5, Appl  
Sequence 8, Appl  
Sequence 113, App  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 5220, Ap  
Sequence 5221, Ap

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US-10-037-182-12  
US-10-369-493-5220  
US-10-369-493-5221

ALIGNMENTS

RESULT 1  
US-10-037-182-20  
; Sequence 20, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-20

Query Match 100.0%; Score 8527; DB 14; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AMDECADEGGRRPQRCMPFVNAENVTVAINTCGTPPEYCVGTGVTGKSCHLCDAG 60  
Qy 61 QQHLLHGAFAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVLKPHTS 120  
Db 61 QQHLLHGAFAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVLKPHTS 120  
Qy 121 RPESFAYKRTREGPIPIQVYSGSCENTYSKANRGFIPTGGDEQQALCTDFESDLSPL 180

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 39.9931 Seconds  
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Title: US-10-037-182-20  
Perfect score: 8527  
Sequence: 1 AMDECADEGGRRPQRCMPFV.....EDIKKTLPTGCFNTFSIEKP 1572

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PTC\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
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- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PTC\_US\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10E\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8527	100.0	1572	14	US-10-037-182-20
2	8527	100.0	1605	14	US-10-037-182-18
3	8460	99.2	1607	9	US-09-938-275-10
4	8038	94.3	1576	14	US-10-037-182-16
5	8038	94.3	1609	14	US-10-037-182-14
6	8038	94.3	1609	14	US-10-299-058-12
7	8034	94.2	1609	9	US-09-938-275-11
8	8034	94.2	1609	15	US-10-372-683-36
9	3586	42.1	1587	9	US-09-845-583-10
10	3585	42.1	1587	12	US-10-262-839-210
11	3583	42.0	1575	12	US-10-262-839-212
12	3193	37.4	1537	12	US-10-369-493-6816
13	2592	30.4	1193	12	US-10-392-113-14
14	2592	30.4	1193	14	US-10-171-311-115
15	2592	30.4	1193	14	US-10-053-662A-31

Db 121 RPESFAIYKRTREDPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180  
Qy 181 TGGNVAFTLEGRPSAYFNPNFVLPQEWVATDIRVTNLNLTGDEVFNDPKVLKSYYY 240  
Db 181 TGGNVAFTLEGRPSAYFNPNFVLPQEWVATDIRVTNLNLTGDEVFNDPKVLKSYYY 240  
Qy 241 AISDPFVGGKCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300  
Db 241 AISDPFVGGKCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 300  
Qy 301 ASECLPCDNGRSQECYFDPPELYASTGHGCHTNCRDNTDGAKCERENFFRLGNTAC 360  
Db 301 ASECLPCDNGRSQECYFDPPELYASTGHGCHTNCRDNTDGAKCERENFFRLGNTAC 360  
Qy 361 SPCHCSVPGSLSTOCDSYGRCSCKPGVMGDKORCPGFHSLTEAGRCPCSCDPSGSTDE 420  
Db 361 SPCHCSVPGSLSTOCDSYGRCSCKPGVMGDKORCPGFHSLTEAGRCPCSCDPSGSTDE 420  
Qy 421 CNVETGRVCVKDNEGFENCKRCKPGFFNLESSPKGCTPCFCFHSVCTNAVGYSYDI 480  
Db 421 CNVETGRVCVKDNEGFENCKRCKPGFFNLESSPKGCTPCFCFHSVCTNAVGYSYDI 480  
Qy 481 SSTQIDEDGWRVQRGSEASLEWSSDRQYIAVISDSYPRYFIAPVKELGNQVLSYG 540  
Db 481 SSTQIDEDGWRVQRGSEASLEWSSDRQYIAVISDSYPRYFIAPVKELGNQVLSYG 540  
Qy 541 NLSFSFRVDRDRTLSAEDLVLEGAGLRVSVPILIAQNSYSPSETTVKYIFRLHEATDYPW 600  
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Qy 601 RPALSPFEFQKLNLSITSIKIRGYSERSAGYLDVLTQARPGPGVPATWVESCPCVG 660  
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Qy 661 YGGQFCETCLPGYRRETPSLGYPVCLCTCNHSETCDPBTGVCDCRDNTAGPHCKCS 720  
Db 661 YGGQFCETCLPGYRRETPSLGYPVCLCTCNHSETCDPBTGVCDCRDNTAGPHCKCS 720  
Qy 721 DGYTGDSTLGTSSDCQPCPCGGSSCAIYPKTKKVTCHTPTGTAGRCBLCDGDFGDP 780  
Db 721 DGYTGDSTLGTSSDCQPCPCGGSSCAIYPKTKKVTCHTPTGTAGRCBLCDGDFGDP 780  
Qy 781 LGSNGPVRCLPCCCNNDIDNAGVNCNLTGECIKCIYNTAGFYCDRCCKEFGFNPLAP 840  
Db 781 LGSNGPVRCLPCCCNNDIDNAGVNCNLTGECIKCIYNTAGFYCDRCCKEFGFNPLAP 840  
Qy 841 NPADCKACACNYGTVOQSSCNPTVTCQCLPHVSGRDCGTDPGYNLTQSGGCBRC 900  
Db 841 NPADCKACACNYGTVOQSSCNPTVTCQCLPHVSGRDCGTDPGYNLTQSGGCBRC 900  
Qy 901 CHALGSTNGQCDIRTGQCECPGFTGQHCERCETHFGFPGEGCKPCDCHHGSLSLQCK 960  
Db 901 CHALGSTNGQCDIRTGQCECPGFTGQHCERCETHFGFPGEGCKPCDCHHGSLSLQCK 960  
Qy 961 DDGRCEGREGFVGNRCDOCEENFYFNRSWPGCQCPACRYLVKDKAAEHRVYKQLESLI 1020  
Db 961 DDGRCEGREGFVGNRCDOCEENFYFNRSWPGCQCPACRYLVKDKAAEHRVYKQLESLI 1020  
Qy 1021 ANLGTGDDMTQAPFEDLKAERVTDLLEAQQVQDQNLMDRLQVNSSLSHSQISR 1080  
Db 1021 ANLGTGDDMTQAPFEDLKAERVTDLLEAQQVQDQNLMDRLQVNSSLSHSQISR 1080  
Qy 1081 LQNIENITTEGILAEARARSVESTQLEIETASRELEKAKAAVNSITQPESTGEPNMT 1140  
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Db 1201 QAKN:SQDLEKQAAHVHEAKGAKAVEIYASVAQLTPVDSEALENEANKI:KEAADLD 1260

Qy 1261 RLIDOKLXDYEDLREDYRGKEHEVKNLLKGAQOQTADQALLARADAALAEBAKGR 1320  
Db 1261 RLIDOKLXDYEDLREDYRGKEHEVKNLLKGAQOQTADQALLARADAALAEBAKGR 1320  
Qy 1321 STLQEPANDILNNLKDFRRVNDNKTAAEEALRRIPAINRTTAAENKKTREQAALGNAAA 1380  
Db 1321 STLQEPANDILNNLKDFRRVNDNKTAAEEALRRIPAINRTTAAENKKTREQAALGNAAA 1380  
Qy 1381 DATEAKNKAHEAERTASAAQKNATSTKADAERTGEVTDLDNEVNGMLRQLEEAENELKR 1440  
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Qy 1441 KQDDADQDMMAGMASQAAQAEALNARKKNSVSLLSQLNNLLPQLGQDLDVLDKLINE 1500  
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Qy 1501 IEGSLINKAKDEKASDLDRKVSIDLESEARKOEAAIMDYNRDIAETIKDHNLEDIKKTL 1560  
Db 1501 IEGSLINKAKDEKASDLDRKVSIDLESEARKOEAAIMDYNRDIAETIKDHNLEDIKKTL 1560  
Qy 1561 TGCFTNTPSIEKP 1572  
Db 1561 TGCFTNTPSIEKP 1572

## RESULT 2

US-10-037-182-18  
; Sequence 18, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-18

Query Match 100.0%; Score 8527; DB 14; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 QOHLQGAFLTDYNNQADTTWQSQTMLAGVQVENSINLTILHKGAFDITVRLKPHTS 120  
Db 94 QOHLQGAFLTDYNNQADTTWQSQTMLAGVQVENSINLTILHKGAFDITVRLKPHTS 153  
Qy 121 RPESFAIYKRTREDPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180  
Db 154 RPESFAIYKRTREDPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 213  
Qy 181 TCGNVAFTLEGRPSAYFNPNFVLPQEWVATDIRVTNLNLTGDEVFNDPKVLKSYYY 240  
Db 214 TCGNVAFTLEGRPSAYFNPNFVLPQEWVATDIRVTNLNLTGDEVFNDPKVLKSYYY 273  
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Db 274 AISDPFVGGKCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATAES 333

QY 301 ASECLPCDNGRSQCYFDPELYRSTGHGCHTNCNDNTGAKCERENFRFLGNTTEAC 360  
DB 334 ASECLPCDNGRSQCYFDPELYRSTGHGCHTNCNDNTGAKCERENFRFLGNTTEAC 393  
QY 361 SPCHSPVGSLSQCDSTYGRSCSKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420  
DB 394 SPCHSPVGSLSQCDSTYGRSCSKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 453  
QY 421 CNVETGRVCCKDNVEGFCNCRCKPGFNLNLSNPKGCTPCFCFHSSVCTNAVGSYVDI 480  
DB 454 CNVETGRVCCKDNVEGFCNCRCKPGFNLNLSNPKGCTPCFCFHSSVCTNAVGSYVDI 513  
QY 481 SSTFOIDEDGWRVEQRDGEASLEWSDRQIVATISDSYFFPRYFIAPVKFLGNQVLSYGQ 540  
DB 514 SSTFOIDEDGWRVEQRDGEASLEWSDRQIVATISDSYFFPRYFIAPVKFLGNQVLSYGQ 573  
QY 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSESTTVKIFRLHEATDPW 600  
DB 574 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSESTTVKIFRLHEATDPW 633  
QY 601 RPALSPFFQKLLNLTGIKIRGTYSERSAGVLDVTLQSRPQPGVPATVBSCTCPVG 660  
DB 634 RPALSPFFQKLLNLTGIKIRGTYSERSAGVLDVTLQSRPQPGVPATVBSCTCPVG 693  
QY 661 YGGQFCETCLPGYRRETSLGYPSPVLCNNGHSETCDPTGVCDCRDNATAGPHCKCS 720  
DB 694 YGGQFCETCLPGYRRETSLGYPSPVLCNNGHSETCDPTGVCDCRDNATAGPHCKCS 753  
QY 721 DGYGDSLTGSSDCQPCPCGSSCAIVPKTKVCTHCTGTAGKCELCDDGYGDP 780  
DB 754 DGYGDSLTGSSDCQPCPCGSSCAIVPKTKVCTHCTGTAGKCELCDDGYGDP 813  
QY 781 LGSNGPVLRCPCQCNNDIPNAVGNCLRTGECCLKIYNTAGFYCDRCBGFNGNPLAP 840  
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DB 874 NPADKCKACACNYGTVOQSSCNPTGQCQLPHVSGRDCGTCDPGYNLSGGCERCD 933  
QY 901 CHALSTNGQCDIRTGQCEQCBQGITGQCERCETNHFGEPCGKPCDCHIEGSLSLQCK 960  
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DB 1234 QAKNTSODLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293  
QY 1261 RLIDQKLDKDYEDLRDMRKEHEVKNLLEKGAQOQTADOLLARADAAKALAEAAKGR 1320  
DB 1294 RLIDQKLDKDYEDLRDMRKEHEVKNLLEKGAQOQTADOLLARADAAKALAEAAKGR 1353  
QY 1321 STLQEBANDILNLIKOPDRVNDNKTAABEALRRIIPAINRTIAEANKEKTRAEQALGNAAA 1380  
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DB 1414 DATEAKNKAHEAERIAASAAQKATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANELKR 1473  
QY 1441 KQDADQDQMMAGMASQAAQAEELNARKAKNSVSSLLSQJNNLLDQLGQDVTVDLNKLE 1500  
DB 1474 KQDADQDQMMAGMASQAAQAEELNARKAKNSVSSLLSQJNNLLDQLGQDVTVDLNKLE 1533  
QY 1501 IEGLSKAKDEMKAASDLDRKVSLESEARKQBAAIMDYNRDAEIIKDIHNLEDIKKTLP 1560  
DB 1534 IEGLSKAKDEMKAASDLDRKVSLESEARKQBAAIMDYNRDAEIIKDIHNLEDIKKTLP 1593  
QY 1561 TGCNFTPSIEKP 1572  
DB 1594 TGCNFTPSIEKP 1605

RESULT 3  
US-09-938-275-10  
; Sequence 10, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: of Laminin and Laminin-Derived Protein Fragments  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1607  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P02468  
; DATABASE ENTRY DATE: 1989-07-01  
; US-09-938-275-10

Query Match 99.2%; Score 8460; DB 9; Length 1607;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1565; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPORCMPEFVNAAFNVTATNTCGTPPEEYCVQTGVTGKTSCHLCDAG 60  
DB 34 AMDECADEGGRPORCMPEFVNAAFNVTATNTCGTPPEEYCVQTGVTGKTSCHLCDAG 93  
QY 61 QOHLQGAFLTDYNNQADTTMWSOTMLAGVQYPSINLTLLHKAFTIYVRLKFTS 120  
DB 94 QOHLQGAFLTDYNNQADTTMWSOTMLAGVQYPSINLTLLHKAFTIYVRLKFTS 153  
QY 121 RPESFALYKRTREDGDPWIPYOYSGSCENTYKANEGRFRTGGDEQOALCTDEFSISPL 180  
DB 154 RPESFALYKRTREDGDPWIPYOYSGSCENTYKANEGRFRTGGDEQOALCTDEFSISPL 213  
QY 181 TGGNVAFTSLTEGRPSAYNFNDSVPLQEWVTATDIRVTLNRLNTFGDEVNPKVLSYYY 240  
DB 214 TGGNVAFTSLTEGRPSAYNFNDSVPLQEWVTATDIRVTLNRLNTFGDEVNPKVLSYYY 273  
QY 241 AISDPAVGRCKNGKNGHASECVKNEFKLMCNKXNTYVDCEKCLPFNDPRPERRATAES 300  
DB 274 AISDPAVGRCKNGKNGHASECVKNEFKLMCNKXNTYVDCEKCLPFNDPRPERRATAES 333  
QY 301 ASECLPCDNGRSQCYFDPELYRSTGHGCHTNCNDNTGAKCERENFRFLGNTTEAC 360  
DB 334 ASECLPCDNGRSQCYFDPELYRSTGHGCHTNCNDNTGAKCERENFRFLGNTTEAC 393  
QY 361 SPCHSPVGSLSQCDSTYGRSCSKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 420  
DB 394 SPCHSPVGSLSQCDSTYGRSCSKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSTDE 453  
QY 421 CNVETGRVCCKDNVEGFCNCRCKPGFNLNLSNPKGCTPCFCFHSSVCTNAVGSYVDI 480

Db	454	CNVETGRCVKNVEGFNCERKPGFNFLESNPKGCTCFCEGHSSVCTNAVGSYDI	513
Qy	481	SSTFDIEDGWRVEQDGSSEASLEWSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	540
Db	514	SSTFDIEDGWRVEQDGSSEASLEWSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	573
Qy	541	NLSFSFRVDRDRLSADLVLGAGLRVSVPILIAOGNSVPSETTVKYIFRLHEATDYPW	600
Db	574	NLSFSFRVDRDRLSADLVLGAGLRVSVPILIAOGNSVPSETTVKYIFRLHEATDYPW	633
Qy	601	RPALSPFEFOKLNNLTSIKIRGYSERSAGYLDVTLQASRPGVPATWVESCTCPVG	660
Db	634	RPALSPFEFOKLNNLTSIKIRGYSERSAGYLDVTLQASRPGVPATWVESCTCPVG	693
Qy	661	YGSQFCETCLPGVRRTPSPGVPCVLCTCNCHSETCPETGVCDCRNTAGPHCEKCS	720
Db	694	YGSQFCETCLPGVRRTPSPGVPCVLCTCNCHSETCPETGVCDCRNTAGPHCEKCS	753
Qy	721	DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGRCCLCDDGDFGDP	780
Db	754	DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGRCCLCDDGDFGDP	813
Qy	781	LGSNGPVRLCRPCQCNNDIPNAGVNCNRLTGELCKIYNTAGFYCDRCKEGFFGNPLAP	840
Db	814	LGSNGPVRLCRPCQCNNDIPNAGVNCNRLTGELCKIYNTAGFYCDRCKEGFFGNPLAP	873
Qy	841	NPADKCKACACN-YGTVOQSSCNPTGQCCLPHVSGRDCGTCDPGYTNLQSGQCERC	899
Db	874	NPADKCKACACN-YGTVOQSSCNPTGQCCLPHVSGRDCGTCDPGYTNLQSGQCERC	933
Qy	900	DCHALGTNGQDITQCCQCPGIGTQHCERCETNHFPGPGGKPCDCHHEGSLQ	959
Db	934	DCHALGTNGQDITQCCQCPGIGTQHCERCETNHFPGPGGKPCDCHHEGSLQ	993
Qy	960	KDDGRCRSGFVGNRCDCQCEENFYNRSWPGQCEPCACVRLVKDKAAEHRVKLQLESL	1019
Db	994	KDDGRCRSGFVGNRCDCQCEENFYNRSWPGQCEPCACVRLVKDKAAEHRVKLQLESL	1053
Qy	1020	IANLGTGDMVTDQAFEDRLKEAREVTDLLRBAQEVKQVDQNLMDRLQRVNSLSQS	1079
Db	1054	IANLGTGDMVTDQAFEDRLKEAREVTDLLRBAQEVKQVDQNLMDRLQRVNSLSQS	1113
Qy	1080	RLQNRITBETGLARARSRVESTBOLTEIASRELEKAKM-AANVSITQPESTGEPPN	1138
Db	1114	RLQNRITBETGLARARSRVESTBOLTEIASRELEKAKM-AANVSITQPESTGEPPN	1173
Qy	1139	MTLLAEARLAEHRKQEAADDIVRAKTANETSAAEYNLLRLTAGENQTALEIEBLNRK	1198
Db	1174	MTLLAEARLAEHRKQEAADDIVRAKTANETSAAEYNLLRLTAGENQTALEIEBLNRK	1233
Qy	1199	YEQAQNTSODLEKQAAARVBEAKGADKAVEIYASVAQLTPVDSEALENEANKIKKEAD	1258
Db	1234	YEQAQNTSODLEKQAAARVBEAKGADKAVEIYASVAQLTPVDSEALENEANKIKKEAD	1293
Qy	1259	LDRLIDOKLDYEDLREDMRGKEHEVNKLEKGAEQQTADQLLARAADAALAEAAKK	1318
Db	1294	LDRLIDOKLDYEDLREDMRGKEHEVNKLEKGAEQQTADQLLARAADAALAEAAKK	1353
Qy	1319	GRSTLQEAANDTLNNLKDFDRVNDNKTAAEALRRIIPAINRTTAAANEKTRQAALGNA	1378
Db	1354	GRSTLQEAANDTLNNLKDFDRVNDNKTAAEALRRIIPAINRTTAAANEKTRQAALGNA	1413
Qy	1379	AADATEAKNKAHAERIASAQKATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANEL	1438
Db	1414	AADATEAKNKAHAERIASAQKATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANEL	1473
Qy	1439	KRQKDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGOLDTVDLNLK	1498
Db	1474	KRQKDDADQDMMWAGMASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGOLDTVDLNLK	1533
Qy	1499	NEIEGSLNKAKDEMKASDLDRKVSQDSEARKQEAAMDNRYDIAEIIKDHNLEDIKKT	1558

Db	1534	NEIEGSLNKAKDEMKASDLDRKVSQDSEARKQEAAMDNRYDIAEIIKDHNLEDIKKT	1593
Qy	1559	LPTGCENTPSTIEKP	1572
Db	1594	LPTGCENTPSTIEKP	1607
RESULT 4			
US-10-037-182-16			
; Sequence 16, Application US/10037182			
; Publication No. US20030044899A1			
; GENERAL INFORMATION:			
; APPLICANT: Trygsvason, Karl			
; APPLICANT: Doi, Masayuki			
; APPLICANT: Thyboll, Jill			
; TITLE OF INVENTION: Recombinant Laminin 10			
; FILE REFERENCE: 99-274-F			
; CURRENT APPLICATION NUMBER: US/10/037,182			
; CURRENT FILING DATE: 2001-12-21			
; PRIOR APPLICATION NUMBER: 60/257,449			
; PRIOR FILING DATE: 2000-12-21			
; PRIOR APPLICATION NUMBER: 60/279,282			
; PRIOR FILING DATE: 2001-03-28			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 16			
; LENGTH: 1576			
; TYPE: PR			
; ORGANISM: Homo sapiens			
US-10-037-182-16			
Query Match 94.3%; Score 8038; DB 14; Length 1576;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;			
Qy	1	AMDECADEGGPQRCMPBEFVNAAFNVTVATNTCGTPPEYCVQTVGTGTSKCHLCDAG	60
Db	3	AMDECTDEGGPQRCMPBEFVNAAFNVTVATNTCGTPPEYCVQTVGTGTSKCHLCDAG	62
Qy	61	QOHLQHGAAFTDYNQADTTWQSQTLQAGVQVNSINLTLHGKAFDIYVRLKFTS	120
Db	63	QPHLQHGAAFTDYNQADTTWQSQTLQAGVQVNSINLTLHGKAFDIYVRLKFTS	122
Qy	121	RPESFAYIKRTREDGPMWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDISPL	180
Db	123	RPESFAYIKRTREDGPMWIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSDISPL	182
Qy	181	TGCVNAPSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVNDPKVLSVY	240
Db	183	TGCVNAPSTLEGRPSAYNFDNSPVLQEWVTATDIRVTILNRLNTFGDEVNDPKVLSVY	242
Qy	241	ALSDFAVGRCCKNGHASECVKNEBFDKLMCKNCKNTYGVDCCKLPPFNDRPWRATAES	300
Db	243	ALSDFAVGRCCKNGHASECMKNEBFDKLVCKNCKNTYGVDCCKLPPFNDRPWRATAES	302
Qy	301	ASECLPCDCNGRSQCYFDPPELYRSTGGHCTNCRDNTDGAACERENFRGNTGAC	360
Db	303	ASECLPCDCNGRSQCYFDPPELYRSTGGHCTNCRDNTDGAACERENFRGNTGAC	362
Qy	361	SPCHSPVGSLSQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLSLTAEGRCPCSDPSGSIDE	420
Db	363	SSCHSPVGSLSQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLSLTAEGRCPCSDPSGSIDE	422
Qy	421	CNVETGRCVCKDNVEGFNCRCKPGFNFLESNPKGCTPCFCFHHSSVCTNAVGSVYDI	480
Db	423	CNVETGRCVCKDNVEGFNCRCKPGFNFLESNPKGCTPCFCFHHSSVCTNAVGSVYDI	482
Qy	481	SSTFOIDEDGWEVQDSEASLEWSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	540
Db	483	SSTFOIDEDGWEVQDSEASLEWSDRQYIAVISDSYFPRFYFIAPVKFLGNQVLSYQ	542
Qy	541	NLSFSFRVDRDRLSADLVLGAGLRVSVPILIAOGNSVPSETTVKYIFRLHEATDYPW	600

Db 543 NLSFSPVRDRRLRLSAEDLVLEAGLRVSVPLIAQNSYSPSETTVKYVFLRLHEATDYPW 602  
QY 601 RPALSPEFQKLNNTSIRKITYSERSAGYLDVTLQASRPGCPVATWVESCCTCPVG 660  
Db 603 RPALTPEFQKLNNTSIRKITYSERSAGYLDVTLQASRPGCPVATWVESCCTCPVG 662  
QY 661 YGQFCETCLPGYRRRTPLSGPSPVCLCTCNHSETCDPETGVCDCRNTAGPCEKCS 720  
Db 663 YGQFCETCLPGYRRRTPLSGPSPVCLCTCNHSETCDPETGVCDCRNTAGPCEKCS 722  
QY 721 DGYGDSITGTSDDCPGCPGSSCAIVPKYKEVVTCHPTGTAGRCGLCDDGYFGDP 780  
Db 723 DGYGDSITGTSDDCPGCPGSSCAIVPKYKEVVTCHPTGTAGRCGLCDDGYFGDP 782  
QY 781 LGSNGPVRCLRCPCQNDNDPNAVCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAP 840  
Db 783 LGSNGPVRCLRCPCQNDNDPNAVCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAP 842  
QY 841 NPADKCKACACN-YGTVOQSSCNPTVGOQCCLPHVSGRDCGTCPGYNLSQGGCERC 899  
Db 843 NPADKCKACACN-YGTVOQSSCNPTVGOQCCLPHVSGRDCGTCPGYNLSQGGCERC 902  
QY 900 DCHALGSTGQCDIRTGQCECQPGITGQHCERCETNHFPGGCKPCDCHHEGSLSLQC 959  
Db 903 DCHALGSTGQCDIRTGQCECQPGITGQHCERCETNHFPGGCKPCDCHHEGSLSLQC 962  
QY 960 KDDGRCEGFGVGNRCDCQCEENFYNRSWPGQCECPACRYLVKDKAAEHRYKLQELSL 1019  
Db 963 KDDGRCEGFGVGNRCDCQCEENFYNRSWPGQCECPACRYLVKDKAAEHRYKLQELSL 1022  
QY 1020 IANLGTGDDWTDQAEFRLKEAREVTDLLREAEVQDVNDQNLDRQVNTLSLSQIS 1079  
Db 1023 IANLGTGDDWTDQAEFRLKEAREVTDLLREAEVQDVNDQNLDRQVNTLSLSQIS 1082  
QY 1080 RLQNIRNTIETGILARARSVESTPEQLIETASRELEKAKN-AANVSTQPESTGEPPN 1138  
Db 1083 RLQNIRNTIETGILARARSVESTPEQLIETASRELEKAKN-AANVSTQPESTGEPPN 1142  
QY 1139 MTLLEAEARLAPRHQAEADDIVRAKATANETSAEAYNLLRLTLAGENOTALIEBELNRK 1198  
Db 1143 MTLLEAEARLAPRHQAEADDIVRAKATANETSAEAYNLLRLTLAGENOTALIEBELNRK 1202  
QY 1199 YEOAKNISQLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSBALENEANKIKKEAAD 1258  
Db 1203 YEOAKNISQLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSBALENEANKIKKEAAD 1262  
QY 1259 LDRIDQKLDYEDLREDNRKGEHEVKNLLEKGAFAQQTADQALLARADAALAEAAK 1318  
Db 1263 LDRIDQKLDYEDLREDNRKGEHEVKNLLEKGAFAQQTADQALLARADAALAEAAK 1322  
QY 1319 GRSTLOEANDILNLLKDFRRVNDNKTAAEALRIPALNRTIAEANEKTRAEALGNA 1378  
Db 1323 GRSTLOEANDILNLLKDFRRVNDNKTAAEALRIPALNRTIAEANEKTRAEALGNA 1382  
QY 1379 AADATKAKNAHEABRIASAAQKNATSTKADARTFEVTDLDNEVNGMLRQLEAEANEL 1438  
Db 1383 AADATKAKNAHEABRIASAAQKNATSTKADARTFEVTDLDNEVNGMLRQLEAEANEL 1442  
QY 1439 KRQDDADQDMWAGASQAQAEALNARKAKNSVLSLSQLNLLDQGLDQDLDLNLK 1498  
Db 1443 KRQDDADQDMWAGASQAQAEALNARKAKNSVLSLSQLNLLDQGLDQDLDLNLK 1502  
QY 1499 NETEGSLNKAQDMKASDLDRKVSDESBAKQEAAMIDNDRDIAEIKIDHNLSDIKKT 1558  
Db 1503 NETEGSLNKAQDMKASDLDRKVSDESBAKQEAAMIDNDRDIAEIKIDHNLSDIKKT 1562  
QY 1559 LPTGCFNTPSIEKP 1572  
Db 1563 LPTGCFNTPSIEKP 1576

RESULT 5  
US-10-037-182-14

; Sequence 14, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-14

Query Match 94.3%; Score 8038; DB 14; Length 1609;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDSACDEGGRPQRCMPDEFVNAAPNVTVAINTCGTPPEEYCVQGTGVTGKSHLCDAG 60  
Db 36 AMDECTDEGGRPQRCMPDEFVNAAPNVTVAINTCGTPPEEYCVQGTGVTGKSHLCDAG 95  
QY 61 QQLHQHGAALFDTNNQADTTWQSQMLAGVQVPSNLTLLHKGAFDITYVRLKEFHTS 120  
Db 96 QQLHQHGAALFDTNNQADTTWQSQMLAGVQVPSNLTLLHKGAFDITYVRLKEFHTS 155  
QY 121 RPESFALYKRTREDGPWIPYQYSSGSCENTYSKANRGFIRTGDEQOALCTDFSDISPL 180  
Db 156 RPESFALYKRTREDGPWIPYQYSSGSCENTYSKANRGFIRTGDEQOALCTDFSDISPL 215  
QY 181 TGGNVASTLEGPSAYNFNDSVPLQEWVTATDIRVTLNRLNTFGDBEVNDPKVLKSY 240  
Db 216 TGGNVASTLEGPSAYNFNDSVPLQEWVTATDIRVTLNRLNTFGDBEVNDPKVLKSY 275  
QY 241 AISDFAVGGRCKNGHASECQNEFDKLMCNCKENTYGVDCERCLPFNFDRPWRRTAES 300  
Db 276 AISDFAVGGRCKNGHASECQNEFDKLMCNCKENTYGVDCERCLPFNFDRPWRRTAES 335  
QY 301 ASECLPCDCNRSOECYFDPDELRYSTGHGCHTNCRDNTGAKCERCFNRLGNTAEAC 360  
Db 336 ASECLPCDCNRSOECYFDPDELRYSTGHGCHTNCRDNTGAKCERCFNRLGNTAEAC 395  
QY 361 SPCHSPVGSLSSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSPSGSTDE 420  
Db 396 SPCHSPVGSLSSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSPSGSTDE 455  
QY 421 CNVETGRVCCKNVGECNRCRCKPGFFNLSSNPKGCTPCFCFHSVSVCTNAVGYSYDI 480  
Db 456 CNVETGRVCCKNVGECNRCRCKPGFFNLSSNPKGCTPCFCFHSVSVCTNAVGYSYDI 515  
QY 481 SSTFQIDEDGWRVORQDSEASLEWSSDROVIAVISDYPFPIAPVKFLGNQVLSYG 540  
Db 516 SSTFQIDEDGWRVORQDSEASLEWSSDROVIAVISDYPFPIAPVKFLGNQVLSYG 575  
QY 541 NLSFSPVRDRRLRLSAEDLVLEAGLRVSVPLIAQNSYSPSETTVKYVFLRLHEATDYP 600  
Db 576 NLSFSPVRDRRLRLSAEDLVLEAGLRVSVPLIAQNSYSPSETTVKYVFLRLHEATDYP 635  
QY 601 RPALSPEFQKLNNTSIRKITYSERSAGYLDVTLQASRPGCPVATWVESCCTCPVG 660  
Db 636 RPALTPEFQKLNNTSIRKITYSERSAGYLDVTLQASRPGCPVATWVESCCTCPVG 695  
QY 661 YGQFCETCLPGYRRRTPLSGPSPVCLCTCNHSETCDPETGVCDCRNTAGPCEKCS 720  
Db 696 YGQFCETCLPGYRRRTPLSGPSPVCLCTCNHSETCDPETGVCDCRNTAGPCEKCS 755



Qy 721 DGYGDSLTGTSQCPGCGSSCAIVPKTKEVWTHCPTGTAGKRCCLDDGFGDP 780  
Db 756 DGYGDSLTGTSQCPGCGSSCAIVPKTKEVWTHCPTGTAGKRCCLDDGFGDP 815  
Qy 781 LGSNGPVLRCPCCNNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKEGFNGPLAP 840  
Db 816 LGRNGPVLRCPCCNNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKEGFNGPLAP 875  
Qy 841 NPADKCKACACN-YGTVOQSSCNPVGTGQCCPLPHVSGRDCGTCDPGYNLQSGQCERC 899  
Db 876 NPADKCKACACN-YGTVOQSSCNPVGTGQCCPLPHVSGRDCGTCDPGYNLQSGQCERC 935  
Qy 900 DCHALGSTNGQCDRTGQCCECGITGHCERCETHFGFPGCKPCDCHHSGSLQ 959  
Db 936 DCHALGSTNGQCDRTGQCCECGITGHCERCETHFGFPGCKPCDCHHSGSLQ 995  
Qy 960 KDDGRCCEGFGVNRCDQCEBENFYNRSPGCGECPACRYLVKDKAAEHRVLOELES 1019  
Db 996 KDDGRCCEGFGVNRCDQCEBENFYNRSPGCGECPACRYLVKDKAAEHRVLOELES 1055  
Qy 1020 IANLGTGDMVTDQAFEDRLKEAREVTDLLREAEVQKVDQNDLMDRLQVNSLSQIS 1079  
Db 1056 IANLGTGDMVTDQAFEDRLKEAREVTDLLREAEVQKVDQNDLMDRLQVNSLSQIS 1115  
Qy 1080 RLQIRNTIETGILARARSRVSTEQIIEIASRELEKAKM-AANYSITQPESTGEPPN 1138  
Db 1116 RLQIRNTIETGILARARSRVSTEQIIEIASRELEKAKM-AANYSITQPESTGEPPN 1175  
Qy 1139 MTLAABEARLAERHKGADIVVAKTANETSABAYNLLRTLAGENQTALEIBELNRK 1198  
Db 1176 MTLAABEARLAERHKGADIVVAKTANETSABAYNLLRTLAGENQTALEIBELNRK 1235  
Qy 1199 YEQAQNISODLEKQARVHEAKRAGDKAVIYASVAQLTPVDSEALENEANKIKKEAD 1258  
Db 1236 YEQAQNISODLEKQARVHEAKRAGDKAVIYASVAQLTPVDSEALENEANKIKKEAD 1295  
Qy 1259 LDRLIDQKDYEDLREDMRGKEHEVKNLEKGAEOQTADQLARADAAKALAEAAK 1318  
Db 1296 LDRLIDQKDYEDLREDMRGKEHEVKNLEKGAEOQTADQLARADAAKALAEAAK 1355  
Qy 1319 GRSTLQEAANDILNLIKDFDRVNDKTAABEALRRIIPAINRTIAEANEKTRAEALAGNA 1378  
Db 1356 GRSTLQEAANDILNLIKDFDRVNDKTAABEALRRIIPAINRTIAEANEKTRAEALAGNA 1415  
Qy 1379 AADATEAKNAKAEABERIASAQKNATSTKADAERTFGEVTDLDNEVNGMLKQLEAEENEL 1438  
Db 1416 AADATEAKNAKAEABERIASAQKNATSTKADAERTFGEVTDLDNEVNGMLKQLEAEENEL 1475  
Qy 1439 KRKQDDADQMMAGASQAAQAEALNARKAKNSVSLLSQNLILDLQGLDQVLDLNLK 1498  
Db 1476 KRKQDDADQMMAGASQAAQAEALNARKAKNSVSLLSQNLILDLQGLDQVLDLNLK 1535  
Qy 1499 NEIEGSLNKADEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLIEDIKT 1558  
Db 1536 NEIEGSLNKADEMKASDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLIEDIKT 1595  
Qy 1559 LPTGCFNTPSIEKP 1572  
Db 1596 LPTGCFNTPSIEKP 1609

RESULT 6  
US-10-299-058-12  
; Sequence 12, Application US/10299058  
; Publication No. US20030103975A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, JONATHAN C.R.  
; APPLICANT: GONZALES, MEREDITH  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION  
; FILE REFERENCE: 1720-1-002 CIP  
; CURRENT APPLICATION NUMBER: US/10/299,058  
; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 09/706,235  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/163,199  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; US-10-299-058-12

Query Match 94.3%; Score 8038; DB 14; Length 1609;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
Qy 1 AMDECADEGRQRCMPFVNAAFNVVAVNTCTGTPPEEYCVQGVGVTKSKCHLCADG 60  
Db 36 AMDECTDEGGRQRCMPFVNAAFNVVAVNTCTGTPPEEYCVQGVGVTKSKCHLCADG 95  
Qy 61 QOHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQYFSSINLTLHLGKAFDITYVRLKFHTS 120  
Db 96 QOHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQYFSSINLTLHLGKAFDITYVRLKFHTS 155  
Qy 121 RPESFAIYKRTREDGFWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 180  
Db 156 RPESFAIYKRTREDGFWIPYQYISGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL 215  
Qy 181 TGNVAFSTLEGRPSAYNFDNSPVLQEWVATDITVTLNRLNTFGDEVFNDPKVLKSYYY 240  
Db 216 TGNVAFSTLEGRPSAYNFDNSPVLQEWVATDITVTLNRLNTFGDEVFNDPKVLKSYYY 275  
Qy 241 AISDFAVGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPPFNDPRWRATAES 300  
Db 276 AISDFAVGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPPFNDPRWRATAES 335  
Qy 301 ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDQAKRCRCENPRLNBTAC 360  
Db 336 ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDQAKRCRCENPRLNBTAC 395  
Qy 361 SFCHSPVGSLSQCDSDYGRCSCKPGVNGDKCDRCQPGFHSLTEAGRCPCSDPGSGTDE 420  
Db 396 SFCHSPVGSLSQCDSDYGRCSCKPGVNGDKCDRCQPGFHSLTEAGRCPCSDPGSGTDE 455  
Qy 421 CNVETGRCKVCKNDVGFNCRCCKPGFNLSSNPGCTPCFCFHSSTVCTNAVGVSVYDI 480  
Db 456 CNVETGRCKVCKNDVGFNCRCCKPGFNLSSNPGCTPCFCFHSSTVCTNAVGVSVYDI 515  
Qy 481 SSTFQIDEGWVEQORDGSEASLEWSSDRQYIAVISDSYFFPRYFIAPVKFLGNQVLSYQ 540  
Db 516 SSTFQIDEGWVEQORDGSEASLEWSSDRQYIAVISDSYFFPRYFIAPVKFLGNQVLSYQ 575  
Qy 541 NLSFSFRVDRRTRLSAEDLVLEGAGLVSVPLIAQNSYSETTVKVIIRLHEATDYPW 600  
Db 576 NLSFSFRVDRRTRLSAEDLVLEGAGLVSVPLIAQNSYSETTVKVIIRLHEATDYPW 635  
Qy 601 RPALSPFEQKLLNLTISKIRGTYSERSAGYLDVTLQSRAPGPGVPATWVSTCTCPVG 660  
Db 636 RPALSPFEQKLLNLTISKIRGTYSERSAGYLDVTLQSRAPGPGVPATWVSTCTCPVG 695  
Qy 661 YGQCFCECLPGYRRTPLSLGYPSCVLCTCNHSETCDPBTGVCDCRNTAGPHECKS 720  
Db 696 YGQCFCECLPGYRRTPLSLGYPSCVLCTCNHSETCDPBTGVCDCRNTAGPHECKS 755  
Qy 721 DGYGDSLTGTSQCPGCGSSCAIVPKTKEVWTHCPTGTAGKRCCLDDGFGDP 780  
Db 756 DGYGDSLTGTSQCPGCGSSCAIVPKTKEVWTHCPTGTAGKRCCLDDGFGDP 815  
Qy 781 LGSNGPVLRCPCCNNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKEGFNGPLAP 840  
Db 816 LGRNGPVLRCPCCNNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKEGFNGPLAP 875  
Qy 841 NPADKCKACACN-YGTVOQSSCNPVGTGQCCPLPHVSGRDCGTCDPGYNLQSGQCERC 899



876 NFADKCKACNCPYGMKQSSCNVPTGQCCLPHVTGQDGCACDPGFYNLQSGQCERC 935  
900 DCHALGSTNGQCDIRTGQCEQFGITGQHCERCETNHFHFGPEGCKPCDCHHEGSLQOC 959  
936 DCHALGSTNGQCDIRTGQCEQFGITGQHCERCETNHFHFGPEGCKPCDCHHEGSLQOC 995  
960 KDGRCCEGREGVGNRCQCEENYFVNSWPGCQCECPACRYLVKDKAAHRVKLOELES 1019  
996 KDGRCCEGREGVGNRCQCEENYFVNSWPGCQCECPACRYLVKDKAAHRVKLOELES 1055  
1020 IANLGTGDDMVTDOAFEDRLKEAEREVTDLLREAEQVKVDQDQNLMDRLQRVNSLSHQS 1079  
1056 IANLGTGDDMVTDOAFEDRLKEAEREVMDLLREAEQVKVDQDQNLMDRLQRVNSLSHQS 1115  
1080 RQONRNTIEETGILAEARBSVSTEQLEIASRELEKAKM-AANYSTIQTPESTGEPNN 1138  
1116 RQONRNTIEETGILAEARBSVSTEQLEIASRELEKAKM-AANYSTIQTPESTGEPNN 1175  
1139 MTLAEEARLAEHKEADDIRVAKTANETSABAYNLLRTLAGENQTALEIEELNRK 1198  
1176 MTLAEEARLAEHKEADDIRVAKTANETSABAYNLLRTLAGENQTALEIEELNRK 1235  
1199 YEQAENISODLEKQARVHEEAKGADKAVEIYASVQLTPVDSEALENEANKIKKEAAD 1258  
1236 YEQAENISODLEKQARVHEEAKGADKAVEIYASVQLTPVDSEALENEANKIKKEAAD 1295  
1259 LDRLTDQKLDYEDLREDMRKEHEVNKLEKGAEOQTADQLARADAKALAEBAEAKK 1318  
1296 LEQLTDQKLDYEDLREDMRKEHEVNKLEKGAEOQTADQLARADAKALAEBAEAKK 1355  
1319 GESTLOEANDILNKKDFDRVNDKTAABEALRRIIPAINRTIABANEKTRAEQALGNA 1378  
1386 GRDTLOEANDILNKKDFDRVNDKTAABEALRRIIPAINRTIABANEKTRAEQALGNA 1415  
1379 AADATEAKNAKAHEAERTASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1438  
1416 AADATEAKNAKAHEAERTASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1475  
1439 KRQDDADQDMMAGMASQAQAEAEIENARKAKNSVSSLLSQANLLDQGLDQDGLDQGLD 1498  
1476 KRQDDADQDMMAGMASQAQAEAEIENARKAKNSVSSLLSQANLLDQGLDQDGLDQGLD 1535  
1499 NEIEGSLNKADEMKASDLDRKVSDELSEARKQEAATMDYNRDIAEIIKDHNLEDKKT 1558  
1536 NEIEGSLNKADEMKASDLDRKVSDELSEARKQEAATMDYNRDIAEIIKDHNLEDKKT 1595  
1559 LPTCFNTPSIEKP 1572  
1596 LPTCFNTPSIEKP 1609

RESULT 7  
US-09-938-275-11  
; Sequence 11. Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE accession number: Swissprot P11047  
; DATABASE entry date: 1991-11-01

US-09-938-275-11  
Query Match 94.2%; Score 8034; DB 9; Length 1609;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1468; Conservative 56; Mismatches 48; Indels 2; Gaps 2;  
QY 1 AMDECADGGGQRCQRCMBEFVNAAFNVTVATNTCGTPEEYCVQTVGTGKTSCHLQDAG 60  
DB AMDECTDGGGRCQRCMBEFVNAAFNVTVATNTCGTPEEYCVQTVGTGKTSCHLQDAG 95  
QY 61 QOHLOHGAFAFTDYNQADTTWQSOQMLAGVQVPSNINLTLLHKGAFDITTVYRLKPHTS 120  
DB QPHLOHGAFAFTDYNQADTTWQSOQMLAGVQVPSNINLTLLHKGAFDITTVYRLKPHTS 155  
QY 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFINTGDEQOALCTDSEFDSPL 180  
DB RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFINTGDEQOALCTDSEFDSPL 215  
QY 181 TGGNVAFSTLEGRSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLSYYY 240  
DB TGGNVAFSTLEGRSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLSYYY 275  
QY 241 AISDPVAGGRCKMGHASECKVNEFDFKLMCNCKHNTYGVDCCKLPFFFNDRPWRRTAES 300  
DB AISDPVAGGRCKMGHASECKVNEFDFKLMCNCKHNTYGVDCCKLPFFFNDRPWRRTAES 335  
QY 301 ASECLPCDCNRSQECYFDPPELYRSTGHGHCCTNCRDNTDGAKECERCFNFRGLNTEAC 360  
DB ASECLPCDCNRSQECYFDPPELYRSTGHGHCCTNCRDNTDGAKECERCFNFRGLNTEAC 395  
QY 361 SPCHSPVGSLSQDSDYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSDPSSGSD 420  
DB SSCHSPVGSLSQDSDYGRCSCKPGVMGDKDRCPQGFHSLTEAGCRPCSDPSSGSD 455  
QY 421 CNVTGRCVKDQNVGECRCRCKPGFNLESNPKCTPCFCFHHSSVCTNAGVSVYDI 480  
DB CNVTGRCVKDQNVGECRCRCKPGFNLESNPKCTPCFCFHHSSVCTNAGVSVYDI 515  
QY 481 SSTQIODEGWRVQDQSGSEASLEWSDROYIAVSDSYPPRYFTAPVFLGNQVLSYQ 540  
DB SSTQIODEGWRVQDQSGSEASLEWSDROYIAVSDSYPPRYFTAPVFLGNQVLSYQ 575  
QY 541 NLSFSPVDRDRTRLAEADLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLEHATDVPW 600  
DB NLSFSPVDRDRTRLAEADLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLEHATDVPW 635  
QY 601 RPALSPPEFQKLLNLTISKIRGTYSERSAGYLDVTLQASAPPGVPATWYESTCTCPVG 660  
DB RPALSPPEFQKLLNLTISKIRGTYSERSAGYLDVTLQASAPPGVPATWYESTCTCPVG 695  
QY 661 YGGQFCETCLPGYRRTPSLGYPSPVLCCTCNHSETCDPCTGVCDCRDNTPAGHCEKCS 720  
DB YGGQFCETCLPGYRRTPSLGYPSPVLCCTCNHSETCDPCTGVCDCRDNTPAGHCEKCS 755  
QY 721 DGYIGDSTLGTSSDQPCPCPGSSCAIIVPKTVVTVHCTPTGTAGKRCCLCDDGYFGDP 780  
DB DGYIGDSTLGTSSDQPCPCPGSSCAIIVPKTVVTVHCTPTGTAGKRCCLCDDGYFGDP 815  
QY 781 LGSNGPVLRCPCQCNNDNDPNAVGNCRNLTCGLKCLYNTAGFYCDCKEGFCGNPLAP 840  
DB LGSNGPVLRCPCQCNNDNDPNAVGNCRNLTCGLKCLYNTAGFYCDCKEGFCGNPLAP 875  
QY 841 NPADKCKACACN-YGTVQOQSSCNVPTGQCCPLPHVSGRDCGTCDPGYNNYLOSQGGCERC 899  
DB NPADKCKACACN-YGTVQOQSSCNVPTGQCCPLPHVSGRDCGTCDPGYNNYLOSQGGCERC 935  
QY 900 DCHALGSTNGQDIRTGQCEQFGITGQHCERCETNHFHFGPEGCKPCDCHHEGSLQOC 959  
DB DCHALGSTNGQDIRTGQCEQFGITGQHCERCETNHFHFGPEGCKPCDCHHEGSLQOC 995  
QY 960 KDGRCCEGREGVGNRCQCEENYFVNSWPGCQCECPACRYLVKDKAAHRVKLOELES 1019  
DB KDGRCCEGREGVGNRCQCEENYFVNSWPGCQCECPACRYLVKDKAAHRVKLOELES 1055



Db 1176 MTLAEEAKLAERHQAEDDIIVRAKTANDTSTAYNLLRLTAGENTAFEIBELNRK 1235  
QY 1199 YEQAQNIISQLEKQAARVHEEAKRAGDKAVEIYASVAQTPVDSEALENEANKIKKEAAD 1258  
Db 1236 YEQAQNIISQLEKQAARVHEEAKRAGDKAVEIYASVAQSPDSETLENEANNIKWEABN 1295  
QY 1259 LORLIDOKLQVEDLREDWKGHEHEVKNLLEKKAECQOTADOLLAPADAALAEAAK 1318  
Db 1296 LEGLIDOKLQVEDLREDWKGHEHEVKNLLEKKAECQOTADOLLAPADAALAEAAK 1355  
QY 1319 GRSTLOEANDILNKLDFORRVNDNKTAABEALRRIPAINRTIAEANEKTBREAQALGNA 1378  
Db 1356 GRDTLOEANDILNKLDFORRVNDNKTAABEALRRIPAINRTIAEANEKTBREAQALGSA 1415  
QY 1379 AADATKAKHAERIASAQAQAEALNARKAKNSVSLLSQNLNLDLQGLDQGLDQGLDQGLD 1438  
Db 1416 AADATKAKHAERIASAQAQAEALNARKAKNSVSLLSQNLNLDLQGLDQGLDQGLDQGLD 1475  
QY 1439 KRQDDADQDMMWAGMASQAQAEALNARKAKNSVSLLSQNLNLDLQGLDQGLDQGLDQGLD 1498  
Db 1476 KRQDDADQDMMWAGMASQAQAEALNARKAKNSVSLLSQNLNLDLQGLDQGLDQGLDQGLD 1535  
QY 1499 NETEGSLINKAKDEMKASDLDKRVSDLESEARKQEAAMIDYNRDIAIIBKDIENLEDIKKT 1558  
Db 1536 NETEGTLINKAKDEMKVSDLDKRVSDLENEAKQEAAMIDYNRDIEBIMKDIRNLEDIRKT 1595  
QY 1559 LPTGCFNTPSIEKP 1572  
Db 1596 LPSGCFNTPSIEKP 1609

RESULT 9  
US-09-845-583-10  
; Sequence 10. Application US/09845583  
; Patent No. US200201429541  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-10

Query Match 42.1%; Score 3586; DB 9; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 3.6e-200;  
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;

QY 2 MDECADEGGRPQRMPBFVNAAFNVTVVATNTCGTPEEYCVGTGVTGKSHLDAQG 61  
Db 22 MGACYDAGRPQRCLPVFNAAFORLAQAGHTCGSPEDFCFHVGAAGAGAHQRCDAAD 81  
QY 62 QHLOHGAFLTDYNNQADTTWQSQTMAGVOYPSNLTLLHGLKAFDITYVRLKFTSR 121  
Db 82 QORHNASLYTDFHSQDESTWQSPSAFVQVQYPTSVNITRLRGKAYEITYVRLKFTSR 141  
QY 122 PESFAIKRTREDGFWIPYQYSGSCENTYSKANRGFIRGTGDEQQALCTDEFSDISPLT 181  
Db 142 PESFAIKRSADGFWPQYQYSGSCENTYSKANRGFIRGTGDEQQALCTDEFSDISPLS 201  
QY 182 GGNVAPSTLEGRPSAYNFESPGLOEWVTSTELLISLRLNTFGDDIFKDPKVLQSYYYA 241

Db 202 GGNVAPSTLEGRPSAYNFESPGLOEWVTSTELLISLRLNTFGDDIFKDPKVLQSYYYA 261  
QY 242 ISDFAVGRCCKNGHASECVKNKFDKLMCKNKNTYGVDCCKLPFFENDPWRATAES 301  
Db 262 VDSFVGRCKCKNGHASECVKNKFDKLMCKNKNTYGVDCCKLPFFENDPWRATAES 321  
QY 302 SECLPCDCNRGRSQCYPDPPELYRSTGGHGTCTNCRDNTDGAKECRERENFRLLNTEACS 361  
Db 322 HECLPCNCSGRSECTFDRELFRSTGGHGTCTNCRDNTDGAKECRERENFRLLNTEACS 381  
QY 362 PCHSPVGLSTQCDSTGRCCKPFGVMDKCDRCQPGFHSLSLTEAGCRPCSDCPSSGSDTEC 421  
Db 382 PCDCQASGLHLQCDTGTCAKPTVTGWKCDRLCPGHSLSSEGGCRPCTCNPAAGSDTC 441  
QY 422 NVETGRVCCKNVGFCNCRCKPGFFNLBSNPKGCTPCFCFHHSSVCTNAVGSVYDIS 481  
Db 442 DPRGRCPCKENVEGNLDCRCRPGTFLNPHNPAGSCSCFCYGHSKVCASATAQFQVHIL 501  
QY 482 STFOIDEDGWRVEORDSEASLEWSRQYIATVSDSYFFRYFTAPVKFLGNQVLSYQCN 541  
Db 502 SDFHQAEGMWARVGGSEHSPWSPN----GVLLSPEDEBELTAPGKFLGDQRFSGQGP 557  
QY 542 LSFSPRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYIFRLH---EATDY 598  
Db 558 LILTRVPDPSPLPVQ-LRLEGTGLALS--LRHSSLSGPQODASASQGGRAQVPLQETSE 614  
QY 599 PWRPALSPEFKLNNLNTSIKIRGYTSERSAG--YLDVTLQARPGPGVPAIWTESCT 656  
Db 615 DVAPPPLPFHFORLLANLTSRLRVSPGSPAGPVFLTEVLTSAEPGLSPASWVEICS 674  
QY 657 CPVGVGQFCETCLPGYRETPSLGYPVCLTCNGHSETCDPETGVCCDRDNTAGPHC 716  
Db 675 CPTGYTGQFCSCAPGYKREMPQGGPYASCVPCTCNQHG--TCDNTGTCVSHHTEGSPC 733  
QY 717 EKSDGYYGDTLGTSSDCQPCPCPGSSCAIIVPKTKXVWCHTCHPTGTAGKRCBLCDGY 776  
Db 734 RECLPGFYGNPFAGQADDQPCPCPGQSACTTIPESGEVWCHTCHPTGTAGKRCBLCDGY 793  
QY 777 FGDPLGNSGVRRLCRPCQCNNDNIDENAVGNRLTGCLKICVNTAGFYCDRCRGGPFGN 836  
Db 794 FGDPLGLFHFQPCQCHQCCQSGNVDFNAVGNCDPLSGHCLRLHNTTGDHCEHCEGFGVS 853  
QY 837 PLAPNPADKCKACACN-YGTVQQSSCNPNVTGQCCQLPHVSGRDCGTGDPGYNLQSQG 895  
Db 854 ALAPNPADKCMPCSCHPGQSVSEQWPCDPVTGQCSCLPHVTARDCSRCPYGFDFLQPGG 913  
QY 896 CERCDHALGTNGQCDIRTCQCCQPGITQHCERCETNHFHGFPGPECKCDCHHESGL 955  
Db 914 CRSCCKHPLGSOEDQCHPKTQCTCRPGVTQACDRQOLGFGFSSIKGCRACRCSPLGAA 973  
QY 956 SLQCKDDGRCREGEFVGNRCDOCEENFYNRSWPGQCEPCACVRLVKDKAAEHRVKLOE 1015  
Db 974 SAQCHYNGTCVCRPGFEGYKCDRCHYNEFLTDGTHCQCCPSCYALVKEETAKLKARLTL 1033  
QY 1016 LESLIANLGTGD----DMVTDQAFEDRLKAEAREVTDLLREAEVQKDVQDNLMDRLQV 1070  
Db 1034 TEGMLQSGDCGSPWPLDILLGEAPRGDVYQGH-----LLPGAREA-----FLEQMGL 1083  
QY 1071 NSSLSQJSLRQNTENTTEETGILAEARSRSVESTQLEIETASRE-LEKAKVANVSITQ 1129  
Db 1084 EGAVKAAEQLQRLNKGARCAQAGSKTCTQADLEAVLESSEBEILHAAALSLAIPQ 1143  
QY 1130 PESTGEPPNMTLLAEARSLAEHRKQEAADDIVRVAKTANETSABAYNLLTLAGENTOTA 1189  
Db 1144 -EGPSQPTKWSHLATEARALARSHRDTATKIAATAWRALLASNTSYALLWNL--EGRA 1200  
QY 1190 LEIE-ELANKYEQAKNIISQDLEKQAAVHEBAKAGDKAVIYASVAQ----- 1237  
Db 1201 LETQDLEDREYQVQEAQAALRTAVAEVLPBAE-----SVLATVQVQADTAPYLL 1253  
QY 1238 -----TPVDSEA--LENEANKIKKEAADLRLIDQKLXDYEDLRE-DMRGKEHEVKNLLE 1289  
Db 1254 ASFGALPQKSRADLGLKAKALEKIVASQWQHMATEAARTLQTAQAATLRQTE---PLTWA 1310

QY 1290 KGKAEQOTADQOLARADAALAEBAEAAKGRSTLOEANDILNKLKDFDRVNDNKTAABE 1349  
Db 1311 RSRLTATFASQHOAGABAALTOASSVQAATVTVMGARTLLADLEGMKLQFFRPKQQAAL 1370  
QY 1350 ALRIPAINRTIAENKTRTQALALGNAADATEAKVKAHAERTASAAQKNATSTKAD 1409  
Db 1371 QRKADSVSDLLADTRKTKQAEMLGNAAPLSSAKKGRGAEVLAQDSAKLAKALLRE 1430  
QY 1410 AERTFGEVTDLONEVNGMLRQL-EEAENELRKQDDADQDMMAGMASQAQAEINARK 1468  
Db 1431 RKQARBRASRLTQOTATLOQASQOVLASAEARQEEAEAEVAGJLS-----EMEQQIRE 1485  
QY 1469 AKNSVSSLLSOLNLLDOLGOLDT--VDLNLKNEIEGSLINKAKDEM-KASDLDRKVSULE 1525  
Db 1486 SRISLEKDIETLSLLARLSLTHQAPALNETQWALERLELQLGSPGSLQRLKLSLE 1545  
QY 1526 SEARKQAAIMYNDNRDAEIKIHNLEDIKKTLPTGC 1563  
Db 1546 QESQOQELQIGFESDLAERADKQNLLEAILHSLPENC 1583

RESULT 10  
US-10-262-839-210  
; Sequence 210, Application US/10262839  
; Publication No. US20040038877A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, John,  
; APPLICANT: Anderson, David W.,  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Burgess, Catherine,  
; APPLICANT: Catterton, Elina,  
; APPLICANT: Edinger, Shomit,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Guo, Xiaojia,  
; APPLICANT: Ji, Weizhen,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Leach, Martin,  
; APPLICANT: Li, Li,  
; APPLICANT: Miller, Charles,  
; APPLICANT: Patturajan, Meera,  
; APPLICANT: Reiger, Daniel,  
; APPLICANT: Rothenberg, Mark,  
; APPLICANT: Shimkets, Richard,  
; APPLICANT: Smithson, Glenada,  
; APPLICANT: Spytek, Kimberly, jr.,  
; APPLICANT: Taupier, Raymond,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Voss, Edward,  
; APPLICANT: Zerhusen, Brian,  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-462A  
; CURRENT APPLICATION NUMBER: US/10262,839  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,029  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,056  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/381,101  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/371,972  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/327,342  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/328,044  
; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/374,738  
; PRIOR FILING DATE: 2002-04-23  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 210  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-839-210

Query Match 42.1%; Score 3586; DB 12; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 3.6e-200; Indels 72; Gaps 23;  
Matches 700; Conservative 258; Mismatches 568;

QY 2 MDECADEGGRPQRCMPPEFVNAAPNTVATNTCGTPPEEYCVQGTGVTGWSCHLCDAQ 61  
Db 22 MGACYDGAQRPCRLPVENAFAFRLAQASHTCGSPPEDFCFHVGAAGAGAHQRCDAAD 81  
QY 62 QHLQHGAAFLTDYNNQADTTWQSTMLAGVQYPSNLTLLHLGKAFDITYVRLKPHTSR 121  
Db 82 QORHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLLKRAYEITYVRLKPHTSR 141  
QY 122 PESFAIYKRTREDGPMIYYQYSGSCENTYKXANRGFIRTCGDEQQALCTDFSDISPLT 181  
Db 142 PESFAIYKESRADGPMIYYQYSGSCENTYKXANRGFIRTCGDEQQALCTDFSDISPLT 201  
QY 182 GGNVAFSTLEGRPSAYNFNSPVLQEWYATDITVTLNRLNTEGDEVNDPKVLKSYTAA 241  
Db 202 GGNVAFSTLEGRPSAYNFNSPVLQEWYATDITVTLNRLNTEGDEVNDPKVLKSYTAA 261  
QY 242 ISDFAYGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATASEA 301  
Db 262 VSDFSVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATASEA 321  
QY 302 SECLPCDCKNGRQOBYDFDELYRSTGHGCHCTNCRDNDGAKCERCFNRLGNTAACS 361  
Db 322 HECLPCNCSGRSECTFDELFRTSTHGRCHCHDHTAGPHCERCQENFYHNPMPQ 381  
QY 362 PCHSPVGSLSLTCDSYGRCSCKPQVMGDKDRCPQPHSLTEACRPSCDPSGSTDEC 421  
Db 382 PCDCQASGSLHLQCDTGTGACKTPTVTGKWCRCRLPGFHSLSSEGGRCPCPCNPAGSLDTC 441  
QY 422 NVETGRVCCKDNVEGFCNCRKPGFNLESNNPKCTPCFCFGHSSVCTNAGVSVYDIS 481  
Db 442 DPRSGRCPCNVEGNLDCRCRPGTFNLPQHPNAGCSCFCYGHSKVCASTAQVHHIL 501  
QY 482 STFOIDEDGRVQORDGSEASLEWSSDRQYIAVISDSYFPYFTAPVKFLGNQLSYQON 541  
Db 502 SDPHQAGWARSVGGSEHSPQNSPN----GVLLSPEDEBELTAPGKFLGDRFSYQGP 557  
QY 542 LSPSPRVDRDRRLGAEDLVLEGAGLRVSVPLIAQGNYSYPSSETTVKIFRLH---EATDY 598  
Db 558 LILTFRVPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDARASQGRAPVLOETSE 614  
QY 599 PWRPALSPEPFQKLNNTSIRKIRCTYERSAG--YLDVTLQASRPGPGVPAWVESCT 656  
Db 615 DVAPPLPFPFHFORLLANTLSLRVSPGSPAGPVFLTEVRLTSARPLSPSPASWVEICS 674  
QY 657 CPVGVGGQFCETCLPQYRRETPSLGYPSPCVLCTCNHSETCDPETGVDCDRDNTAGPHC 716  
Db 675 CPTGYTGQFCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDPNTGLCVCSHTEGSPC 733  
QY 717 EKSDGYGDSYLTGTSDDCPCPCPGSSCAIVPKTKHVVCTHCTGTGTAGKRLCDDGY 776  
Db 734 ERCLFGFYGNPPAGQADDCQPCFCGQSGACTTIPESGEWCTHCPGQGRRCRVCDDGF 793  
QY 777 FGDPLGSGNPFVRLCRPCCNNDNDPNAVCNRLTGECLKCIYNTAGYCDRCCKGFFGN 836  
Db 794 FGDPLGLFGHPQPCQCCQCSGNVDNAVNCNDPLSGHCLRLCHNTTGDHCEHCQEGVGS 853

QY 837 PLAPNADYCKKACACN-YGTVOOQSSCNVPTGQCQCCLPHVSGRDCGTCDPGYNNLQSGQ 895  
Db 854 ALAPNADYCKKACACN-YGTVOOQSSCNVPTGQCQCCLPHVSGRDCGTCDPGYNNLQSGQ 913  
QY 896 CERCDHALGNGQCDIRGTGCEQPGITGQHCECETNHFPGPEGCKPCDCHHEGSL 955  
Db 914 CRSCCKHPJGSEBQCHPTGCTCRPGVTGACDRQCQLGFGSSIKGCRACRCSPLGAA 973  
QY 956 SLQCKDDGCECREGFGVNRCDQCEENYPYNSWFGCECPACYRLVKDKAAHEHVKLOE 1015  
Db 974 SAQCHYNGTCVCRPGEGYKCDRCHYCNFFLTADGTHCQCPCSYALVKEETAKLRLTL 1033  
QY 1016 LESLIANLTGD-----DMVTOQAFEDRLKEAREVTDLLREAQEKVDQVQNLMDRLQV 1070  
Db 1034 TEGWJGSCGSPGWLILLGEPAGPDVYQGH-----LLPGAREA-----FLSQMGL 1083  
QY 1071 NSLSHSQISRLQNRINTIETGILAEARSRSVESTQEOLIEIASRE-LEKAKAAVNSITQ 1129  
Db 1084 EGAVKAAREQLQRLNKGARCAQAGSQTCTQLADLEAVLESSEEEILHAAATLASLEIPQ 1143  
QY 1130 PESTGPNWMTLLAEARLARERHKEADDIYRVAKTANETSAEYNLLRLTAGENQTA 1189  
Db 1144 -EGPSQFTKWSHLAEARALARSHRDATKIAATAWRALLASNTSYALLWNL--EGRVA 1200  
QY 1190 LEIE-ELNKRKYQAKNISQLEKQARVHEEAKRAGDKAVEIYASVAQL----- 1237  
Db 1201 LETQRLDEBYQEVQAAQKALTAVAEVLPEAE-----SVLATVQVGDATPYLALL 1253  
QY 1238 -----TPVDSEA--LENEANKIKKEADLDRLIDQKLKDYEDLRE-DMRGKEHEVKNLLE 1289  
Db 1254 ASFGALPQKSRABDLGKAKALEKTVASQHWATEARTLQTAQAATLRQTE---PLTWA 1310  
QY 1290 KGAEQQTADOLLARADAALAEAAKGRSTLQEAANDILNNLKDFFRRVNDNKTAAEE 1349  
Db 1311 RSLTATFASQLHCGARALTOASSSVQATVTVMGARTLLADLSGKMLQFFRPKQAA 1370  
QY 1350 ALRRIPAINTTAEANEKTRQAALGNAAADATEANKKAHAERIAASAAQKNTSTKAD 1409  
Db 1371 QRKADSVSDELLADTRKTKQAERMLGNAAPLSSSAKKKGREAEVLAKDSAKLAKALLRE 1430  
QY 1410 AERTFCEVDLDNEVNGMLRQL-EEAENELKRDQDADODMMAGWASQAAQAEELNARK 1468  
Db 1431 RQKHRRARSLTSQTAQLQASQCVLASEARQEELEAEERVQAGLS-----EMEQQIRE 1485  
QY 1469 AKNSVSLLSQNLNLDQLDQDIT--VDLNKLEIEGSLINKADEM-KASDLDLRKVSLE 1525  
Db 1486 SRISLEKDIETLSSELLARLSLDTHQAPAAQALNETQWALERLRLQLGSPGSLQKLSLLE 1545  
QY 1526 SEARKQERAIMDYNRIADIIKDIHNLIEDIKTLPTGC 1563  
Db 1546 QESQOQELQIQGPESDLAEIRADKQNLZAILHSLPENC 1583

RESULT 11  
US-10-262-839-212  
; Sequence 212, Application US/10262839  
; Publication No. US20040038877A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook, John,  
; APPLICANT: Anderson, David W.,  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Burgess, Catherine,  
; APPLICANT: Catterton, Elina,  
; APPLICANT: Edinger, Shlomit,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Guo, Xiaojia,  
; APPLICANT: Ji, Weizhen,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Leach, Martin,  
; APPLICANT: Li, Li,  
; APPLICANT: Miller, Charles,

; APPLICANT: Patturajan, Meera,  
; APPLICANT: Reiger, Daniel,  
; APPLICANT: Rothenberg, Mark,  
; APPLICANT: Shimkets, Richard,  
; APPLICANT: Smithson, Glennda,  
; APPLICANT: Spytek, Kimberly,  
; APPLICANT: Taupier, Raymond, jr.,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Voss, Edward,  
; APPLICANT: Zethusen, Brian,  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.  
; FILE REFERENCE: 21402-462A  
; CURRENT APPLICATION NUMBER: US/10/262,839  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,029  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,056  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/381,101  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/371,972  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/327,342  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/328,044  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,849  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/374,738  
; PRIOR FILING DATE: 2002-04-23  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 212  
; LENGTH: 1575  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-839-212

Query Match 42.0%; Score 3583; DB 12; Length 1575;  
Best Local Similarity 44.3%; Pred. No. 5.3e-200;  
Matches 704; Conservative 249; Mismatches 570; Indels 66; Gaps 23;

QY 2 MDECADEGGPQRCMPBEFVNAENVTVAINTCTGPPEEYCVQTVGTGKSHLCDAGQ 61  
Db 22 MGACYDAGRPQRCPLPVFENAAFGRLAQASHTCGSPEDFCPHVGAAGAGAHQRCDAAD 81  
QY 62 QHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVYPSNINLTILHLGKAPDITVRLKFTSR 121  
Db 82 QRHHNASYLTDFHSQDESTWQSPSMAFGVQVPTSVNITRLGKAYEITVRLKFTSR 141  
QY 122 PESTAIYKRTREDGPMIPYQVYSGSCENTYKANKRGFIRTTGGDBEQOALCTDEFSDISPLT 181  
Db 142 PESTAIYKRSRADGFWPEYQVYFYSACQKTVRPGQVLRPGEDERVAFTSEFSDISPLS 201  
QY 182 GGNVAFSTLEGRPSAYNFDSNPSVLQEWVTATDIRVTNLRNLNTFGDEVNPNKVLKSYIA 241  
Db 202 GGNVAFSTLEGRPSAYNFDSNPSVLQEWVTSTELLISLRLNTFGDDIFKDPKVLQSYIA 261  
QY 242 ISDFAVGRCCKNGHASECVKNEFDKLMCKNKNYGVDCBKLPFFENDRWRRAEASA 301  
Db 262 VSDFSVGRCCKNGHASECGPDVAGLACRCQHTTGTDCERCCLPFFQDRPWARGTAA 321  
QY 302 SECLPCDCNGRSQECYDFDPELYRSTGHGGHCTNCRDNTDGAKCRCRCRNFRLNGTEACS 361  
Db 322 HECLPCNCSGSEECTFDFELFRSTGHGRCRCHCRDHTAGPHCERCQENFYHWDPRMPCQ 381  
QY 362 PCHCSFVGSLSLTQDSYGRCSCKPFGWMDKDCRCQPGFHSLTEAGCRFCSGSDSTDEC 421

Db 382 FDCQSSAGSLHLCDDDTGTCACTVTGTGKDCRCLPGLFSLSEGGCRPCTCNFAGSLDTC 441  
Qy 422 NVETGRVCVKNVGEFNCERCKPGFNLESSNPKGCTPCFCGSHSSVCTNAVGSYVDIS 481  
Db 442 DPRSGRCPCXENVGNLDCRGTGNLPHNPAGSCSCFCYGHKVCACSTAPQVHIL 501  
Qy 482 STQIDEDGWRVQRDGSSEASLEWSDRQVIASVDSYFPRFVIAFVPLGQVLSYQGN 541  
Db 502 SDPHQGAEGHWARSVGGSEHSPQWSPN---GYLLSPDEDEBELTAPGKGLDGRFSYQGP 557  
Qy 542 LSFSTRVDRDRLSLAEDLVLEGAGLRVSLPLAQNYSVPSETTVKVIPLHLH---EATDY 598  
Db 558 LILTRFVPPGDSPLVQ-LLESTGLALS--LEHSSLSPQPARASQGRAGVPLQETSE 614  
Qy 599 FWPALSPFPFQKLLNNLTSIKIRGTYSERSAG--YLDVTLQSRAPGPGVPATWVSECT 656  
Db 615 DVAPPLPPFPFQKLLNNLTSIRLURVSPGSPAGPVLTEVRLTSARPGLSPASVVEICS 674  
Qy 657 CPVGYGQGCETCLPGVRRTPSLGYPSPCLCTCNHSETCDPBTGVCDCRDNATAGPHC 716  
Db 675 CPTGYTGQFCESCAPGYKREMPGGYASVPCCTCNQHG--TCDPNTGICVSHRTEGSC 733  
Qy 717 EKSDGYGSDSTLGTSSDQPCPCPGSSCAIVPKTKVCTHCTGTAGKRCCLDDGY 776  
Db 734 ERLCPGYGNPFAQADDQPCPCPGQSACTTIPESGEVVCVCHCPGQGRRCCEVDDGF 793  
Qy 777 FGDPLGNSGVRLCRPCQNDNDPNAVGNCRNLTCGLKCTIYTAGFYCDRCRKGPPGN 836  
Db 794 FGDPLGLFHPQCHQOCQSGNVDPNAVGNCPFLSCHCLRLNHTGTGHCHECBGFGS 853  
Qy 837 PLAPNPADKCAKACN-YGTVOQSSCNVPTQCCLPHVSGRDCGTCDPGYNLQSQG 895  
Db 854 ALAPNPADKCMPCSCHPQGSVSEMPCEPVTQCCCLPHVTARDCSRCPYGFDFLQPGRG 913  
Qy 896 CERCDCHALGSTNGQCDIIRTCQCECOPGITGQHCERCETNHFGEFGPECKPCDCHHEGL 955  
Db 914 CRSCKHPLGSEDQCHPKTGCTCRPGVTGACDRCLGFGSSIKGRACRCSPLGAA 973  
Qy 956 SLOCKDDRCCEGREGVGNRCQCBENFYNRSWFGQCEPCACVLYLVDKAAERHVKLQE 1015  
Db 974 SAQCHYNGTCVCRPGFEGYKCDCHYNFFELTADGTHCQCCPSYALVKEETAKLKAULTL 1033  
Qy 1016 LESLIANLGTGD---DMVTDQAFEDRLKEAREVTDLLREAOBVKDQDNLMDRLQV 1070  
Db 1034 TEGWLOGSDCGSPWGLDILLGEAPRGDYYQGH---LLPGAREA-----FLEQWGL 1083  
Qy 1071 NSSLSQISRLQNRNITBETGILAEARSERVESTEQLIEIASRE-LEKAKMAANVSITQ 1129  
Db 1084 EGAVKAAREQLQRLNKARGACAQAGSQKCTQLADLEAVLESSEEBEILHAAAILASLETPQ 1143  
Qy 1130 PESTGPNNTLLAEERLAEARHKEOADDIVRVAKTANETSABAYNLLLATLAGENOTA 1189  
Db 1144 -EGPSQPTKWSHLAIEARALARSHRDTATKIATAWRALLASNTSYALLNLL--EGEVA 1200  
Qy 1190 LEIE-EINKRYEQAQKNIQDLKQVYEDUREDMRKEHEVKNLLEKGAEOOTADQ--- 1244  
Db 1201 LETQDLEDRYOEVAQAKALATAVAEVLPEAE-----SVLATVQVQADTAPYLL 1253  
Qy 1245 LENEANKIKKEAADRLDQKLKQYEDUREDMRKEHEVKNLLEKGAEOOTADQ--- 1300  
Db 1254 ASFGALPQKSRADL---GLAKALEKTVAHQWMAFEARTLQ--TAAQATLQTEPL 1307  
Qy 1301 --LLARADAKALAEBAKKGSTSTQANDILNLIKOFDRRVNDNKTAAEBALRRIPAIN 1358  
Db 1308 TKLHQEARAALTOASSVQAATVTVNGARTLLADLEGKMLQPPRPKDOAALQKADSVSD 1367  
Qy 1359 RTIAENAKTREAOALGNAADATKAKNAHEARERIASAQKQATSTPKAAERTFGEVT 1418  
Db 1368 RLADTFTKTKQAEKRLGNAAPLSSAKKKGAEAVLAKDSKLAKALLERKQARRAS 1427  
Qy 1419 DLNENVGMLRQL-EBAENELKRRQDDADQDMMAGMASQAQAEALNARKAKNSVSSL 1477

Db 1428 RLTSQATLQOASQOVLASEARROELBEAERVGAGLS-----EMEQQIRSRISLEKDI 1482  
Qy 1478 SOLNNLLDOLGOLDT--VDLNKLNIEGSLNKADEM-KASDLDRKVDLSEARKQEA 1534  
Db 1483 ETLSSELLARGLSLDTHQAQAALNTQWALERLQLQSPGLQRLKLSILEQESQOQELQ 1542  
Qy 1535 IMDYNRDIAIILKIDHNLEDIKKTLPTGC 1563  
Db 1543 IQGFESDLAEIRADKONLEAILHSLPENC 1571

RESULT 12  
US-10-369-493-6816  
; Sequence 6816, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6816  
; LENGTH: 1557  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6816

Query Match 37.4%; Score 3193; DB 15; Length 1557;  
Best Local Similarity 38.2%; Pred No. 2,9e-177;  
Matches 626; Conservative 289; Mismatches 543; Indels 180; Gaps 30;

Qy 5 CADEGR-PQRCMPBFVNAAFNVTVVATNTGTP-PREYCVQTVGTGVTXSKHLCDAQQ 62  
Db 25 CYDRATPQRCVDFVNAAFNVTVVATNTGTP-PREYCVQTVGTGVTXSKHLCDAQQ 84  
Qy 63 HLQGAFTLVNNQADTTWQSTMLAGVQPSINLTLHLKAFDITVRLKFTSRP 122  
Db 85 GFSHPAKYLTDFVNNQADTTWQSTMLAGVQPSINLTLHLKAFDITVRLKFTSRP 144  
Qy 123 ESFAIYKRTREDGPWIPYQYYSGCNTYKANKRGFTTGGDEQOALCTDEFSISPLTG 182  
Db 145 ESFTIYKRTREDGPWIPYQYYSGCNTYKANKRGFTTGGDEQOALCTDEFSISPLTG 203  
Qy 183 GNVAFSTLEGPSAYNFNSPVLQSVTATDIRVTLNRLNTFGDEVNDPKVLKSYVYAI 242  
Db 204 GNIAFSTLEGPSAYNFNSPVLQSVTATDIRVTLNRLNTFGDEVNDPKVLKSYVYAI 263  
Qy 243 SDFAVGGRCKNGHASECVKNEF---DKLMCNKNTYGVDCBKCLPFPNDPWRATA 296  
Db 264 SDFAVGGRCKNGHASECVKNEF---DKLMCNKNTYGVDCBKCLPFPNDPWRATA 323  
Qy 299 ESASECLPCDNGRSGQCYFDPPELVRSYTHGCHCTNCRDNTDGAKECRKRENFRLNTE 358  
Db 324 VZANECLACNSQLSNRCYFQQLFEETHGCHCTNCRDNTDGAKECRKRENFRLNTE 383  
Qy 359 ASPCCHCPVSGSLSTQDSYGRCSCKPGWMDKDRQCPGFHSLTEAGCRPCSDPGSGT 418  
Db 384 YCVACGCGNEISLSTQDSYGRCSCKPGWMDKDRQCPGFHSLTEAGCRPCSDPGSGT 443  
Qy 419 D---ECNVETGRVCKDNGVGFNCERCKPGEFNLESSNPKGCTPCFCGSHSSVCTNAVGY 475  
Db 444 KNPQRCDSGSSGSCSKLVNVEGRQCKKPGYFDLSTENQFGCTPCFCGSHSSVCTNAVGY 503  
Qy 476 SYDTSSTFQIDEDGWRVQRDGSSEASLEWSDRQVIASVDSYFPRFVIAFVPLGQVLSYQGN 535

Db 504 FAMVSSVFDQDKQKWAQONRIGLO-DTQWAEADKAVAVSDTNSPVVFAVPEQFLGDQR 562  
QY 536 LSYQNLSFSFRVDRDRRLSAEDLVLEGAGLR-VSVPLIAQNSYSESTTVKVIIFRLHE 594  
Db 563 SSYNQDLVFTLKAVHVTNODVKDIIIVGADRQELSTITAQGNPPFTTEAQYRFRVHA 622  
QY 595 ATDYPWRPALGFFBPKLNNLNTSKIRGTYSERSAGVLDVTLQSAARPGV-----PAT 650  
Db 623 DPFQWYPRINELDFIGILSNITAIKIRGTYSYKIDIGYLSVNLGTAGVAPSANPKQAT 682  
QY 651 WVESCTCPVGGGFCETCLPGYRETPSLGYPSPVCLCTCNHSETCDPPTGVCDPDRDN 710  
Db 683 WIEHCECLPGFVGQFCESCEGFRRETKFGGPFNHCIKCDCHNSCSAEASGSCIEHN 742  
QY 711 TAGHCEKCSGYGDSLTGLTSSQCPGSSCAIVPKTKVWCTHPTGACRCS 770  
Db 743 TAGDTCERCAGYGDALQGTTEOCQKCPENDGFC-ILHAGDVICTECPNGYTGRRCD 801  
QY 771 LCDDGYGDPGLSGNPVRLCRPCQCNNDNIDPNVAGNCNRLTGCLKCIYNTAGFYCDRCK 830  
Db 802 ECSDDGYGNPKDGTG---CVCACSGNTDPSNGCDKITGCKKCIYNTAGFYCDRCK 857  
QY 831 EGFGNPLAPNPAKCKACACNYCTVQOQSS-----CNPTGOCCLPHVSRDGTCD 884  
Db 858 PFGYGDALI-BPKNCSCGCGFAAGTRRPNNDYTLLECNDQDQCCDCLPNVIGIQDQCA 916  
QY 885 PGYNLSQGCRCRCDHALGSTNGQCDIRTGQCEQCPGIGTGHCRCETNHFQFEGC 944  
Db 917 HGFYNTISGLQCECNCNDPLGSEGTCDVNTGQCKQKPGVTGQRCDCRCDYHFGPSANGC 976  
QY 945 KPCCHHEGSLLOCK-DDGRCCEGFGVNRDCEENYFYNRSWPGCOECPACVRLVK 1003  
Db 977 QPCCEVIGSNQCDVNSGQCLCKENVEGRDQCAENRY---GITQGLPDDCDVTLQ 1034  
QY 1004 DKAHEHVKLESLIANLGTGDMVTDOAFEDRLKEAPREVTDLREA-QEVKDVQON 1062  
Db 1035 SRVNVFEKVKSLDNTLQETIENPAPVNDTKFEKVKETSRASAEVWAVKQTKEGGT 1094  
QY 1063 LMDRLQVNSLSHQSISLQNIENRTIETGILAEARSSEVEQLEIASREL----- 1116  
Db 1095 IKTSKAIKDEIVAALEKLSIDESAQAKGADAENDKRWEIIEIENARIEENLVH 1154  
QY 1117 -----EKAKVAAVNSTIPESTGEPN-NMTLAEAPKLAERHKEADDIRVAKTANE 1169  
Db 1155 LETEGERAQTAVNAS---QKYGEQSKMSSELASGTREBAEKHLQKASEIQLSEQAIA 1210  
QY 1170 TSABAYNLLFTLAGENQTALETELNRKYEQA-KNISQDLEKQARVHEBAKQAGKAV 1228  
Db 1211 NATQANKESDAIYGGGQISQIAELKEKQONQUNESIHTLD-----LAEQKKSADAN 1265  
QY 1229 EIYA-----SVAQLTPVDSEALENANKIKKEAADLRLIDQKLD---YEDLREDMRG 1279  
Db 1266 NLAAVSLTNVEAVKIPSPDKELRNDVAGVLES---ENLVDSSVKENSANDELFDVNR 1322  
QY 1280 KEHEVKNLLEKGAEOQTADQLARADAALAEAAKGRSTLQEBANDILNMLKDFDR 1339  
Db 1323 SVADARNELSSQDQKVSQDLMELEKSKRERIVDSVSTADTKLDAEAALQVLEFGAK 1382  
QY 1340 VNDNKTAAEALRIPAINR---TIAEANEKTR-----BAQALAGNAAD 1381  
Db 1383 IEKSRNDVAFAGVEGQINQRLDDIIDAOQKRNLSLPDKQFVIDYRKSADVLLNETHAL 1442  
QY 1382 ATEAKNAHEARITASAQKQAT-STKADAERTFGEVTDLDNEVNGMLRQLEAEENELK 1440  
Db 1443 ADYKDIH-----SDVDFRDSSTEAVQYDIEQLMEBLTDSNENL-----QYK 1485  
QY 1441 QDDADQDDMMAGWASQ-----AAQAEELNARKAKNSVSLLSQLNLLQQLQDVT 1493  
Db 1486 KOAEDDKQMAATEAVRKQLLPRIPLFSKQMLPFLSRKMKRSKSLWL----- 1532  
QY 1494 DLNKLNIEGSLNKADEMKASDLDRKVSLESEARKQEAATWYNDRIAEIIKDHNLE 1553  
Db 1533 -----NLE 1535

QY 1554 DIKKTLPFGFNTSPSIEK 1571  
Db 1536 EIRNMLPTKCFNVINLEQ 1553

RESULT 13

US-10-392-113-14  
; Sequence 14, Application US/10392113  
; Publication No. US20030224993A1  
; GENERAL INFORMATION:  
; APPLICANT: Land, Hartmut  
; APPLICANT: Deleu, Laurent  
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION  
; TITLE OF INVENTION: OF CANCER CELLS  
; FILE REFERENCE: 21108.000503  
; CURRENT APPLICATION NUMBER: US/10/392,113  
; PRIOR FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: 60/365,078  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: PCT/US01/32127  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/239,705  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-392-113-14

Query Match 30.4%; Score 2592; DB 12; Length 1193;  
Best Local Similarity 39.1%; Pred. No. 2-2e-142;  
Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;  
QY 284 CLPFFNDPWRRTAESAECPLPCDNGRSQSCYDPPELYRSTGHGHTNCRDWTGAK 343  
Db 9 CLCFSLLPAARATSRRE---VDCNGKSRQCFDEHLRQTGNGFRCNLCNDNTDGIH 64  
QY 344 CERCENPFFRLGNTACSPCHSCVLSSTQCDSDYGRCSKPGVMDKCDRCQPGFHSIT 403  
Db 65 CEKCKNGFYHREDRCLPCNCKNGKLSARCDNSGRCSCKPGVTGARCDCLPFGHMLT 124  
QY 404 EAGC-----RPSCDPSGSDTDECNVETGRCVCKDNVVEGNCRCRKPFGFNLESSNPK 455  
Db 125 DAGCTQDQRLLSKDCDPAIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGGNPE 182  
QY 456 GCTPCFCFGHSSVCTNAVGSYVDISSLTFOIDEGWVEQRDGSASLEWSSDRQYIAVI 515  
Db 183 GCTCCFCYGHSSASCRSSAEYSVHKITSTFHQDVQKAVQNRGSPAKLQWSRQHQDVFS 242  
QY 516 SDSYFRYFIAPVKFIGNQVLSYQNLGSLFSPFRVDRDRRLSAEDLVLEGAGLRVSVPLIA 575  
Db 243 AQRLDVPYFVAPAKFLGNOQVSGQSLSPDYRVDRGRHPSAHVDILEGAGLRITAPLMP 302  
QY 576 QGNSYSESTTVKYPRLHEATDYPWRPALSPPEFQKLNLTSTIKIRGTYSERSAGYLD 635  
Db 303 LGKTLPCGLTKYTYFLNNEHPSNWSPOLSYFEYERLLNLTALIRATYGEYSTGYDN 362  
QY 636 VTLOSARPGFVPATWBSCTCPVGYGGQFCETCLPGYRRETPSLGYPSPVCLTCNHS 695  
Db 363 VTLSARVSGAPAPVMEQICIPVGYKGFQCDASGYKRSARLPGPFGTCIPCNQCG-G 421  
QY 696 ETCDPBTGVCDCRDNATAGPHCKCSGDYGYGSTLTGTSDDCQPCPCPGSSCAIVPKTKEV 755  
Db 422 GACDPTDGCYSGDENPDIECADCPIGFYNDP--HDPKRCPCPCCHNGFSCSVMPTEV 479  
QY 756 VCTHCTPTAGKRCCLCDDGYEGDPLGSGNVPRLCPCQCNNDNIDPNVAGNCNLTGEC 815



480 VCNPCPGVTGARCCELADGDFGDPFGHGPVVRPQPCQCNVNNVPSASGNCRLTGRCL 539  
QY 816 KCIYNTAGFYCDRCCKGFFGNPLAPNADKCKACACNYGTVOQSSCNPTVGOCCLPHV 875  
Db 540 KCIHNTAGIYCDQCKAGIFGDFPLAPNADKCRACN 576  
QY 876 SGRDGTGDPYNYNLOGGOCERCDCALGSTNGQCDIRTGQCEQPGITGQHCHERCETN 935  
Db 577 576  
QY 936 HFGFGPEGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCQCEENYFYNRSWPGQCEC 995  
Db 577 576  
QY 996 PACYRLVKDAAEHRVKLOELESILIANLGTGDMVTDQAFEDRLKEAREVTDLLREAOE 1055  
Db 610 PACYNOVKIQMDQFMQOLQORMEALISKAQGGGVDPDTELEGRMQQAQALQDILDAQI 669  
QY 1056 VKDQDQNLMDRLQVNSLSHSQISRLQNTIETGILAEARARSVESTQLIEIASRE 1115  
Db 670 SEGASRSLGLQAKVRSQENSQSRLLDDUKMIVRVALGSQYQNRVDRTHRLITQWOLS 729  
QY 1116 LERAKMA-ANVSTQPESTGEPNNMTLLAEAEARLAEHRKQADDIRVAKTANETSABE 1174  
Db 730 LAESEASLGNITNIPASDHYVGNPKSLAQEAETRLAESHVESASNMQLTRETEDYSKOA 789  
QY 1175 YNLLRLT-----AGENQTALEIEELNRKVEQAKNISQDLERKQAAEVHEEAKRAGDKA 1227  
Db 790 LSVLRKALHEGVSGSGSPDGA-VGLVKELEKYSQAQQTREATQAEIADRSYQHS 848  
QY 1228 VEIYASVAQITPVDSPALE-NEANKIKKEAADLBDLQKLDYEDLREDMRGKEHEVKN 1286  
Db 849 LRLDSVSLQGVSDQSFQVEEAKRIKQKADSLTLVTRHMDFFKRTOKLGNKKEEAAQ 908  
QY 1287 LLEKGAEOCTDOLLARADAALAEAEAAKKGSTLOEANDILNNLKDFFRRVNDNKA 1346  
Db 909 LLONGKSGREKSDQLSRANLAKSRAQEALEFVEVESILKNLREFDLQVNDKAE 968  
QY 1347 ABEALRIPAINRTIAANEKTRQAQLAGNAAADATKAKNAHEAEIASAAQNAIST 1406  
Db 969 ABEAMRLSYISKVSDASDKTQQAERALGSAADAQAKXGAGEALEISIEBQETGSL 1028  
QY 1407 KADAERTFGEVTDLDNEVNGMLRQLEAEENEUKRKQDDADODMMAGVASQAQAEALNA 1466  
Db 1029 NLEANTADGALAMEGLASLASEMREVEGELELEFEDNMDAVQVMTAEAKVDTA 1088  
QY 1467 RKAKNSVSLLOQLNLLDQLQDQDVLNKLNEIEGSLNKAQDEMKASDIDRKYSDLES 1526  
Db 1089 KNAGVTIQDTLNTLDGLLHMDQPLSVDBEGLVLEQLSRAKTQIN-SQLRPMMSLEE 1147  
QY 1527 EARKQEAAMVDYNRDIAETIKDIHNLEDIKTLPTGCFNTPSIEK 1571  
Db 1148 RARQGRHLLHLETSIDGLADVKVLENIRDLNLPCCNTQALDQ 1192

## RESULT 14

US-10-171-311-115  
; Sequence 115, Application US/10171311  
; Publication No. US20030087270A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Chen, Yan  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Monahan, John  
; APPLICANT: Kamatkar, Shubhang  
; APPLICANT: Glatt, Karen  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Hoerh, Sebastian  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
; FILE OF INVENTION: OF CERVICAL CANCER  
; FILE REFERENCE: MRI-035  
; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US 60/298,159  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,155  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/335,936  
; PRIOR FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-171-311-115

Query Match 30.4%; Score 2592; DB 14; Length 1193;  
Best Local Similarity 39.1%; Pred. No. 2.2e-142;

Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;

QY 284 CLPFPNDPWRATASASECLPCDCNGRSEOCYFDPDELYRSTGHGHCNTCNDTDAK 343  
Db 9 CLCFSLLLPAARATSRRE-----VCDCKGSRQCFIDRELHROTGNFRLCNCNDNDTGIH 64  
QY 344 CERCENFRRLGNTAEACSPCHCSVPGSLSTOCDYGRCSCKPGVMGDKDCRCQCPGPHSLT 403  
Db 65 CEKCKNGFYRHRERDRCLPCNCKSGSLSARCDSRCCKPGVTGARCDCCLPGFHMILT 124  
QY 404 EAGC-----RPCSCDPSGSTDECNVETGRCVKCNVEGPNCEKRCCKPGFFNLESNPK 455  
Db 125 DAGTCQDQRLDLSKDCDDCPAGIAGPC--DAGRCVCPEAVTGERCDRCRSYYNLDGDNPE 182  
QY 456 GCTPCFCFCHSVCNTNAVGVSVYDISSTFQIDEDGNRVEORDGSEASLESWSSDRQYIAVI 515  
Db 183 GCTQCFYCHSASCSSSAEYSVHKITSTFHQVDGKAVQNRGSPAKLQWSRQHVDFSS 242  
QY 516 SDSYFPRPIAPVFLGNQVLSYQNLVSFDFRVDRTRLSAEDLVLEGAGLVSVPLIA 575  
Db 243 AORLDPVYFVAPAKPLGNCQVYSGSLSFYRVDGRGHPSAHDVILEGAGLEITAPLMP 302  
QY 576 QGNSYPSSTTVKTYIFRLHEATDYPWRPALSPFFBQKLLNNLTISKIRGYTSERASGYLD 635  
Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSPLSYFEYVRLRLNLTALRIRATYVEYSTGYIDN 362  
QY 636 VTLOSARPGVPATWVESCCTPVYGGQRCETCLPGYRRETSLGSPVCLTCNGHS 695  
Db 363 VTLISARVSGAPAPWVEQCIQPVYGGQRCQDCASGKXKDSARLGGFFGTCIPCNQCG-G 421  
QY 696 ETCDPETGVCDCRNTAGPHCEKSGDYGGDSTLGTSSDCQPCPCPGSGSSCAIVPKTKEY 755  
Db 422 GACDDPTGDCYSGDENPDIECADCPIGFYNDP--HDPSCCKPCPCCHNGSPSCSVMPETEEV 479  
QY 756 VCTHCTGTAGRCCELCDGDFGDPGDSNGPVLRCQCNQNDIDPNVAGNCNRLTGECL 815  
Db 480 VCNPCPGVTGARCCELADGDFGDPFGHGPVVRPQPCQCNVNNVPSASGNCRLTGRCL 539  
QY 816 KCIYNTAGFYCDRCCKGFFGNPLAPNADKCKACACNYGTVOQSSCNPTVGOCCLPHV 875  
Db 540 KCIHNTAGIYCDQCKAGIFGDFPLAPNADKCRACN 576  
QY 876 SGRDGTGDPYNYNLOGGOCERCDCALGSTNGQCDIRTGQCEQPGITGQHCHERCETN 935  
Db 577 576  
QY 936 HFGFGPEGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCQCEENYFYNRSWPGQCEC 995  
Db 577 576  
QY 996 PACYRLVKDAAEHRVKLOELESILIANLGTGDMVTDQAFEDRLKEAREVTDLLREAOE 1055  
Db 610 PACYNOVKIQMDQFMQOLQORMEALISKAQGGGVDPDTELEGRMQQAQALQDILDAQI 669  
QY 1056 VKDQDQNLMDRLQVNSLSHSQISRLQNTIETGILAEARARSVESTQLIEIASRE 1115



Db 670 SEGASRSLGLQAKVRSQENSVQSRDLDDLKMTVEKVRALGSQYQNRVDRDTHRLITQMOLS 729  
QY 1116 LEKAKMA-ANVSITQPESTGEPNNMTLLAEAEARLAEHKEADDDIVRVAKTANETSAAE 1174  
Db 730 LAESEAISLGNITNIPASDHVYVGNPKSLAQEATRLAESHVESASNMQLTRETEDYSKQA 789  
QY 1175 YNLLRLT-----AGENQTALEIEELNRKVEQAKNISQLEKQAAARVHEBAKAGDKA 1227  
Db 790 LSLVRKALHEGVSGSGSPDGA-VQGLVEKLEKTKSLAQQLTREATQAEIBADRSYQHS 848  
QY 1228 VEIYASVAQLTPVDSEALE-NEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKN 1286  
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QY 1287 LLEKGAEOQTADOLLARADAARAKAABEAKKGRSTLOEANDILNNLKDFORVNDKTA 1346  
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QY 1347 ABEALRRIPAINRTIAEANEKTRAEALGNAADAATEAKNKAHAEARIASAQAOKNATST 1406  
Db 969 ABEAMKRLSYISQKVSADSKTQAAERALGSAADAQKXNGAGEALEISSEIEQIGSL 1028  
QY 1407 KADAEFTGEVTDLDNEVNGMLRQLBEAENELKQKDDADQDMMAGMASQAQAQAEALNA 1466  
Db 1029 NLEANTVADGALAMEKGLASKESEMEVEGELEKELEFDTNMDAVQMVITEAQKVDTRA 1088  
QY 1467 RKARNSVSLLSQNLNLLDQLGOLDTVDLNLKNEIEGSLNKADEMKASDLDRKVSDES 1526  
Db 1089 KNAGVTIQDTLTLDGLLHMDQPLSVDEGLVLEQLSRKATQIN-SQLRPMWSELES 1147  
QY 1527 EARKQEAAMDMYNRDAEIIKDHNLDIKKTLPTGCFNTPSIEK 1571  
Db 1148 FARQQRGHLHLETSIDGILADVKNLENIRDNUPPGCYNTQALEQ 1192

RESULT 15  
US-10-053-662A-31  
; Sequence 31, Application US/10053662A  
; Publication No. US20030143545A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandra Charlesworth  
; APPLICANT: Falvia Spirito  
; APPLICANT: Guerrino Meneguzzi  
; APPLICANT: John Baird  
; APPLICANT: Keith Linder  
; TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN  
; TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS  
; TITLE OF INVENTION: BULLOSA  
; FILE REFERENCE: p84us4  
; CURRENT APPLICATION NUMBER: US/10/053.662A  
; CURRENT FILING DATE: 2002-01-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; OTHER INFORMATION:  
US-10-053-662A-31

Query Match 30.48; Score 2592; DB 14; Length 1193;  
Best Local Similarity 39.18; Pred. No. 2.2e-142;  
Matches 510; Conservative 235; Mismatches 422; Indels 138; Gaps 13;  
QY 284 CLPFFNDPWRRTAESAECPLCDNCRSQECYFDPPELYSTGHGHCNCRDNTDGAK 343  
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QY 344 CERENFFPLGNTAECSPCHSPVGLSTQDCSYSCSKGVMDKCDRCQRFHSIT 403  
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QY 404 EAGC-----RPSCDSPSGSTDECNVETGRCVCKDNVEGFNCERCCKPGFFNLESSNPK 455  
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QY 456 GCTPCFCGHSSVCTNAGVSVYDISTSFTQIDEDGHWVEQDQSGSEASLEWSSDRQYIAVI 515  
Db 183 GCTQCFYCHSASCRSAEYSVHKITSTPHQDVGWKAVQNGSPAKLOWSRHQDVFSS 242  
QY 516 SDSYFPYFIAFVKFLGNQVLSYQNLSPFRVDRDRTRLSAEDLVLEGAGLRSVPLIA 575  
Db 243 AQRUDPVYFAPAKFLGNQVSYQSLSFYDVRGRGHPHSAHDVILEGAGLITAPLMP 302  
QY 576 QGNYSPESTTVKYIFRLHEATDYPWRPALSPFFOKLNNLTISKIRGTYSERSAGYLD 635  
Db 303 LKTLPCGLTKTYTFLRNEHPSNNWSPQLSYFYRLLRLNLTALRATRYGEYSTGYDN 362  
QY 636 VTLOSARPGVPATWTVESCTCPVYGCGQFCETCLPGYRRETSPSLGYPSPCVLCTCNGHS 695  
Db 363 VTLISARPVSGAPAPWVEQCICPVYKQFCQDCASGYKEDSARLPGFTGTCIPNCQG-G 421  
QY 696 ETCDPETGVCDRCRNTAGPHCEKSDGYDSTLGTSTSDCQPCPCPGGSSCAIVPKTEV 755  
Db 422 GACDPDTCGDCYSGDENPDIEACDCPIGFYNDP--HDPRCKPCPCPNHGFSCSVMPETEV 479  
QY 756 VTCHPTGTAGKRCCELDDGDFGDPGLSGNPFVRLCRPCQCNNDIDPNVGNCRNLTGEC 815  
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QY 816 KCIYNTAGVCDRCCKEFGFNPLAPADKCAKACAGNVTVOOQSCNVPVTCQCLPRV 875  
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Db 577 ----- 576  
QY 936 HFGPGEGCKPCDCHHSGLSLOCKDGRCEGREGFVGNRCQCBENYFNRSWGCQEC 995  
Db 577 -----VGRSDGTGCVCKPGFGPNCEH-----GAFSC 609  
QY 996 PACYLVKDKAAEHVKLQLESILANLGTGDDMTVDQAFEDRLKEAREVTDLLREAE 1055  
Db 610 PACYNVKIQMDQFMQOLQSMALISKAQGGVGVDPTELEGRMQQAEALQILRDAQI 669  
QY 1056 VKQVDQNLRLQVNSLSHLSQISRLQNTNIEETGILAEARSRVSTEOILLIASE 1115  
Db 670 SEGASRSLGLQAKVRSQENSVQSRDLDDKMTVERVRLGSGYQNRVDRDTHRLITQMOLS 729  
QY 1116 LEKAKMA-ANVSITQPESTGEPNNMTLLAEAEARLAEHKEADDDIVRVAKTANETSAAE 1174  
Db 730 LAESEAISLGNITNIPASDHVYVGNPKSLAQEATRLAESHVESASNMQLTRETEDYSKQA 789  
QY 1175 YNLLRLT-----AGENQTALEIEELNRKVEQAKNISQLEKQAAARVHEBAKAGDKA 1227  
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QY 1287 LLEKGAEOQTADOLLARADAARAKAABEAKKGRSTLOEANDILNNLKDFORVNDKTA 1346  
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QY 1407 KADAEFTGEVTDLDNEVNGMLRQLBEAENELKQKDDADQDMMAGMASQAQAQAEALNA 1466  
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QY 1467 RKARNSVSLLSQNLNLLDQLGOLDTVDLNLKNEIEGSLNKADEMKASDLDRKVSDES 1526

Wed May 19 10:47:44 2004

db	1089	KNAGVTIQDTLNTDGLHLMQDPLSVDEGLVLEQKLSRAKTQIN-SQLRPMSELEE	1147
Qy	1527	EARKQEAAMVDNRYDAEIIKOIHNLEDIKTLPTGCENTPSTIEK	1571
db	1148	RAFQQRGHLHLETSIDGILADVKNLENIRDNLPQCIYNTQALEQ	1192

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Job time : 46.9931 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 11.8919 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-20  
Perfect score: 8527  
Sequence: 1 AMDEADGGRRQRCMPFV.....EDIKTLTGCFNPSIEKP 1572

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
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5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8527	100.0	1572	4	US-09-562-702A-32
2	8527	100.0	1572	4	US-09-561-818A-28
3	8527	100.0	1605	4	US-09-562-702A-30
4	8527	100.0	1605	4	US-09-561-818A-26
5	8038	94.3	1576	4	US-09-562-702A-24
6	8038	94.3	1576	4	US-09-561-818A-24
7	8038	94.3	1584	4	US-09-562-702A-28
8	8038	94.3	1609	4	US-09-562-702A-22
9	8038	94.3	1617	4	US-09-561-818A-22
10	8038	94.3	1617	4	US-09-562-702A-26
11	3586	42.1	1587	4	US-09-561-709B-3
12	3586	42.1	1587	4	US-09-561-709B-1
13	2591	30.4	1193	1	US-08-317-450B-13
14	2591	30.4	1193	3	US-08-800-593-13
15	2476.5	29.0	1111	3	US-08-317-450B-15
16	2476.5	29.0	1111	3	US-08-800-593-15
17	2306.5	27.0	1171	1	US-08-445-135-1
18	1812.5	21.3	3106	4	US-09-562-702A-10
19	1807.5	21.2	3084	4	US-09-562-702A-12
20	1790	21.0	3088	4	US-09-562-702A-8
21	1790	21.0	3089	4	US-09-562-702A-4
22	1790	21.0	3110	4	US-09-562-702A-2
23	1790	21.0	3110	4	US-09-562-702A-6
24	1790	21.0	3110	4	US-09-561-709B-7
25	1789.5	21.0	3111	2	US-08-460-309-4
26	1789.5	21.0	3111	2	US-08-125-077-4
27	1704	20.0	3075	2	US-08-460-309-5

28	1704	20.0	3075	2	US-08-125-077-5	Sequence 5, Appli
29	1677	19.7	1765	4	US-09-562-702A-16	Sequence 16, Appl
30	1677	19.7	1765	4	US-09-561-818A-16	Sequence 16, Appl
31	1677	19.7	1786	4	US-09-562-702A-14	Sequence 14, Appl
32	1677	19.7	1786	4	US-09-561-818A-14	Sequence 14, Appl
33	1677	19.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
34	1661.5	19.5	1786	4	US-09-562-702A-18	Sequence 18, Appl
35	1661.5	19.5	1786	4	US-09-561-818A-18	Sequence 18, Appl
36	1637.5	19.2	1725	4	US-09-562-702A-20	Sequence 20, Appl
37	1637.5	19.2	1725	4	US-09-561-818A-20	Sequence 20, Appl
38	1630	19.1	1761	4	US-09-561-709B-1	Sequence 1, Appli
39	1526	17.9	1799	4	US-09-845-583A-6	Sequence 6, Appli
40	1477.5	17.3	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1472.5	17.3	1798	4	US-09-845-583A-8	Sequence 8, Appli
42	1357	15.9	251	1	US-08-152-019A-37	Sequence 37, Appl
43	1347.5	15.8	3635	4	US-09-845-583A-2	Sequence 2, Appli
44	1346	15.8	252	2	US-08-460-309-12	Sequence 12, Appl
45	1346	15.8	252	2	US-08-125-077-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-562-702A-32  
; Sequence 32, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-32

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		0	Indels	0
		0	Gaps	0
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DB	61	QOHLQHGAAFTDYNQADTTWQSOOTMLAGVQVNSINLTLLHGKAFDITVYRLKHTS	120	
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DB	121	RPESFAIKYKTRREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPL	180	
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Db 361 SPCHCSPVGLSTQCDISYGRCSCKPGVWGDKDRCPGFHSLHTEACRCPSCDPSGSTDE 420
QY 421 CNVETGRVCVCKDNVEGFCNCRKPGFPFNLESSNPKGCTPCFCFGHSSVCTNAVGYSYVDI 480
Db 421 CNVETGRVCVCKDNVEGFCNCRKPGFPFNLESSNPKGCTPCFCFGHSSVCTNAVGYSYVDI 480
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Db 1201 QAKNISODLEKQAAARVHEAKRAGDKAVEIYASVAQLTPVDSEALENANKIKKEAADLD 1260
QY 1261 RLIDQKLDYEDLREDMRGKEHEVKNLLEKGAKEQQTADQLLARADAALAEAAKKGK 1320
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Db 1501 IEGSLNKADEKMSKASDLDRKVSIDLESEBARKQEAAMIDYNRDIAEIIKDHNLEDKITLP 1560
QY 1561 TGCNTPSIEKP 1572
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RESULT 2
US-09-561-818A-28
; Sequence 28, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-28

Query Match 100.0%; Score 8527; DB 4; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 TGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTTGFDEVNDPKVLSYYY 240
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601 RPALSPFEFOKLNNLTSIKIRGYTSERSAGYLDVTLQASRPGPGVPATWVESCPCPVG 660  
661 YGQFQFETCLPGVRRTPSLGYPSPVCLCTCNHSETCDPBTGVCDCRONTAGPHCEKCS 720  
661 YGQFQFETCLPGVRRTPSLGYPSPVCLCTCNHSETCDPBTGVCDCRONTAGPHCEKCS 720  
721 DGYGSGTSLGTSDDCPCPCPGSSCAIYVKTKEVVCTHCPTGTAGRCCELDDGDFGDP 780  
721 DGYGSGTSLGTSDDCPCPCPGSSCAIYVKTKEVVCTHCPTGTAGRCCELDDGDFGDP 780  
781 LGSNGPVRLCRPCQNDNDPNAVGNCRNLTGELKCIYNTAGFYCDRCKEGFFGNPLAP 840  
781 LGSNGPVRLCRPCQNDNDPNAVGNCRNLTGELKCIYNTAGFYCDRCKEGFFGNPLAP 840  
841 NPADKCKACACNYGTVOQSSCNFVTGQCCLPHVSGRDCGTCDPGYNNLQSGGCERC 900  
841 NPADKCKACACNYGTVOQSSCNFVTGQCCLPHVSGRDCGTCDPGYNNLQSGGCERC 900  
901 CHALGSTNGQCDIRTOCEBQPGITQCHERCERTNHFPGPEGCKPCDCHHGSLSLQCK 960  
901 CHALGSTNGQCDIRTOCEBQPGITQCHERCERTNHFPGPEGCKPCDCHHGSLSLQCK 960  
961 DDCRCREGFVGNRCDOCEENFYNRSPWGOCECPACVRLVKDKAAERVKLOLESIL 1020  
961 DDCRCREGFVGNRCDOCEENFYNRSPWGOCECPACVRLVKDKAAERVKLOLESIL 1020  
1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSLSHSQSR 1080  
1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSLSHSQSR 1080  
1081 LQNIIRNTIETGLAERARSVESTQLIEIASRELEKAKMAANSITQPESTGBPNMT 1140  
1081 LQNIIRNTIETGLAERARSVESTQLIEIASRELEKAKMAANSITQPESTGBPNMT 1140  
1141 LLAEBARRLAERHKQADDIIVRAKTANETSAEAYNLLRTLAGENQTALEIEELNRKYE 1200  
1141 LLAEBARRLAERHKQADDIIVRAKTANETSAEAYNLLRTLAGENQTALEIEELNRKYE 1200  
1201 QAKNIISDLEKQAAHVHESAKAGDKAVIYASVAOLTVPDSEALENEANKIKKGAADLD 1260  
1201 QAKNIISDLEKQAAHVHESAKAGDKAVIYASVAOLTVPDSEALENEANKIKKGAADLD 1260  
1261 RLIDQKLKDYEDLRDMRGKEHEVKNLLBKGAEOQTADOLLARADAALAEAAKKGR 1320  
1261 RLIDQKLKDYEDLRDMRGKEHEVKNLLBKGAEOQTADOLLARADAALAEAAKKGR 1320  
1321 STLQEANDILNNLKDFDRVNDNKTAAEBALRRIPAINRTIAEANEKTRQAALGNAAA 1380  
1321 STLQEANDILNNLKDFDRVNDNKTAAEBALRRIPAINRTIAEANEKTRQAALGNAAA 1380  
1381 DATEAKNKAHEABRIASAKQKATSTKADAERTFGEVTDLDNEVGNMLQLEAEANELK 1440  
1381 DATEAKNKAHEABRIASAKQKATSTKADAERTFGEVTDLDNEVGNMLQLEAEANELK 1440  
1441 KQDADQDMMWAGMASQAAQAEALNARKAKNSVSLLSQNLNLLDQGLQDITVDLNKLE 1500  
1441 KQDADQDMMWAGMASQAAQAEALNARKAKNSVSLLSQNLNLLDQGLQDITVDLNKLE 1500  
1501 IEGSLNKADEMKASDLDRKVSDESEARKOEAAMNDYNRDAEIIKDHNEDEIKTLP 1560  
1501 IEGSLNKADEMKASDLDRKVSDESEARKOEAAMNDYNRDAEIIKDHNEDEIKTLP 1560  
1561 TGCFTNTPSIEKP 1572  
1561 TGCFTNTPSIEKP 1572

RESULT 3  
US-09-562-702A-30  
; Sequence 30, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-562-702A-30

Query Match 100.0%; Score 8527; DB 4; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMDECADEGGPQRCMPEFVNAAFNVTVAATNTCGTPEEYCVQGTGVTGKSHCLDAG 60  
DB 34 AMDECADEGGPQRCMPEFVNAAFNVTVAATNTCGTPEEYCVQGTGVTGKSHCLDAG 93  
QY 61 QOHLQHGAAFLTDYNNQADTTWQSQTLAGVQVPSNINLTGKGAFTIYVRLKHEHTS 120  
DB 94 QOHLQHGAAFLTDYNNQADTTWQSQTLAGVQVPSNINLTGKGAFTIYVRLKHEHTS 153  
QY 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSISPL 180  
DB 154 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIRTTGGDEQALCTDEFSISPL 213  
QY 181 TGGNVASTLEGRPSAYNFQNSPVLQSEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240  
DB 214 TGGNVASTLEGRPSAYNFQNSPVLQSEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 273  
QY 241 AISDFAVGGRCKNGHASECVKNEBFDKLMCNKXHTYGVDCCKLPFFNDRPWRATAES 300  
DB 274 AISDFAVGGRCKNGHASECVKNEBFDKLMCNKXHTYGVDCCKLPFFNDRPWRATAES 333  
QY 301 ASECLPCDCNRSQECYFDPBELYSTGHHGCTNCRONTGAKCERENFERLGNTEAC 360  
DB 334 ASECLPCDCNRSQECYFDPBELYSTGHHGCTNCRONTGAKCERENFERLGNTEAC 393  
QY 361 SPCHSPVGSLSLTQCDSYGRCSCKPVGMDKCDRCQPGFHSLTEAGRCPCSDPSGSTDE 420  
DB 394 SPCHSPVGSLSLTQCDSYGRCSCKPVGMDKCDRCQPGFHSLTEAGRCPCSDPSGSTDE 453  
QY 421 CNVETGRVCVKNDVEGNCERCPGPFNLESSNPKGCTPCFCGHSSVCTNAVGYSYVDI 480  
DB 454 CNVETGRVCVKNDVEGNCERCPGPFNLESSNPKGCTPCFCGHSSVCTNAVGYSYVDI 513  
QY 481 SSTSFIQIDEDGWRVQRQDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 540  
DB 514 SSTSFIQIDEDGWRVQRQDGESEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 573  
QY 541 NLSFSFRVDRDRRLSAEDLVLEGALRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
DB 574 NLSFSFRVDRDRRLSAEDLVLEGALRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 633  
QY 601 RPALSPFEFOKLNNLTSIKIRGYTSERSAGYLDVTLQASRPGPGVPATWVESCPCPVG 660

Db 634 RPALSPFQKLLNNLTSIKIRGYTSERSAGYLDVTLQASRPGPGVPATWVESCPCPVG 693  
Qy 661 YGQFCETCLPGVRRTPSLGPPSPCVLTCNGHSETCDPETHGVCDCRONTAGPHCEKCS 720  
Db 694 YGQFCETCLPGVRRTPSLGPPSPCVLTCNGHSETCDPETHGVCDCRONTAGPHCEKCS 753  
Qy 721 DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGTCAGRCCLCDGDFGDP 780  
Db 754 DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGTCAGRCCLCDGDFGDP 813  
Qy 781 LGSNGPVRCLCRPCQCNNDIPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKEGFGNPLAP 840  
Db 814 LGSNGPVRCLCRPCQCNNDIPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKEGFGNPLAP 873  
Qy 841 NPADKCKACACNVTGVOQSSCNPVTCQCCLPHVSGRDCGTCDPGVYNLQSGQGERCD 900  
Db 874 NPADKCKACACNVTGVOQSSCNPVTCQCCLPHVSGRDCGTCDPGVYNLQSGQGERCD 933  
Qy 901 CHALGSTNGQCDITRTGCECQPGITGHCRCETNHFPGPECKPCDCHHEGSLQCK 960  
Db 934 CHALGSTNGQCDITRTGCECQPGITGHCRCETNHFPGPECKPCDCHHEGSLQCK 993  
Qy 961 DDGCECREGFGVNRCDQCEENFYNRWPGCECPACVRLVKDKAAHRVKLOELESIL 1020  
Db 994 DDGCECREGFGVNRCDQCEENFYNRWPGCECPACVRLVKDKAAHRVKLOELESIL 1053  
Qy 1021 ANLGTGDMVTDQAFEDRLKEAREVTDLLREAEQVNDQNLMDRLQRVNSLSHSQISR 1080  
Db 1054 ANLGTGDMVTDQAFEDRLKEAREVTDLLREAEQVNDQNLMDRLQRVNSLSHSQISR 1113  
Qy 1081 LONIRNTIETGILAEARSRVSTEOLEIIRASRELEKAKAANVSITOPESGEPNNMT 1140  
Db 1114 LONIRNTIETGILAEARSRVSTEOLEIIRASRELEKAKAANVSITOPESGEPNNMT 1173  
Qy 1141 LLAEARLARLAEHRKQEAADDIVRAKTANETSAAYNLLRLTAGENQTALEIIEELNRKYE 1200  
Db 1174 LLAEARLARLAEHRKQEAADDIVRAKTANETSAAYNLLRLTAGENQTALEIIEELNRKYE 1233  
Qy 1201 QAKNISQDLEKQARVHEERAKRAGDKAVEIYASVAQLTPVDSALEANEANKIKKEAADLD 1260  
Db 1234 QAKNISQDLEKQARVHEERAKRAGDKAVEIYASVAQLTPVDSALEANEANKIKKEAADLD 1293  
Qy 1261 RLIDOKLKYEDLREDNRGKEHEVKNLLEKGAEQQTADQLLARAADAALAEAAKGR 1320  
Db 1294 RLIDOKLKYEDLREDNRGKEHEVKNLLEKGAEQQTADQLLARAADAALAEAAKGR 1353  
Qy 1321 STLQEAANDILNKLKDFRRVNDNKTAAEALRIPALNRTIABANEKTRQAQLALGNAAA 1380  
Db 1354 STLQEAANDILNKLKDFRRVNDNKTAAEALRIPALNRTIABANEKTRQAQLALGNAAA 1413  
Qy 1381 DATEAKNKAHEABERIASAAQKNATSTKADAERTFGEVTDLDNEVGMRLROLEAEANELKR 1440  
Db 1414 DATEAKNKAHEABERIASAAQKNATSTKADAERTFGEVTDLDNEVGMRLROLEAEANELKR 1473  
Qy 1441 KODDADQDMWAGMASQAQAEALNARKAKNSVSSLSQLNNLLDQLGQDQDVTDLNKLNE 1500  
Db 1474 KODDADQDMWAGMASQAQAEALNARKAKNSVSSLSQLNNLLDQLGQDQDVTDLNKLNE 1533  
Qy 1501 IEGSLNKAQDMKASDILDRKVSDESEARKQOEAALMDYNDRIAEIINKDHNLSDIKKTLP 1560  
Db 1534 IEGSLNKAQDMKASDILDRKVSDESEARKQOEAALMDYNDRIAEIINKDHNLSDIKKTLP 1593  
Qy 1561 TGCFTNTPSIEKP 1572  
Db 1594 TGCFTNTPSIEKP 1605

## RESULT 4

US-09-561-818A-26  
; Sequence 26, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:

; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99, 274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-561-818A-26

Query Match 100.0%; Score 8527; DB 4; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMDECADSGGRPQRCMPEFVNAAFNVTVAATNCGTTPPEEYCVQGTGVTKSKHLCADAG 60  
Db 34 AMDECADSGGRPQRCMPEFVNAAFNVTVAATNCGTTPPEEYCVQGTGVTKSKHLCADAG 93  
Qy 61 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAPDITFYVRLKEHTS 120  
Db 94 QOHLQHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITFYVRLKEHTS 153  
Qy 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIITGGDEQCALCTDEFSDSL 180  
Db 154 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIITGGDEQCALCTDEFSDSL 213  
Qy 181 TGGNVAFTSLGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYV 240  
Db 214 TGGNVAFTSLGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYV 273  
Qy 241 AISDPAGGRCKNGHASECVKNEFDFKLMCKNKTGYDCEKCLPFENDEPWRATAES 300  
Db 274 AISDPAGGRCKNGHASECVKNEFDFKLMCKNKTGYDCEKCLPFENDEPWRATAES 333  
Qy 301 ASECLPCDCNCRSQCVCYFDPPELYRSTGHGCHTNCRDNTDGAKCERCRENPFRLGTEAC 360  
Db 334 ASECLPCDCNCRSQCVCYFDPPELYRSTGHGCHTNCRDNTDGAKCERCRENPFRLGTEAC 393  
Qy 361 SPCHSPVGSJSTQCDYSYGRCSCKPVGMDKCDRCQCFHSLTEAGCPSCDPSGSTDE 420  
Db 394 SPCHSPVGSJSTQCDYSYGRCSCKPVGMDKCDRCQCFHSLTEAGCPSCDPSGSTDE 453  
Qy 421 CNVETGRVCVCKDNVGENCERCKPGFNLSSNPKGCTPCFCFGHSSVCTNAVGSYVDI 480  
Db 454 CNVETGRVCVCKDNVGENCERCKPGFNLSSNPKGCTPCFCFGHSSVCTNAVGSYVDI 513  
Qy 481 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYQ 540  
Db 514 SSTFQIDEDGWRVEQORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYQ 573  
Qy 541 NLSFSPFRVDRDTRLASDELVLGAGLVSPLIAQGNYSPESTTVKYIFRLHEATDYPW 600  
Db 574 NLSFSPFRVDRDTRLASDELVLGAGLVSPLIAQGNYSPESTTVKYIFRLHEATDYPW 633  
Qy 601 RPALSPFQKLLNNLTSIKIRGYTSERSAGYLDVTLQASRPGPGVPATWVESCPCPVG 660  
Db 634 RPALSPFQKLLNNLTSIKIRGYTSERSAGYLDVTLQASRPGPGVPATWVESCPCPVG 693  
Qy 661 YGQFCETCLPGVRRTPSLGPPSPCVLTCNGHSETCDPETHGVCDCRONTAGPHCEKCS 720  
Db 694 YGQFCETCLPGVRRTPSLGPPSPCVLTCNGHSETCDPETHGVCDCRONTAGPHCEKCS 753  
Qy 721 DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGTCAGRCCLCDGDFGDP 780  
Db 754 DGYGDSLTGSDQCPGCPGSSCAIVPKTEVVTCHTCTAGTCAGRCCLCDGDFGDP 813  
Qy 781 LGSNGPVRCLCRPCQCNNDIPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKEGFGNPLAP 840  
Db 814 LGSNGPVRCLCRPCQCNNDIPNAVGNCRNLGTGCLKCIYNTAGFYCDRCKEGFGNPLAP 873

841 NPADKCKACACNYGTVOQSSNPVTGQCQCLPHVSGRDCGTCDPGYNNLQSGQCERCD 900  
874 NPADKCKACACNYGTVOQSSNPVTGQCQCLPHVSGRDCGTCDPGYNNLQSGQCERCD 933  
901 CHALGSTNGQCDIRTCQCCQCPGIGTQHCERCETNHFPGPGCKPCDCHHEGSLSLQCK 960  
934 CHALGSTNGQCDIRTCQCCQCPGIGTQHCERCETNHFPGPGCKPCDCHHEGSLSLQCK 993  
961 DGRCECRGFGVGNRCDCQCEBNFYNNRSPGQCEPCACVRLVKDKAAAEHRVKLQLESIL 1020  
994 DGRCECRGFGVGNRCDCQCEBNFYNNRSPGQCEPCACVRLVKDKAAAEHRVKLQLESIL 1053  
1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLRBAEQEVKVDQNLMDRLQRVNSLSHSQISR 1080  
1054 ANLGTGDDMVTDQAFEDRLKEAREVTDLLRBAEQEVKVDQNLMDRLQRVNSLSHSQISR 1113  
1081 LQNIIRNTIETGILAEARSRVESITQLEIETASRELEKAKMAANVSITQPESTGPNNT 1140  
1114 LQNIIRNTIETGILAEARSRVESITQLEIETASRELEKAKMAANVSITQPESTGPNNT 1173  
1141 LLAEEARRLAERHKQADDIIVRAKTANETSABAYNLLRTLAGENQTALEIEELNRKYE 1200  
1174 LLAEEARRLAERHKQADDIIVRAKTANETSABAYNLLRTLAGENQTALEIEELNRKYE 1233  
1201 QAKNIISQDLEKQAAHVHEAKRAGDKAVIYASVAQLTPVDSEALENEANKIKKSAADLD 1260  
1234 QAKNIISQDLEKQAAHVHEAKRAGDKAVIYASVAQLTPVDSEALENEANKIKKSAADLD 1293  
1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLBKGAEQOQTADQLLARADAAKALAEAAKGR 1320  
1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLBKGAEQOQTADQLLARADAAKALAEAAKGR 1353  
1321 STLOEANDILNKKDFDRVNDNKTAAEALRRIPAINRTIAEANEKTRAEQALGNAAA 1380  
1354 STLOEANDILNKKDFDRVNDNKTAAEALRRIPAINRTIAEANEKTRAEQALGNAAA 1413  
1381 DATEAKNKAHEARISAAQKATSTKADAERTFGEVTDLDNEVGNMLQLEAEANELK 1440  
1414 DATEAKNKAHEARISAAQKATSTKADAERTFGEVTDLDNEVGNMLQLEAEANELK 1473  
1441 KQDADQDMMAGWASQAAQAEALNARKAKNSVSLLSQNLNLLDQLGDTVDNLKNE 1500  
1474 KQDADQDMMAGWASQAAQAEALNARKAKNSVSLLSQNLNLLDQLGDTVDNLKNE 1533  
1501 IEGSLNKADEMKASDLDRKVSLESEAPKQEAAMDYNRDIAEIIKDIHNLEDIKKTL 1560  
1534 IEGSLNKADEMKASDLDRKVSLESEAPKQEAAMDYNRDIAEIIKDIHNLEDIKKTL 1593  
1561 TGCFTNPSIEKP 1572  
1594 TGCFTNPSIEKP 1605

## RESULT 5

US-09-562-702A-24  
Sequence 24, Application US/09562702A  
Patent No. 6632790  
GENERAL INFORMATION:  
APPLICANT: Yurchenco, Peter  
TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
FILE REFERENCE: 99-274-B  
CURRENT APPLICATION NUMBER: US/09/562, 702A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/155,945  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: 60/143,289  
PRIOR FILING DATE: 1999-07-12  
PRIOR APPLICATION NUMBER: 60/139,198  
PRIOR FILING DATE: 1999-06-15  
PRIOR APPLICATION NUMBER: 60/131,720  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 1576  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-562-702A-24

Query Match 94.3%; Score 8038; DB 4; Length 1576;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDESCADGGRRPQRCMPFEFVNAAFNVTVATNTCGTPPEEYCVGTGTVTKSCHLCDAG 60  
DB 3 AMDESCADGGRRPQRCMPFEFVNAAFNVTVATNTCGTPPEEYCVGTGTVTKSCHLCDAG 62  
QY 61 QQLHGHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFTHS 120  
DB 63 QQLHGHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITYVRLKFTHS 122  
QY 121 RPESFAIYKRTREGPMIPYQYSGSCENTYSKANRGFIETGGDEQCALCTDESDISPL 180  
DB 123 RPESFAIYKRTREGPMIPYQYSGSCENTYSKANRGFIETGGDEQCALCTDESDISPL 182  
QY 181 TGGNVAFSTLLEGPSAYNFONS PVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 240  
DB 183 TGGNVAFSTLLEGPSAYNFONS PVLQEWVTATDIRVTNLRLNTFGDEVFNDPKVLKSY 242  
QY 241 AISDFAVGGRCKNGHASECVKNEBFDKLMCNKXNTYGVDCCKCLPFNDPRWRRAAES 300  
DB 243 AISDFAVGGRCKNGHASECVKNEBFDKLMCNKXNTYGVDCCKCLPFNDPRWRRAAES 302  
QY 301 ASECLPCDCNCRSQECYFDPDELRYSTGHGCHCTNCRONTDGAKCERENFFRLGNTEAC 360  
DB 303 ASECLPCDCNCRSQECYFDPDELRYSTGHGCHCTNCRONTDGAKCERENFFRLGNTEAC 362  
QY 361 SPCHSPVGSLSQCDYSYGRCSCKPVGMDKDRCPQGFHSLTEAGORPCSDPSGSTDE 420  
DB 363 SSCCHSPVGSLSQCDYSYGRCSCKPVGMDKDRCPQGFHSLTEAGORPCSDPSGSTDE 422  
QY 421 CNVTGRCVKNDVNGFNCERCKPFPNLESSNPKGCTPCFCFHHSSVCTNNAVGSYVDI 480  
DB 423 CNVTGRCVKNDVNGFNCERCKPFPNLESSNPKGCTPCFCFHHSSVCTNNAVGSYVDI 482  
QY 481 SSTFQIDEDGWRVQRDGESEASLEWSSDRQVIAVISDSYFPFYPIAPVKFLGNQVLSYG 540  
DB 483 SSTFQIDEDGWRVQRDGESEASLEWSSDRQVIAVISDSYFPFYPIAPVKFLGNQVLSYG 542  
QY 541 NLSFSFVDRDRDTLSAEDLVLEGAGLRVSVPLTAQNSYPSSETTKYIIFRLHEATDPW 600  
DB 543 NLSFSFVDRDRDTLSAEDLVLEGAGLRVSVPLTAQNSYPSSETTKYIIFRLHEATDPW 602  
QY 601 RPALSPPEFQKLLNLLTSIKIRGTYSERSAGYLDVTLQSAEPGPGVPATWVESCTCPVG 660  
DB 603 RPALTPPEFQKLLNLLTSIKIRGTYSERSAGYLDVTLQSAEPGPGVPATWVESCTCPVG 662  
QY 661 YGQFCETCLPGYRRETPSLGPVPCVLCTCNHSETCDPETHVCDNRDNTAGPHCKCS 720  
DB 663 YGQFCETCLPGYRRETPSLGPVPCVLCTCNHSETCDPETHVCDNRDNTAGPHCKCS 722  
QY 721 DGYGDSLTGTSQCPGSSCAIVPKTKEVVCTHCTGTAGTKRCELCDGDEGDP 780  
DB 723 DGYGDSLTGTSQCPGSSCAIVPKTKEVVCTHCTGTAGTKRCELCDGDEGDP 782  
QY 781 LGSNGPVRLLRPPCCNDNIDPNVGNCRNLTGCECLKIYNTAGYCDRCCKEFGFNFLAP 840  
DB 783 LGRNGPVRLLRCLCQSDNIDPNVGNCRNLTGCECLKIYNTAGYCDRCCKEFGFNFLAP 842  
QY 841 NPADKCKACACN-YGTVOQSSCNPNVTGQCQCLPHVSGRDCGTCDPGYNNLQSGQCERC 899  
DB 843 NPADKCKACACNPNVTGQCQCLPHVSGRDCGTCDPGYNNLQSGQCERC 902  
QY 900 DCHALGSTNGQCDIRTCQCCQCPGIGTQHCERCETNHFPGPGCKPCDCHHEGSLSLQ 959

Db 903 DCHALSTNGQCDIRTCQCEQCPGIGTQHCECEVNHFGFEGEGCKPCDCHPEGSLSLQC 962  
Qy 960 KDGRCCEBGFVGNRCDCCEENYFYNRSWPGCECPACRYRLVDDKAAAEHRVYKLELES 1019  
Db 963 KDGRCCEBGFVGNRCDCCEENYFYNRSWPGCECPACRYRLVDDKAAAEHRVYKLELES 1022  
Qy 1020 IANLGTGDDVMTDQAFEDRLKAEAREVTDLLREAEVVDVNDLMDRLQRVNSLHLSOIS 1079  
Db 1023 IANLGTGDDVMTDQAFEDRLKAEAREVTDLLREAEVVDVNDLMDRLQRVNSLHLSOIS 1082  
Qy 1080 RLQINRTIETGILAEARSRVSTEQIEIASRELEKAKM-AANVSITQPESTGEPNN 1138  
Db 1083 RLQINRTIETGILAEARSRVSTEQIEIASRELEKAKM-AANVSITQPESTGEPNN 1142  
Qy 1139 MTLLEAEARLAEHRKQAEADIVRVAKTANETSAAEYNLLSTLAGENOTALEIEELNRK 1198  
Db 1143 MTLLEAEARLAEHRKQAEADIVRVAKTANETSAAEYNLLSTLAGENOTALEIEELNRK 1202  
Qy 1199 YEOAKNISODLEKQAEARVHEEAKRAGDXAVEIYASVAQLTPVDSPEALENEANKIKBAAD 1258  
Db 1203 YEOAKNISODLEKQAEARVHEEAKRAGDXAVEIYASVAQLTPVDSPEALENEANKIKBAAD 1262  
Qy 1259 LDLLEIDOKLKDVEDLEEDVRGKEHEVKNLLEKGAEOQTADOLLARADAALAEBAK 1318  
Db 1263 LEQLIDOKLKDVEDLEEDVRGKEHEVKNLLEKGAEOQTADOLLARADAALAEBAK 1322  
Qy 1319 GRSTLOEANDILNNLKDFDRVNDNKTAAEALRIPAINRTIAPANEKTRAEALGNA 1378  
Db 1323 GRSTLOEANDILNNLKDFDRVNDNKTAAEALRIPAINRTIAPANEKTRAEALGNA 1382  
Qy 1379 AADATKAKNAHEARIEASAGVQNAITSTKAEARTFAEVTDLDEVNMLKQLEAEKEL 1438  
Db 1383 AADATKAKNAHEARIEASAGVQNAITSTKAEARTFAEVTDLDEVNMLKQLEAEKEL 1442  
Qy 1439 KRQDDADQDMWAGMASQAQAEALNARKANSYSLLSOLLNLLDQLDQDLDVLDNKL 1498  
Db 1443 KRQDDADQDMWAGMASQAQAEALNARKANSYSLLSOLLNLLDQLDQDLDVLDNKL 1502  
Qy 1499 NEIEGSLNKADEMKSADLDKVSLESEARKQEAAMDYNRDIAEIIKDIHNLIEDIKKT 1558  
Db 1503 NEIEGSLNKADEMKSADLDKVSLESEARKQEAAMDYNRDIAEIIKDIHNLIEDIKKT 1562  
Qy 1559 LPTGCFNTPSIEKP 1572  
Db 1563 LPTGCFNTPSIEKP 1576

## RESULT 6

US-09-561-818A-24  
; Sequence 24, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortesmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99-274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-24

Query Match 94.3%; Score 8038; DB 4; Length 1576;  
Best local similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 1 AMDECADEGGRPQRCMPFVNAAFNVTVVATNTCTGTPPEEYCVGTGVTGKSHCLCDAG 60  
Db 3 AMDECTDSGRPQRCMPFVNAAFNVTVVATNTCTGTPPEEYCVGTGVTGKSHCLCDAG 62

Qy 61 QOHLQHGAAFLTDYNNQADTTWQSQTLWAGVQVPSINLTLHLGKAFDITVYVLFKFTS 120  
Db 63 QOHLQHGAAFLTDYNNQADTTWQSQTLWAGVQVPSINLTLHLGKAFDITVYVLFKFTS 122  
Qy 121 RPSFAIYKRTREDGPMWIPYQYSGSCENTYSKANRGFIPTGGDEQOALCTDESDISPL 180  
Db 123 RPSFAIYKRTREDGPMWIPYQYSGSCENTYSKANRGFIPTGGDEQOALCTDESDISPL 182  
Qy 181 TCGNVAFTLEGRPSAYNFDSVPLQEWVTATDTRVTLNRLNTLFGDEVFNDPKVLKSYI 240  
Db 183 TCGNVAFTLEGRPSAYNFDSVPLQEWVTATDTRVTLNRLNTLFGDEVFNDPKVLKSYI 242  
Qy 241 ALSDFAVGRCCKNGHASECKNPFKLMCKNKENTYGVDCCKLPFPNDRPWRATAES 300  
Db 243 ALSDFAVGRCCKNGHASECKNPFKLMCKNKENTYGVDCCKLPFPNDRPWRATAES 302  
Qy 301 ASECLPCDCNGRSQCYFDPPELYRSTGHGHCCTNCRDNTDGAKCERENFFRLGNTEAC 360  
Db 303 ASECLPCDCNGRSQCYFDPPELYRSTGHGHCCTNCRDNTDGAKCERENFFRLGNTEAC 362  
Qy 361 SPCHSPVGSLSSTOCDYSYGRSCCKPGVWMDKDCQPGFHSLTEAGCRPCSDPSGSTE 420  
Db 363 SPCHSPVGSLSSTOCDYSYGRSCCKPGVWMDKDCQPGFHSLTEAGCRPCSDPSGSTE 422  
Qy 421 CNVETGRCVCKDNVEGFNCERCKPGFNLSSNPKGCTPCFCFCHSSVCTNAVGSYDI 480  
Db 423 CNVETGRCVCKDNVEGFNCERCKPGFNLSSNPKGCTPCFCFCHSSVCTNAVGSYDI 482  
Qy 481 SSTFOIDEDGRVREORDGSEASLEWSSDROVIAVISDYPRTYFAPVFLGHQVLSYG 540  
Db 483 SSTFOIDEDGRVREORDGSEASLEWSSDROVIAVISDYPRTYFAPVFLGHQVLSYG 542  
Qy 541 NLSFGRVDRDTRLSAEDLVLEAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYP 600  
Db 543 NLSFGRVDRDTRLSAEDLVLEAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYP 602  
Qy 601 RPALSPPEFQKLLNLSISIKIRGYTSERSAGYLDVLTQASARPGVPATWVSSCTCPVG 660  
Db 603 RPALTPPEFQKLLNLSISIKIRGYTSERSAGYLDVLTQASARPGVPATWVSSCTCPVG 662  
Qy 661 YGQPCETCLPGYRRETPSLGYPVCLTCNGHSETCDPETGVCDRDNMTAGPHCEKS 720  
Db 663 YGQPCETCLPGYRRETPSLGYPVCLTCNGHSETCDPETGVCDRDNMTAGPHCEKS 722  
Qy 721 DGYGDSLTGTSDDQPCPCPGSSCAIYKTKVWCTHCTGTAGRCCLDDGVYFGDP 780  
Db 723 DGYGDSLTGTSDDQPCPCPGSSCAIYKTKVWCTHCTGTAGRCCLDDGVYFGDP 782  
Qy 781 LGSNGFVLCRPPCCNDNIDPNVNGNRLTGBCCLKCIYNTAGFYCDRCKEGFFGNLAP 840  
Db 783 LGSNGFVLCRPPCCNDNIDPNVNGNRLTGBCCLKCIYNTAGFYCDRCKEGFFGNLAP 842  
Qy 841 NPADKCKACACN-YGTWQSSCNPNVTGQCCLPHVSGRCGTCDPGYNLSQGCQCERC 899  
Db 843 NPADKCKACACN-YGTWQSSCNPNVTGQCCLPHVSGRCGTCDPGYNLSQGCQCERC 902  
Qy 900 DCHALGSTNGQCDIRTCQCEQCPGIGTQHCECEVNHFGFEGEGCKPCDCHPEGSLSLQC 959  
Db 903 DCHALGSTNGQCDIRTCQCEQCPGIGTQHCECEVNHFGFEGEGCKPCDCHPEGSLSLQC 962  
Qy 960 KDGRCCEBGFVGNRCDCCEENYFYNRSWPGCECPACRYRLVDDKAAAEHRVYKLELES 1019  
Db 963 KDGRCCEBGFVGNRCDCCEENYFYNRSWPGCECPACRYRLVDDKAAAEHRVYKLELES 1022  
Qy 1020 IANLGTGDDVMTDQAFEDRLKAEAREVTDLLREAEVVDVNDLMDRLQRVNSLHLSOIS 1079  
Db 1023 IANLGTGDDVMTDQAFEDRLKAEAREVTDLLREAEVVDVNDLMDRLQRVNSLHLSOIS 1082  
Qy 1080 RLQINRTIETGILAEARSRVSTEQIEIASRELEKAKM-AANVSITQPESTGEPNN 1138  
Db 1083 RLQINRTIETGILAEARSRVSTEQIEIASRELEKAKM-AANVSITQPESTGEPNN 1142



Qy	1139	MTLLAEARLAEARHKKQEADDIVRVAKTANETSAEAYNLLLRLLAGENOTALEIEEELNRK	1199
Db	1143	MTLLAEARLAEARHKKQEADDIVRVAKTANDTSTEAYNLLLRLLAGENOTAPEIEELNRK	1202
Qy	1199	YEQAKNTSQLEKQAAARVHEEAKRAGDKAVEIIVASVAQLTPVDSEALEHANKIKKEAAD	1258
Db	1203	YEQAKNTSQLEKQAAARVHEEAKRAGDKAVEIIVASVAQSPPLDSELEHANNIKKEAEN	1262
Qy	1259	LDRLIDQKLKQYEDLRDMDGKEHEVKNLLEKGAKEQQTADQLLARADAALAEAEAAKK	1318
Db	1263	LEQLIDQKLKQYEDLRDMDGKELEVKNLLEKGTQEQQTADQLLARADAALAEAEAAKK	1322
Qy	1319	GRSTQLEBANDILNNLKQDFDRVNDNKTAAEEALRRIPAINRTTAAENAKETREBAQLALGNA	1378
Db	1323	GRDTQLEBANDILNNLKQDFDRVNDNKTAAEEALRKIPAINQTITEANEKTRTAAQALGSA	1382
Qy	1379	AADATEAKNKAHEAERTASAAQKNAETSKADAEPTFGEVTDLDNEVNGMLRQLEEAENEL	1438
Db	1383	AADATEAKNKAHEAERTASAVQKNAETSKAEAEPTFAEVTDDLNEVNNMLKQLEBAEKEL	1442
Qy	1439	KRKQDDAQDQMMWAGMASQAQAEALNARKAKNSVSLLSQNLNLDQGLQDTVDLNLK	1498
Db	1443	KRKQDDAQDQMMWAGMASQAQAEINARKAKNSVTLSSLIINDLLEQLQGLQDTVDLNLK	1502
Qy	1499	NEIEGSLINKAKDENKASDLORKVSDLESEARKQEAATMDYNRDIAETIKDIHNLEDIKKT	1558
Db	1503	NEIEGTLINKAKDENKVSDLORKVSDLENEAKQEAATMDYNRDIEELMKDIRNLEDIRKI	1562
Qy	1559	LPTGCFNTPSIEKP	1572
Db	1563	LPSCGFNTPSIEKP	1576
RESULT 7			
US-09-562-702A-28			
; Sequence 28, Application US/09562702A			
; Patent No. 6632790			
; GENERAL INFORMATION:			
; APPLICANT: Yurchenco, Peter			
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use			
; FILE REFERENCE: 99-274-B			
; CURRENT APPLICATION NUMBER: US/09/562,702A			
; CURRENT FILING DATE: 2000-04-28			
; PRIOR APPLICATION NUMBER: 60/155,945			
; PRIOR FILING DATE: 1999-09-24			
; PRIOR APPLICATION NUMBER: 60/143,289			
; PRIOR FILING DATE: 1999-07-12			
; PRIOR APPLICATION NUMBER: 60/139,198			
; PRIOR FILING DATE: 1999-06-15			
; PRIOR APPLICATION NUMBER: 60/131,720			
; PRIOR FILING DATE: 1999-04-30			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 28			
; LENGTH: 1584			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-562-702A-28			
Query Match 94.3%; Score 8038; DB 4; Length 1584;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 1469; Conservative 47; Indels 2; Gaps 2;			
Qy	1	AMDCADGGGPPQRCMPEFVNAAPNVTVAATNTCGTTPPEYCVQGTGVTGKSKCHLCDAG	60
Db	3	AMDECTDEGGPPQRCMPEFVNAAPNVTVAATNTCGTTPPEYCVQGTGVTGKSKCHLCDAG	62
Qy	61	QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTLLHGKAFDITYYRLKAFHTS	120
Db	63	QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTLLHGKAFDITYYRLKAFHTS	122
Qy	121	RPESFAIYKTRDEGPPIPYQYSGSCENTYSKANRGFIRTGDEQALCTDFSDISPL	180

123	RPESFAIYKTRBDGPWIPYQYYSGSCENTYSKANGFIRITGDEQALCTDFSDISPL	182
181	TGGNVAESTLEGPSAYNFNSPVLOEWVATDIRVTLNRLNTFGDSVNDPKVLKSY	240
183	TGGNVAESTLEGPSAYNFNSPVLOEWVATDIRVTLNRLNTFGDEVNDPKVLKSY	242
241	AISDPAVGRCKCNHASECVKHEFDKLMCNKHNNTYGVDCBKCLPFENDRPERATAES	300
243	AISDPAVGRCKCNHASECMQIEFDKLVNCKHNNTYGVDCBKCLPFENDRPERATAES	302
301	ASECLPCDCNCRSCECYFDPYELRYSTRGHGHCCTNCRDNTGAKCERENFFALGNTEAC	360
303	ASECLPCDCNCRSCECYFDPYELRYSTRGHGHCCTNQDNTGAHCERENFFALGNNEAC	362
361	SPCHCSPVGLSLTQCDYGRCSCKPGVWGDKDRCPGFHSLTEAGCRPCSCDPSGSTDE	420
363	SSCHCSPVGLSLTQCDYGRCSCKPGVWGDKDRCPGFHSLTEAGCRPCSCDPSGSIDE	422
421	CNVETGRCKDNVGEFNCERCKPGFNLBNSSNPKGCTPCFCFHSSVCTNNAVGSYVDI	480
423	CNVETGRCKDNVGEFNCERCKPGFNLBNSSNPRGCTPCFCFHSSVCTNNAVGSYVSI	482
481	SSTFOIDEDGMRVEQRDGSSEASLEWSDRQYIAVISDSYPRVFIAPVKFLGNQVLSYGQ	540
483	SSTFOIDEDGMRABORQDGSSEASLEWSSERQDIAVISDSYPRVFIAPAKFLGHQVLSYGQ	542
541	NLSFSFVDRDRDTELSAEDVLVLEGAGURVSVPVLAQNSYPSSETTVKYIFRLHEATDYPW	600
543	NLSFSFVDRDRDTELSAEDVLVLEGAGURVSVPVLAQNSYPSSETTVKYIFRLHEATDYPW	602
601	RPALSPFEFQKLLNLTISIIRGTYSSRSAGYLDVLTQOSARPGPGVPATWVESCTCPVG	660
603	RPALTPEFQKLLNLTISIIRGTYSSRSAGYLDVLTQASARPGPGVPATWVESCTCPVG	662
661	YGGFCETCLPGYRETFPSLGPYSPCVLCTCNHGHSETCDSETGVCDRDNATGPHCBKCS	720
663	YGGFCETCLPGYRETFPSLGPYSPCVLCTCNHGHSETCDSETGVCDRDNATGPHCBKCS	722
721	DGYTGDSTLGTSSDCQPCPCPGSSCAIYVPKTKEWCTHCTPTGTAGKRCCLCDDGYGDP	780
723	DGYTGDSTLGTSSDCQPCPCPGSSCAVVPKTKEWCTHCTPTGTAGKRCCLCDDGYGDP	782
781	LGSGNPFVRLCRPCOCDNIDPNVAGNCRLTGTECLKCIYNTAGFYCDRCKEGFGNPLAP	840
783	LGRNGFVRLCRLOCSNIDPNVAGNCRNLTGTECLKCIYNTAGFYCDRCXGDFGPNPLAP	842
841	NPAUKKACACN-YGTVOQSSCNPTVQCQCLPHVSGRDCGTCDPGYNLQSGQGCERC	898
843	NPAUKKACACNPGYTKWQSSCNPTVQCQCLPHVTDGQDAGCDPGFYNLQSGQGCERC	902
900	DCHALGSTNGOCDIRTCGCEQPGITQHCERETNHFHFGPGCEKPCDCHHGSLSLQC	958
903	DCHALGSTNGOCDIRTCGCEQPGITQHCERCEVNHFGPGCEKPCDCHHGSLSLQC	962
960	KDDGRCECREGFVGNRCDOCEENFYNRSWPGQCECPACVRLVKDKAAHRVKLQELSL	1018
963	KDDGRCECREGFVGNRCDOCEENFYNRSWPGQCECPACVRLVKDVADHRVKLQELSL	1022
1020	IANLGTGDMVTDQAFEDRLKEAREVTDLLRREAQEVKVDQNDLMDRLQRVNSLSHSQIS	1078
1023	IANLGTGDMVTDQAFEDRLKEAREVYDMLRQAQDKVDQNDLMDRLQRVNNLTSSQIS	1082
1080	FLQINRTIETGTILAEARARSVESTEQLEIETASRELEKAKM-AANYISITQPESTGPNN	1138
1083	FLQINRTIETGTILAEARARSVENTERLEIETASRELEKAKVAANYISITQPESTGPNN	1142
1139	MTLLAEARRLAERHKEQADDIVRAKANTETSAEYNLLRLTLAGSNQTALETIEELNRK	1198
1143	MTLLAEARRLAERHKEQADDIVRAKANTDSTEAYNLLRLTLAGSNQTALETIEELNRK	1202
1199	YEQAQNTSODLEKQAARVHEAKGACGKAVEIYASVAQLTPVDSEALENEAKTIKKAAD	1258
1203	YEQAQNTSODLEKQAARVHEAKGACGKAVEIYASVAQLSPDSELENNANIKKAEN	1262

QY	1259	LDRLIDQKLDYEDLRDMRGKEHEVNKLEKGAEOQTADQOLARADAAKALAEBAAKK	1318
DB	1263	LEQLIDQKLDYEDLRDMRGKEHEVNKLEKGAEOQTADQOLARADAAKALAEBAAKK	1322
QY	1319	GRSTLOANDILANKDFDRVNDNKTAABENLRRIIPAINRTIAEANEKTRAEQALGNA	1378
DB	1323	GRDTLOANDILANKDFDRVNDNKTAABENLRRIIPAINRTIAEANEKTRAEQALGSA	1382
QY	1379	AADATEAKNKAHEAERIAASAAQKATSTKADAERTFGEVTDLDNEVNGMLRQLLEAENEL	1438
DB	1383	AADATEAKNKAHEAERIAASAVQKATSTKADAERTFAEVTDLONEVNNMLKQLQEAKEKEL	1442
QY	1439	KRKQDDADQMMAGMASAAQAEAELEARNKAKNSVSSLLSOLNNLLDQLOLQDVTDLNKL	1498
DB	1443	KRKQDDADQMMAGMASAAQAEAEINARKAKNSVTSLLSIIINDLLQLOLQDVTDLNKL	1502
QY	1499	NEIEGSLNKADEMKASDLRKVSDLESEARKQEAAMINDYNRDIABIIKDIHNLIEDIKKT	1558
DB	1503	NEIEGSLNKADEMKVSDLRKVSDELNEAKQEAAMINDYNRDIEEIMKDIRNLEDIRKT	1562
QY	1559	LPTGCFNTPSIEKP	1572
DB	1563	LPSGCFNTPSIEKP	1576
RESULT 8			
US-09-562-702A-22			
; Sequence 22, Application US/09562702A			
; Patent No. 6632790			
; GENERAL INFORMATION:			
; APPLICANT: Yurchenco, Peter			
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use			
; FILE REFERENCE: 99-274-B			
; CURRENT APPLICATION NUMBER: US/09/562,702A			
; CURRENT FILING DATE: 2000-04-28			
; PRIOR APPLICATION NUMBER: 60/155,945			
; PRIOR FILING DATE: 1999-09-24			
; PRIOR APPLICATION NUMBER: 60/143,289			
; PRIOR FILING DATE: 1999-07-12			
; PRIOR APPLICATION NUMBER: 60/139,198			
; PRIOR FILING DATE: 1999-06-15			
; PRIOR APPLICATION NUMBER: 60/131,720			
; PRIOR FILING DATE: 1999-04-30			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 22			
; LENGTH: 1609			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-562-702A-22			
Query Match 94.3%; Score 8038; DB 4; Length 1609;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;			
QY	1	AMDECADEGRPQRCMPFNAAFNVTVAATTCCTPPEEYCVGTGVTGKSHLCDAG	60
DB	36	AMDECTDEGRPQRCMPFNAAFNVTVAATTCCTPPEEYCVGTGVTGKSHLCDAG	95
QY	61	QOHLQGAFLDYNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITVRLKPHTS	120
DB	96	QOHLQGAFLDYNQADTTWQSQTMLAGVQYPSNLTLLHKGAFDITVRLKPHTS	155
QY	121	RPEFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDFQOALCTDFSDISPL	180
DB	156	RPEFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDFQOALCTDFSDISPL	215
QY	181	TGQNVAFSTLEGPSPAYNFDNSVLQEWYATDIRVTNLRLNTFGDFVNDPKVLKSYYY	240
DB	216	TGQNVAFSTLEGPSPAYNFDNSVLQEWYATDIRVTNLRLNTFGDFVNDPKVLKSYYY	275
QY	241	AISDPVAGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATAES	300

DB	276	ALISDPVAGGRCKNGHASECMKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATAES	335
QY	301	ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDGAKEBCHRENFRLGNTBAC	360
DB	336	ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDGAKEBCHRENFRLGNTBAC	395
QY	361	SPCHSPVGSJSTOCDSSYGRCSCKPGVMGDKDRQCPGFHSLTEAGCRPCSCDPSGSTDE	420
DB	396	SSCHSPVGSJSTOCDSSYGRCSCKPGVMGDKDRQCPGFHSLTEAGCRPCSCDPSGSTDE	455
QY	421	CNVETGRVCYCKDNVEGFNCERCKPGFFNLSSNPKGCTPCFCFGHSSVCTNAVGSVYDI	480
DB	456	CNVETGRVCYCKDNVEGFNCERCKPGFFNLSSNPKGCTPCFCFGHSSVCTNAVGSVYDI	515
QY	481	SSTFOIDEDCHRVORDSGSEASLEWSRDROYTAVLSDSYEBRYFTAPVKFELGNVLSYGO	540
DB	516	SSTFOIDEDCHRVORDSGSEASLEWSRDROYTAVLSDSYEBRYFTAPVKFELGNVLSYGO	575
QY	541	NLSFSPFRVDRRTRLSAEDLVLEGAGLAVSVPLIAQGNSTPSETTVKYIFRLHEATDYPW	600
DB	576	NLSFSPFRVDRRTRLSAEDLVLEGAGLAVSVPLIAQGNSTPSETTVKYIFRLHEATDYPW	635
QY	601	RPALSPFPFQKLLNNLTSIKIRGTYSERSAGVLDVDTLOSARPPGPGVATWVESCTCPVG	660
DB	636	RPALSPFPFQKLLNNLTSIKIRGTYSERSAGVLDVDTLOSARPPGPGVATWVESCTCPVG	695
QY	661	YGGQFCETCLPGYRRTPSLGYPSPCVLCTCNHSETCDPETGVCDRCRNTAGPCEKCS	720
DB	696	YGGQFCETCLPGYRRTPSLGYPSPCVLCTCNHSETCDPETGVCDRCRNTAGPCEKCS	755
QY	721	DGYGDSLTGTSDDQCPGCGSSCAIVPKTKVWVCHTCTGTAGKCELCDDCGVFGDP	780
DB	756	DGYGDSLTGTSDDQCPGCGSSCAIVPKTKVWVCHTCTGTAGKCELCDDCGVFGDP	815
QY	781	LGNGPVRLCRPCQCNNDNDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKGFFGNPLAP	840
DB	816	LGNGPVRLCRPCQCNNDNDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKGFFGNPLAP	875
QY	841	NPADKCKACACN-YGTVQQSSCNVPTGQCCLPHVSGRDCCTCDPGYNYNLSGGGCERC	899
DB	876	NPADKCKACACN-YGTVQQSSCNVPTGQCCLPHVSGRDCCTCDPGYNYNLSGGGCERC	935
QY	900	DCHALGSTNGQCDIRTGQCECOPGITGQHCERTNHFGEPCGKPCDCHHEGSLSQC	959
DB	936	DCHALGSTNGQCDIRTGQCECOPGITGQHCERTNHFGEPCGKPCDCHHEGSLSQC	995
QY	960	KDDGRCECREGFGVGNRCDCENYFYNRSWPQCBPCYRLVVKOKAABHRVKLOLESL	1019
DB	996	KDDGRCECREGFGVGNRCDCENYFYNRSWPQCBPCYRLVVKOKAABHRVKLOLESL	1055
QY	1020	IANLGTGDDMTDQAFEDRLKEAREVTDLLREARQVVDQNDQNDLRLQVNSLSHQSIS	1079
DB	1056	IANLGTGDDMTDQAFEDRLKEAREVTDLLREARQVVDQNDQNDLRLQVNSLSHQSIS	1115
QY	1080	RLQNIIRNTIETGILAEARARSVESTPEQLEIASRELEKAKM-AANVSTQPESTGEPPN	1138
DB	1116	RLQNIIRNTIETGILAEARARSVESTPEQLEIASRELEKAKM-AANVSTQPESTGEPPN	1175
QY	1139	MTLLAEARLARLRHQEADDDIVRVAKTANETSAEANYLLIRTAGENOTALEIEBLNK	1198
DB	1176	MTLLAEARLARLRHQEADDDIVRVAKTANETSAEANYLLIRTAGENOTALEIEBLNK	1235
QY	1199	YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEKIKKEAAD	1258
DB	1236	YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEKIKKEAAD	1295
QY	1259	LDRLIDQKLDYEDLRDMRGKEHEVNKLEKGAEOQTADQOLARADAAKALAEBAAKK	1318
DB	1296	LEQLIDQKLDYEDLRDMRGKEHEVNKLEKGAEOQTADQOLARADAAKALAEBAAKK	1355
QY	1319	GRSTLOANDILANKDFDRVNDNKTAABENLRRIIPAINRTIAEANEKTRAEQALGNA	1378

Db 1356 GRDTLQEAANDILNLLKDPDRVNDNKTAAEEALRKIPALNQITTEANEKTRQAALGSA 1415  
QY 1379 AADATEAKNAHEAERIAAGAAKNATSTKADARTFGEVTDLDNEVNGMLRQLEAEANEL 1438  
Db 1416 AADATEAKNAHEAERIAAGAAKNATSTKAEARTFAEVTDLNENNNMLKQLEAEKEL 1475  
QY 1439 KKKQDDADQDMMAGWASQAQAEALNARKAKNSVSSLLSQNLNLLDOLGQDCTVDLNLK 1498  
Db 1476 KKKQDDADQDMMAGWASQAQAEALNARKAKNSVSSLLSIINDLLEQLGQDCTVDLNLK 1535  
QY 1499 NEIEGSLNKADEMKAASDLDRKVSDBLESEARKOEAAMNDYNRDIAEIIKDHNLEDIKKT 1558  
Db 1536 NEIEGTLNKADEMKAASDLDRKVSDBLESEARKOEAAMNDYNRDIEBIMKDIEJEDIRKT 1595  
QY 1559 LPTGCENTPSIEKP 1572  
Db 1596 LPSGCCENTPSIEKP 1609

RESULT 9  
US-09-561-818A-22  
; Sequence 22, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-22

Query Match 94.3%; Score 8038; DB 4; Length 1609;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPORCMPEFVNAAAFNVTVAINTCGTPPEYCVQGTGVTGKTSCHLCDAG 60  
Db 36 AMDECTDEGGRPORCMPEFVNAAAFNVTVAINTCGTPPEYCVQGTGVTGKTSCHLCDAG 95  
QY 61 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLKAFDITYVRLKFHTS 120  
Db 96 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLKAFDITYVRLKFHTS 155  
QY 121 RPESFALYKTRTDGPMIPYQYSGSCENTYSKANRGFRTGGDEQOALCTDEFSDISPL 180  
Db 156 RPESFALYKTRTDGPMIPYQYSGSCENTYSKANRGFRTGGDEQOALCTDEFSDISPL 215  
QY 181 TGGNVAFTSLGPRSAYNFQNSPVLQEWVTATDIRVTLNRLNTFTGDEVFNDPKVLKSYYY 240  
Db 216 TGGNVAFTSLGPRSAYNFQNSPVLQEWVTATDIRVTLNRLNTFTGDEVFNDPKVLKSYYY 275  
QY 241 AISDFAVGGRCKNGHASECVKNEFPLKMCNCKHNTYGVDCBKLPFFNDRPWRRTAES 300  
Db 276 AISDFAVGGRCKNGHASECVKNEFPLKMCNCKHNTYGVDCBKLPFFNDRPWRRTAES 335  
QY 301 ASECLPCDCNCRGQECYFDPFLYRSTGHGGHCTNCRDNTDGAKCERCRNFRLGNTEAC 360  
Db 336 ASECLPCDCNCRGQECYFDPFLYRSTGHGGHCTNCRDNTDGAKCERCRNFRLGNNEAC 395  
QY 361 SPCHSPVGSLSLQCSYGRCSKPGVMGDKDRCPQFGHSLTEACRPSCDPSGSTDE 420  
Db 396 SSCHSPVGSLSLQCSYGRCSKPGVMGDKDRCPQFGHSLTEACRPSCDPSGSTDE 455  
QY 421 CNVETGRCKNDVNGNFCRCKPFPNLFSSNPKCTPCFCFGHSSVCTNAGVSVYDI 480  
Db 456 CNVETGRCKNDVNGNFCRCKPFPNLFSSNPKCTPCFCFGHSSVCTNAGVSVYDI 515

QY 481 SSTFOIDEDCWRVEORDGSEASLEWSSDROYIAVSDSYPPRYFIAPVKFLGNQVLSYGQ 540  
Db 516 SSTFOIDEDCWRVEORDGSEASLEWSSDROYIAVSDSYPPRYFIAPVKFLGNQVLSYGQ 575  
QY 541 NLSFSFVDRDRDRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600  
Db 576 NLSFSFVDRDRDRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 635  
QY 601 RPALSPEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLQASRPGVPVPAWVESCTCPVG 660  
Db 636 RPAUTPEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLQASRPGVPVPAWVESCTCPVG 695  
QY 661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPBTGVCDORDNTAGPHCKSKS 720  
Db 696 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPBTGVCDORDNTAGPHCKSKS 755  
QY 721 DGYGDSLTGTSDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGRCCLCDDGYFGDP 780  
Db 756 DGYGDSLTGTSDCQPCPCPGSSCAIVPKTKEVVCTHCTGTAGRCCLCDDGYFGDP 815  
QY 781 LGSNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCRKEGFPGNLAP 840  
Db 816 LGRNGPVRLCRPCQCNNDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCRKEGFPGNLAP 875  
QY 841 NPADKCKACACN-YGTVOQSSCNPTVTCQCCPLPHUSGRDCGTCDPGYNLSQSGCERC 899  
Db 876 NPADKCKACACNPGYTMKQSSCNPTVTCQCCPLPHUSGRDCGTCDPGYNLSQSGCERC 935  
QY 900 DCHALGSTNGQCDIRTCQCCPGITGQHCERCEBTHFGFPGECPCDCHHSGSLQ 959  
Db 936 DCHALGSTNGQCDIRTCQCCPGITGQHCERCEBTHFGFPGECPCDCHHSGSLQ 995  
QY 960 KDGRCRCEGFGVGNRCQCEENFYNRSWPGQCECPACVRLVKDKAAERVKLOELES 1019  
Db 996 KDGRCRCEGFGVGNRCQCEENFYNRSWPGQCECPACVRLVKDKAAERVKLOELES 1055  
QY 1020 IANLGTGDDMTDQAFEDRLKEAREVTDLLREAEQVQDVQNLMDRLQVNSLSHQIS 1079  
Db 1056 IANLGTGDDMTDQAFEDRLKEAREVTDLLREAEQVQDVQNLMDRLQVNSLSHQIS 1115  
QY 1080 FLQIRNTIETGILABRARSRVESTQLEIIEASRELEKAM-AANYSITQPESTGPN 1138  
Db 1116 FLQIRNTIETGILABRARSRVESTQLEIIEASRELEKAM-AANYSITQPESTGPN 1175  
QY 1139 MTLAEARRLAERHKEADDIVRVAKTANETSAEYNLLRLTLAGENOTALIEEELNRK 1198  
Db 1176 MTLAEARRLAERHKEADDIVRVAKTANETSAEYNLLRLTLAGENOTALIEEELNRK 1235  
QY 1199 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALENANKIKKEAAD 1258  
Db 1236 YEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSALENANKIKKEAAD 1295  
QY 1259 LDRLIDQKLKDYEDLREDMRKEHEVKNLLEKGAEOCTADOLLARADAKALAEAAK 1318  
Db 1296 LEQIDQKLKDYEDLREDMRKEHEVKNLLEKGAEOCTADOLLARADAKALAEAAK 1355  
QY 1319 GRSTLQEAANDILNLLKDPDRVNDNKTAAEEALRKIPALNQITTEANEKTRQAALGSA 1378  
Db 1356 GRSTLQEAANDILNLLKDPDRVNDNKTAAEEALRKIPALNQITTEANEKTRQAALGSA 1415  
QY 1379 AADATEAKNAHEAERIAAGAAKNATSTKADARTFGEVTDLDNEVNGMLRQLEAEANEL 1438  
Db 1416 AADATEAKNAHEAERIAAGAAKNATSTKADARTFGEVTDLDNEVNGMLRQLEAEANEL 1475  
QY 1439 KKKQDDADQDMMAGWASQAQAEALNARKAKNSVSSLLSQNLNLLDOLGQDCTVDLNLK 1498  
Db 1476 KKKQDDADQDMMAGWASQAQAEALNARKAKNSVSSLLSIINDLLEQLGQDCTVDLNLK 1535  
QY 1499 NEIEGSLNKADEMKAASDLDRKVSDBLESEARKOEAAMNDYNRDIAEIIKDHNLEDIKKT 1558  
Db 1536 NEIEGTLNKADEMKAASDLDRKVSDBLESEARKOEAAMNDYNRDIEBIMKDIEJEDIRKT 1595

QY 1559 LPTGCFNTPSIEKP 1572  
Db 1596 LPSCGCFNTPSIEKP 1609

RESULT 10  
US-09-562-702A-26  
; Sequence 26, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 1617  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-26

Query Match 94.3%; Score 8038; DB 4; Length 1617;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 1 AMDECADEGGPQRCMBPFVNAAFNVTVATNCTGTPPEYCVQTVGTGTSCHLDCAG 60  
Db 36 AMDECTDEGGPQRCMBPFVNAAFNVTVATNCTGTPPEYCVQTVGTGTSCHLDCAG 95

QY 61 QOHLQHGAAFTLDYNNQADTTWQSQTLAQVQVPSINLTLHLGKAFDITYVRLKPHTS 120  
Db 96 QPHLQHGAAFTLDYNNQADTTWQSQTLAQVQVPSINLTLHLGKAFDITYVRLKPHTS 155

QY 121 RPESFAIYKRTREDPGMPYQYSGSCENTYSKANRGFIRTGDEQALCTDFSDISPL 180  
Db 156 RPESFAIYKRTREDPGMPYQYSGSCENTYSKANRGFIRTGDEQALCTDFSDISPL 215

QY 181 TGGVAFSTLEGRPSAYNFDSVPLQEWVTATDIRVTLNRLNLTGDEVFNDPKVLSYYY 240  
Db 216 TGGVAFSTLEGRPSAYNFDSVPLQEWVTATDIRVTLNRLNLTGDEVFNDPKVLSYYY 275

QY 241 AISDPAVGRCKNGHASECVKNEFDKLMCNCKENTYGVDCCKLPFFNDRPMRRATAES 300  
Db 276 AISDPAVGRCKNGHASECVKNEFDKLMCNCKENTYGVDCCKLPFFNDRPMRRATAES 335

QY 301 ASECLPCDNGRSQCYDPELYRSTGHGCHTNCRDNTDCAKCCRENFRLGNTEAC 360  
Db 336 ASECLPCDNGRSQCYDPELYRSTGHGCHTNCRDNTDCAKCCRENFRLGNTEAC 395

QY 361 SPCHSPVGSLSSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPCSDPSGSTDE 420  
Db 396 SSCHSPVGSLSSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPCSDPSGSTDE 455

QY 421 CNVETGRVCXNDVGFNCRCCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSYDI 480  
Db 456 CNVETGRVCXNDVGFNCRCCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSYDI 515

QY 481 SSTFOIDEGWEVORDGSEASLEWSSDQYTAVIDSYFFRYFIAPVKFLGNQVLSYQG 540  
Db 516 SSTFOIDEGWEVORDGSEASLEWSSDQYTAVIDSYFFRYFIAPVKFLGNQVLSYQG 575

QY 541 NLSFSFRVDRRTRLASDLVLEGAGLRVSVPFLIAQGNSSYPSETTVKIVFLHEATDYPW 600

RESULT 11  
US-09-845-583A-10

Db 576 NLSFSFRVDRRTRLASDLVLEGAGLRVSVPFLIAQGNSSYPSETTVKIVFLHEATDYPW 635  
QY 601 RPALSPFFQKLLNNLTSIKIRGTYSERSAGYLDVDTLOSARPGPGVATWVSECTCPVG 660  
Db 636 RPALTFFQKLLNNLTSIKIRGTYSERSAGYLDVDTLOSARPGPGVATWVSECTCPVG 695

QY 661 YGGQFCETCLPGYRRETPSLGYPSPVLCNTHGSETCDPETGVCDCRDNATAGHCEKCS 720  
Db 696 YGGQFCENCLSGYRRETPNLGYPSPVLCNTHGSETCDPETGVCNCRDNATAGHCEKCS 755

QY 721 DGYGDSLTGTSDDQPCPCPGSSSCAIVPTKVVCHTCTGTAGKRCCLCDGYPGDP 780  
Db 756 DGYGDSLTGTSDDQPCPCPGSSSCAIVPTKVVCHTCTGTAGKRCCLCDGYPGDP 815

QY 781 LGSNGPVLRLCRPCQCNNDNIDNAVGNLRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAP 840  
Db 816 LGRNGPVLRLCLRCQSDNIDNAVGNLRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAP 875

QY 841 NPADKCKACAN - YGTVOQSSCNPVTCQCLPHVSGRDCGTCDPGYNYLQSGGCEC 899  
Db 876 NPADKCKACNPNYGTMTKQSSCNPVTCQCLPHVTQDCGACDPGFYNLQSGGCEC 935

QY 900 DCHALGSTNGQCDIRTGQCECQPGITGOHCERTNHFHGFEGPEGCKPCDCHHESLSLQ 959  
Db 936 DCHALGSTNGQCDIRTGQCECQPGITGOHCERTNHFHGFEGPEGCKPCDCHHESLSLQ 995

QY 960 KDDGRCECREGFGVGNRCQCEENFYFNRSWPQCECPACYLKDKAAHVRKVLQELSL 1019  
Db 996 KDDGRCECREGFGVGNRCQCEENFYFNRSWPQCECPACYLKDKAAHVRKVLQELSL 1055

QY 1020 IANLGTGDDMTDQAFEDRLKEAREVTDILAREQVQKVDONLMDRLQVRNSSLHQSIS 1079  
Db 1056 IANLGTGDDMTDQAFEDRLKEAREVMDLLREADQVQKVDONLMDRLQVRNSSLHQSIS 1115

QY 1080 RLQNRITTEETGILAEARSRVSETEQLIETIASRELEKAKM - AANVSITPESTGEPNN 1138  
Db 1116 RLQNRITTEETGILAEARSRVSETEQLIETIASRELEKAKM - AANVSITPESTGEPNN 1175

QY 1139 MTLAABEARLAEKHOADDIVRVAKTANETSBAYNLLILRTLAGENQTALEIIEELNRK 1198  
Db 1176 MTLAABEARLAEKHOADDIVRVAKTANDTSTBAYNLLILRTLAGENQTALEIIEELNRK 1235

QY 1199 YEOAKNISODLEKQAAHVHEAKRAGDKAVEIYASVAQLTFVDSALENEANKIKKEAAD 1258  
Db 1236 YEOAKNISODLEKQAAHVHEAKRAGDKAVEIYASVAQLTFVDSALENEANKIKKEAAD 1295

QY 1259 LDRLIDQKLYEDLREDMRGHEHEVKNLLEKGAQOQTADQLARADAALAEAAK 1318  
Db 1296 LEQLIDQKLYEDLREDMRGHEHEVKNLLEKGAQOQTADQLARADAALAEAAK 1355

QY 1319 GRSTLOEANDILNLLKDPDRVNDNKTAAEALRRI - PAIRNTIABANEKTRAEQALGNA 1378  
Db 1356 GRSTLOEANDILNLLKDPDRVNDNKTAAEALRRI - PAIRNTIABANEKTRAEQALGNA 1415

QY 1379 AADATEAKNAHEAERIASAAQKATSTKADABRTFGEVTDLDNVEVGNLQLEAEANEL 1438  
Db 1416 AADATEAKNAHEAERIASAAQKATSTKADABRTFGEVTDLDNVEVGNLQLEAEANEL 1475

QY 1439 KRQDDADQDMWAGWASQAQAEELNARKKNSVSLLSOLNLLDOLGOLDTVDLANK 1498  
Db 1476 KRQDDADQDMWAGWASQAQAEELNARKKNSVSLLSOLNLLDOLGOLDTVDLANK 1535

QY 1499 NEIEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDYNDRIAEIHKDHNLSIDIKT 1558  
Db 1536 NEIEGSLNKADEMKAASDLDRKVSLESEARKQEAAMIDYNDRIAEIHKDHNLSIDIKT 1595

QY 1559 LPTGCFNTPSIEKP 1572  
Db 1596 LPSCGCFNTPSIEKP 1609

Sequence 10, Application US/09845583A  
Patent No. 6635616  
GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert  
APPLICANT: Brunken, William Joseph  
APPLICANT: Champlaud, Marie-France  
APPLICANT: Hunter, Dale  
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
FILE REFERENCE: 10287-056001  
CURRENT APPLICATION NUMBER: US/09/845,583A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/200,863  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 1587  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-845-583A-10

Query Match 42.1%; Score 3586; DB 4; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 4.3e-206;  
Matches 700; Conservative 258; Mismatches 568; Indels 72; Gaps 23;

QY 2 MDECAEGGRPQPCMEFEVNAENVTVATNTCGTPPEYCVQTVGTGKSHLCLDAQ 61  
DB 22 MGACYGAGRPQRCLEPVFAEAGRAQASHTCGSPFDFCPHVGAAGAGACQRCDAAD 81  
QY 62 QHLQHGAFTDYNNQADTWMQSTWLAGVQVQVPSINLTGLKAFDITYVRLKPHTSR 121  
DB 82 PORHNASYLTDFHSQDESTWQSPMAFGVQVPTSVNITLRLGKAYEITYVRLKPHTSR 141  
QY 122 PESFAYKRTREGPWIPYQYSGSCENYISKANRGFIRITGDEQALCTDFDISPLT 181  
DB 142 PESFAYKRSRAGPWEYQYFASCCQKYRGEQYLRPGEDRYAFCTSFSDISPLS 201  
QY 182 GGNVASTLEGPSAYNFNSPVLQBWATATDTRVTLNLTNFGDEVNDPKVLSYYVA 241  
DB 202 GGNVASTLEGPSAYNFNSPVLQBWATATDTRVTLNLTNFGDEVNDPKVLSYYVA 261  
QY 242 ISPAVGRCKNGHASECVKNEFDKLMCNKNTYGVCEKLPFPNDRPWRRTAESA 301  
DB 262 VDSFVGRCKNGHASECPDVAGQLACRCQHNTGTDCERCLPFPQDRPWARGTAEAA 321  
QY 302 SECLPCDCNRSOECYFDEPILVSTGHGHCNCRDNTGAKCERENFEALGNTEACS 361  
DB 322 HECLPCNCSRSBECTFDFELFSTGHGRCCHCRDHTAGPHCERCOENFYHWDPMPCQ 381  
QY 362 PCHCSPVGSLSLTCDSYGRCSKPGYMGDKDRCPQFPHSLTEAGRCPCSDPSTGDC 421  
DB 382 PCDCQAGSLHLQCDTDTGTCAKPTVTGWKCDRLCPGHSLSBGGCRPCTCNPAGSLDT 441  
QY 422 NVETGRVCNDVGENCERCKGFFNLSSNPKGTCTPCFCGHSSVCYNAGYSYVDIS 481  
DB 442 DPRSGRCPCKENYEGNLCDRCFGTNLQPHNPAGCSCFCYGHKVCACSTAQFQVHHIL 501  
QY 482 STFOIDEDGWRVEQRQDSEASLSWSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYGN 541  
DB 502 SDFHQAGRWARSVSGSEHSPQWSPN- ---GVLLSPEDEBELTAPGKFLGQDRFSYGP 557  
QY 542 LSFSPFRVDRDRLSADLVLGAGLRVSVPLIAQNSYSPSETTVKVIYRLH- ---EATDY 598  
DB 558 LIUTFRVPPGDSPLPVQ- LLEGTLGLALS- LRSLSLSPQDARASQGGRAQVPLQETSE 614  
QY 599 PWRPALSPPFFOKLLNLTIKIRGTVSERSAG- -YLDVVTLOSARPGPGVPATWYESTC 656  
DB 615 DVAPLPFPFFQRLANLTSLRLRVSPGSPAGPVFLTEVRLTSARPLSPASWYELCS 674  
QY 657 CPVYGGQFCETCLPGVRRTPSLGYPSPVCLTCNGHSETCPETGVCDRCRNTAGPHC 716  
DB 675 CPTGYTQFCESCAPGYKREMPQGPVASCVPCTCNQHG- TCDPNTGICVCSHHTGPSC 733

717 EKSDGYVSTIGTSSDQPCPCPGSSCAIVPKTKEVVTCHTCTAGRCCLCDDG 776  
734 ERCLFGYGNFPAGQADDQPCPCPGSACTTIPESGEVVTCTCPGQRRCEVCDG 793  
777 FGDPLSGNPVRLCRPCQCNNDNDPNAVGNCRNLGTCLKCIYNTAGFYCDRCKEGFFN 836  
794 FGDPLGLFGHPQPCQCCSGNVDNAGNCDPLSGHCLRLHNTTGDHCEHCQEGYGS 853  
837 PLAPNPADKCKACACN- YGTVQOQSSCNVTVGQCCQLPHVSGRDCGTGCGYNYLQSGQ 895  
854 ALAPNPADKCMPCSCHPQGSVSEQPCDPVTGQCSCLPHVTARDCSRCEYFGFLOQGRG 913  
896 CERCDHALSTNGCCDIRTCQCECPGITHGHCERCETNHFPGPGCKPCDCHHESGL 955  
914 CRSCKHPGSGEDQCHPKTGCTCRFGVTGQACDRCLQGFSSSIKGCACRSPJGAA 973  
956 SLOCKDGRCEGREGFVGNRCDCQCEENFYNRSWPGQCECPACVRLVKOAAEHRVKQE 1015  
974 SAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCPSCYALVKEETAKLKLTL 1033  
1016 LESLIANLGTGD- ---DMVTDOAFEDRLKEAREVTDLLREAOEVKDVQNDMLDRQV 1070  
1034 TEGWQSGDCSPGPDILLGEAPRGDVYQGH- ---LLPGAREA- ---FUEQWGL 1083  
1071 NSSLSQISRLQNTIRNTIETGILAEARSRSVESTEQIIEIASRE-LEKAKMAANVSITQ 1129  
1084 EGAVKAAEQQLRNLKNGARCAQAGSQKTCQLADLEAVLSSEBEEILHAAAILASLPIQ 1143  
1130 PESTGEPNNMTLAEABARRLAERHKQADDIRVAKTANETSABAYNLLRTLAGENQTA 1189  
1144 -EGPSQPTKNSHLAEARALARSHRDATKIAATAMPALLASNTSYALLNLL-EGRVA 1200  
1190 LEIS-ELNRKYEOAKNTSQLEKQAAVHEEAKGAGDKAVEIVASVAQL- --- 1237  
1201 LETORDLEDYQVQAAQAKALRTAVAEVLPEAE- ---SVLATVQOVGADTAPYLALL 1253  
1238 -TPVDSA- -LENEANKIKKEAADRLIDQKLYOEDURE-DMRKEHEVKNLLE 1289  
1254 ASPGALPOKSAEDLGLKAKALEKTVAWSQHMATEAARTLQTAQATLROTE- ---PLTMA 1310  
1290 KGAEQQTADOLLARADAAKALAEAAKGRSTLQEAANDILNLIKDFDRVNDNKTAEE 1349  
1311 RSRUTATFASLHGQARAALTQASSVQAATVTVNGARTLLADLEGKLOFPFPRKQAL 1370  
1350 ALRRIPAINRTIABANEKTRQAALGNAADATEAKNKAHEAFRIASAAQKNATSTKAD 1409  
1371 QRKADSVSDRLAATRKTKQABRMGLGNAAPLSSAKKGRAEVLAQAKLAKALLRE 1430  
1410 AERTFGEVTDLDNEVGNLRLQ-EEAENELKRKODDADQDMMAGVASQAQAEELNARK 1468  
1431 RQAHRRASRLTSQTATLQOASQOVLASEARROELEBEAEVAGLS- ---EMEQQIRE 1485  
1469 AKNSVSSLLSOLLNLLDQGLD- -VDLNKLINEIEGLNKADEM-KASDLDKRVSDLE 1525  
1486 SRISLEKDIETSELLARLSLDTHQAPALNETOWALERLRLQLGSPGLQKLSILE 1545  
1526 SEARKQEAINDYNRDIAEIKIHNLEDIKTLPTGC 1563  
1546 QESQOQELIQPFESDLAETRADKONLEAILHSLPENC 1583

RESULT 12  
US-09-561-709B-3  
Sequence 3, Application US/09561709B  
Patent No. 6682911  
GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert  
APPLICANT: Champlaud, Marie-France  
APPLICANT: Olson, Pamela  
APPLICANT: Koch, Manuel  
APPLICANT: Brunken, William  
TITLE OF INVENTION: LAMININS AND USES THEREOF  
FILE REFERENCE: 10287-060001

;; CURRENT APPLICATION NUMBER: US/09/561,709B  
;; CURRENT FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 09/169,949  
;; PRIOR FILING DATE: 1998-10-09  
;; PRIOR APPLICATION NUMBER: US 60/061,609  
;; PRIOR FILING DATE: 1997-10-10  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 1587  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-561-709B-3

Query Match 42.1%; Score 3586; DB 4; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 4.3e-206; Indels 72; Gaps 23;  
Matches 700; Conservative 258; Mismatches 568;  
Qy 2 MDECADGGRRQRCMPBFVNAAFNVTVVATNTCGTPPEYCVQVGTGVTKSHLDAQG 61  
Db 22 MGACVYDAGRRQRCMPBFVNAAFNVTVVATNTCGTPPEYCVQVGTGVTKSHLDAQG 81  
Qy 62 QHLQGHAAFLTDYNNQADTTWQSQOTMLAGVOYFNSINLTLHLGKAFDITYVRLKHTSR 121  
Db 82 PORHNASYLTDFHSQDESTWQSPMAFGVQYFPTSVNITRLRGKAYEITYVRLKHTSR 141  
Qy 122 PESFALYKRTREDGFWPTVQYYSGCENTYSKANRGPIRTGGDEQQALCTDEFSDISPLT 181  
Db 142 PESFALYKRSRADGPWFQYFYSASCKTYGRPEGYLRPGEDERVAFTSEFSDISPLS 201  
Qy 182 GGNVAFSTLEGRPSAYNPDNSVLOEWWTATDTRVNTLRNTFGDEVPNDPKVLSYYA 241  
Db 202 GGNVAFSTLEGRPSAYNPFESFGLQEWVWTSHELLISLDRNTFGDDIFDKPKVLSYYA 261  
Qy 242 LSDFAVGRCKNGHASCNVNEFDKMCNCKHNTYGVDCBCKLPFFNDPFRARRATAESA 301  
Db 262 VDSFVSGRCKNGHASCNVNEFDKMCNCKHNTYGVDCBCKLPFFNDPFRARRATAESA 321  
Qy 302 SECLPCDCNRSQECYFDPYLYRSTGHGHTNCRDNDTGAKCRDRENFRLGNTBACS 361  
Db 322 HECLPCNCSGRSECTFRELFRSTGHGHRCHCRDHTAGPHCERCQENFYHMDPRMPCQ 381  
Qy 362 PCHSPVGLSTQCDSTYRCSCKGVGMDKDCRQCPGHSITTEAGRCPCSCDPSGSDDEC 421  
Db 382 PCDCQASGLHLQDDDTGTACKPTVTGWKCDRLPGFHSUSEGCRPCTCNPAGSLDTC 441  
Qy 422 NVETGRVCCKDNVEGFCNCRCKPFFNLSSNPKGCTPCFCFGHSSVCTNAGVSVYDIS 481  
Db 442 DPRSGRCPCKENVEGNCDCRCPGTFNLQPHNPAGSCSCFCYGHSKVCASTAQOVHIL 501  
Qy 482 STFOIDEDGWEQEDGSEASLEWSSDQYTAVIDSYFPRYFTAPVKFLGNVLSYQON 541  
Db 502 SDFHQAEGWARSVGGSEHSPQSPFN----GVLLSPDEBELTAPKFLQDQRFYSYGP 557  
Qy 542 LSFSPVRDRDRLSAEDLVLEGAGLRVSLPIAQGNSYSPSETTVKYIFRLH----EATDY 598  
Db 558 LILTRVPGDSPLVQ--LRLEGTGLALS--LRHSLSGPDARASQGRAGVPLQSTSE 614  
Qy 599 PWRPALSPEFQKLNUNTSIKRTYSERAG--YLDVTLQARPGVGPATWESCT 656  
Db 615 DVAPPLPFFHFORLANLTSRLRVSPGSPAGPVFLTVLTVLTSARPLGSPFASWVICS 674  
Qy 657 CPVGGGFCETCLPGYRRETPSLGYPFCVLCTCNHSETCDPETHGVCDRDNATAGPHC 716  
Db 675 CPTGTGTGFCESCAFGYKREMPQGGPYASCVPCTCNQHG--TCDPNTGVCVSHHTEGPGSC 733  
Qy 717 EKCSGYYGDSLTGTSQCPQCPGSGSCAIVPTKEVWCHTPTGTAGRCBLDDGY 776  
Db 734 ERCLPGYGNPAGADDDQCPQCPQSGACTTIPESGEVWCTHCPGQGRGRCEVCDGFG 793  
Qy 777 FGDPLGNGCPVLCRPPCCNDNIDNAGVNCNRLTGECLKCIYNTAGCYDCRCKEGPFGN 836  
Db 794 FGDPLGLFQHPQCHQCQSGNVDPNAGVNCNRLTGECLKCIYNTAGCYDCRCKEGPFGN 853

Qy 837 ELAPNPADCKKACACN--YGTVOQSSCNPNVTGQOCLPHVSGRDCGTCDPGYVNLQSQG 895  
Db 854 ALAPNPADCKMPCSCHPOGSSVSEQMPCDPVTGQSSCLPHVTARDCSRCPGPFDDLPGRG 913  
Qy 896 CERCDHALGSTNGQCDIRTCQCBQPGITGOHCERCETNHFPGFPGCKPCDCHHESGL 955  
Db 914 CRSCKCHPLGSOEDQCHPKTQCTCRPGVTGQACDRCLGFGSSIKGCRACRCSPLGAA 973  
Qy 956 SLOCKDDGRCCEGFGVGNRCDCQCBENFYNRSWPGCOECPACVRLVKDAEHRVKLQE 1015  
Db 974 SAQCHYNGTCVCRPGFEGYKDCRCHYNFFLTADGTHCQOCFSCYALVKEETAKLAKRTL 1033  
Qy 1016 LESLIANLGTGD-----DMVTDQAFEDRLKEAREVTDLLREAOEVKDVONQMLDRLQRV 1070  
Db 1034 TEGWLQGGDCGSPWGPLDILLGEAPRGDGYQGH-----LLPGAREA-----FLEQMGL 1083  
Qy 1071 NSSLSQISRLQNIENRTIETGILAEARARSVESTEQLEIEASRE--LEKAKAAANVSITQ 1129  
Db 1084 EGAVKAREEQURLKNGKARCAQAGSKTCTQLADLEAVLESEEEIILHAAAILASLETPQ 1143  
Qy 1130 PESTGEPNMTLLABEARLAEHRKQEAADDIVRVAKTANETSAEAYNLLLTLAGENOTA 1189  
Db 1144 -EGPSQTKWSHLAIEARALARSHRDTATKIAATAWRALLASNTSYALLNLL--EGRVA 1200  
Qy 1190 LEIE-ELARKYTOAKNVSQDLEKQARVHEERAKRAGDKAVIYASVQL----- 1237  
Db 1201 LETQRDLDRYQEVQAAQKALTAVAEVLPBAE-----SVLATVQVQGDATPYLALL 1253  
Qy 1238 ----TPVDSEA--LENEANKIKKEAADLRLDIQKLDYEDLRE--DMRGKEHEVKNLLE 1289  
Db 1254 ASFGALPKQSRADLGLKAKALEKTVASQHWATEAARTLQTAQAATLRQTE---PLTMA 1310  
Qy 1290 KQKASQQTADQLLADARAAKALAEBAKKGSTLOENDILNNLKDFPRVNDKNTAAEE 1349  
Db 1311 RSELTATFASQHLQGAARALTOASSVQAATVTVNGAETLLADLEGMLQFPKPKQAAAL 1370  
Qy 1350 ALRRIPATRTTAEANEKTRAEALAGNAADATAEAKNAHEAERIAASAAKNATSTKAD 1409  
Db 1371 QKASVSDRLADTRKTKQAEKRMGLNAPLSSSAKKKGREAEVLAKSALAKALLRE 1430  
Qy 1410 ABRTFGEVTDLDNEVNGMLRQL--EBAENELKRXQDDADQDMMAGMASQAQAEALNARK 1468  
Db 1431 RQAHRRASRLTSQTQATLQASQOVLASEARRQLEBAERVAGLS-----EMEQQIRE 1485  
Qy 1469 AKNSVSSLLSQLNLLDQLGQDGT--VDLNKLNTEGSLINKAKDEM--KASDLDRKVSOLE 1525  
Db 1486 SRISLEKDIETJSELLARLGLSDTHQAPAAQALNETQWALERLRLQLGSPGSLQKLSLE 1545  
Qy 1526 SEARKQEAAMNDYNRDIAEIIKDIIHNLEDIKKTLPTGC 1563  
Db 1546 QSSQOQELQIGFESDLAEIRADKQNLBAIHLSPENC 1583

RESULT 13  
US-08-317-450B-13  
; Sequence 13, Application US/08317450B  
; Patent No. 5660982  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Kallunki, Pekka  
; APPLICANT: Pyke, Charles  
; TITLE OF INVENTION: Laminin Chains: Diagnostic and  
; TITLE OF INVENTION: Therapeutic Use  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
; STREET: Ten South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/317,450B  
APPLICATION NUMBER: 37,293  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-317-450B-13

Query Match 30.4%; Score 2591; DB 1; Length 1193;  
Best Local Similarity 39.1%; Pred. No. 9.8e-147;  
Matches 510; Conservative 233; Mismatches 424; Indels 138; Gaps 13;

QY 284 CLPFFNDRPWRRTASASECLPCDNGRSQECYFDPYLRSTGHGHCTNCRDNTDGAK 343  
DB 9 CLCFSLLLPAARATSRRE-----VDCNCGSKSRQCFIDRELHRTGTGFRCLNCNDNDTGDH 64

QY 344 CERENRFFELGTEACSPCHCSFVGLSLTQCDYSGRCCKPGVMGDKDCRQCPGPHSLT 403  
DB 65 CEKCKGFFYHRERDRCLPCNCKSKLSARCNSGRCSCKPGVTGARCDRCCLPGEHMLT 124

QY 404 EAGC-----RPSCDPSGSTDECNVETGRVCCKDNVEGFCNRCCKPGFFNLSSNPK 455  
DB 125 DAGCTQDQRLDSKCDPDAGIAGPC--DAGRCVCKPAVTGBRCDCRCRSGYNNLDGNDPE 182

QY 456 GCTPCFCFCHSSVCTNAGVSVYDSTQIDEDGWRVQRQDSLEWSDDRQVIATV 515  
DB 183 GCTQCFCYGHSACSRSAEYSHKISTFHQDVGWKAVERNPSAKLQWSQRHODVFSS 242

QY 516 SDSYFFRYFLAPVKFLGNVLSYQNLSPSFRVDRDRDTRLSABDLVLEGALRVSVPILTA 575  
DB 243 AQRLLDPYFVAPAKFLGNQVSYQSLSPDYRVDGRHPSAHDVILEGALRIATPLMP 302

QY 576 QGNSYPSSETTKIIFRLHEATDYWRPALSPPEFQKLLNNLTSIKIRGTYSRSAGYLD 635  
DB 303 LGKTLPCGLTKYTFRLNHPNSNNWSFOLSYFEYRELLNLTALRIRATYGYSTGYIDN 362

QY 636 VTLOSARPGGVPATWVESCTCPVYGQFCETCLPGYRRETPSLGPYSPCVLCTCNHGS 695  
DB 363 VTLLSARPVSGAPAPWVEQCICPVGYGQFCQDCASGYKDSARLQFFGTCTPCNCG-G 421

QY 696 ETCDPTGVCDRNTAGPHCEKCSQGYGDSLTGTSQCPGCGSSCAIVPTKXEV 755  
DB 422 GACDPTGDCYSDENPDIEACDPIGFYNDP--HDPKSCXPCPCNCHGFSVCVPIETEV 479

QY 756 VCTHCPGTAGKECLCDGFGDPLSGNGPRLCRPCOCDNDIDPNAVGNCRNLGTGCL 815  
DB 480 VCNCPGVTGARCELCADGYFDGPEHGPVPCQPCQNSNVDPSASGNCRLTGRL 539

QY 816 KCIYNTAGFYCDCKEGFGNPLAPNADKCAACNVTGVOQQSCNPVTGQCCLPHV 875  
DB 540 KCIHNTAGYCDCKAGYFGDPLAPNADKCAACN----- 576

QY 876 SGRDCGTCDPGYNNLQSGCCERCDCCHALGSTNGQCDIRTGCECQPGITGHCERCEN 935  
DB 577 ----- 576

QY 936 HFGFGECKPCDCHHEGSLSLQCKDDGRCEGFGVGNRCQCBENFYNRSWFGCQEC 995

577 -----PMGSEP-----VGCSDGTCTVCKPFGGPNCEH-----GAFSC 609  
996 PACYRLVKDKAAEHRVKLESLIANLGTGDDVWTOAPEDRLKEAREVETDILLRAQE 1055  
610 PACYNQVKIQNDQFQQQORMEALISKAQGDGVVPTTELEGRMQQAQALODILRAQI 669  
1056 VKVDONLMDRLQVNSLSHQISRLQNRNTIETGILAEARSRSVSTEQLEIASRE 1115  
670 SEGASRSLGLQAKVRSQENSYSQRLDLMKMTVERVALGSQYQNRVDRTHRLITQMQLS 729  
1116 LEKAKMA--ANVSITQPESTGEPNNMTLLAEAREALAEHKKOEADDIVRVAKTANETSAEA 1174  
730 LAESEASLGNTNIPASDHYVGPNGFKSLAQEATLAESHVESASMBQLFRETEDYSKQA 789  
1175 YNLLRLTL-----AGENOTALEIEELNRKYEQAKNISQLEKQAAVHVEAKRAGDKA 1227  
790 LSLVRKALHEGVGSGSGSPDGA--VQGLVEKLEKTSLAQOLTREATQABTEADRSYQHS 848  
1228 VEIYASVAQLTPVDSEALE--NEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKN 1286  
849 LRLLDVSPLOGVSDQSPQVEEAKRIKQKADSLSVTRHMDFFRTQKNGNWKBAQQ 908  
1287 LLEKGAEQQTADQOLLARADAALAEAAKKGRSTLQEAANDILNNLKDFFDRYNDNKTA 1346  
909 LLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFVEVESILKNLREFDLQVDRKAE 968  
1347 ABEALRRIPAINRTIAEANEXTREAOALGNAADATEAKNKAHEASRIASAAQKNATST 1406  
969 ABEAMKLSYISQKVSADSKTQOARALGSAADAQAKNGAGEALEISSEIEQETGSL 1028  
1407 KADARITFGEVTDLDNENVMGLRLAEAENELKFKQDDADQDMMWAGMSQAQAEALNA 1466  
1029 NLEANTADGALAMEKGLASKSEMEVEGELEKELEFDINMDAVQMVITEAQKVDTA 1088  
1467 RKAKNSVSSLSQNLNLDQGLDQDLDVNLKLNIEGSLNKADEMKAASDLDRKVSLES 1526  
1089 KNAGVITQDNTLTDGLLHMDQPLSVDBEGLVLEQKLSRAKQTQIN--SOLRPMVSELEE 1147  
1527 EARQOAAIMDYNDRDIAEIIKIDHNLEDIKKTLPTGCFNTPSIEK 1571  
1148 PARQORHLLHLETSIDGILADVKNLENIRDNLPPGCTYNTQALEQ 1192

RESULT 14  
US-08-800-593-13  
; Sequence 13, Application US/08800593  
; Patent No. 6143505  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Kallunki, Pekka  
; APPLICANT: Pyke, Charles  
; TITLE OF INVENTION: Laminin Chains: Diagnostic and  
; TITLE OF INVENTION: Therapeutic Use  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,593  
; FILING DATE: 18-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/317,450  
; FILING DATE: 04-OCT-1994



CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-593-13

Query Match 30.4%; Score 2591; DB 3; Length 1193;  
Best Local Similarity 39.1%; Pred. No. 9.8e-147;  
Matches 510; Conservative 233; Mismatches 424; Indels 138; Gaps 13;

QY 284 CLPFDNRPWRATAEASASECLPCDCNGRSGQCYFDPFLYRSTGHGCHTNCNDTNGAK 343  
DB 9 CLCFSLLLPAARATSRRE---VDCNGKSRQCIFDRELHRTGTGNGFRCCLNCNDTNDGIIH 64  
QY 344 CERCRENPFRLGNTEACSPCHSCPVSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSIT 403  
DB 65 CEKCKNGFYHREDRLCLPCNCSKSGLSARCDNSGRCSCKPGVTGARCDRLPGFHMILT 124  
QY 404 EAGC-----RPSCDPSGSTDECNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPK 455  
DB 125 DAGTQDQRLDSDKCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYNNLDGNGPE 182  
QY 456 GCTPCFCFGHSSVCTNAGVSGVYDISFTQFIDEGWEVEORDGSEASLEWSSDRQYIAVI 515  
DB 193 GCTQCFCHGSACRSRGAESVHKITSTFTQDVGKAVQVNGSPAKLQWSQRHQDVFS 242  
QY 516 SDSYFPRYFIAPKFLGNQVLSYQNLFSFPRVDRDTRLAEDLVLEGAGLVSVPLIA 575  
DB 243 AQRLDVYFVAPAKFLGNQVSYGSLSFYRVRDGRHPSAHDVILEGAGLITAPLMP 302  
QY 576 QGNSYFETTVKTYIFRLHEATDYWRPALSPFPEFKLLNLTSTKIRGTYSSESAGVLD 635  
DB 303 LGKTLPCGLTKTYIFRLNHPHNSNWSPLSYFYRRLRLNLTALRIHATYGEYSTGYDN 362  
QY 636 VTLQASRPGVPATWESCTCPVGYGQFCETCLPGYRRRTSLGSPYCVLCTCNGHS 695  
DB 363 VTLISARVSPAPAPWVEQCICPVGYGQFCQDCASGYKDSARLGFPGCIPCNQCG-G 421  
QY 696 ETCDPETGVCDCRNTAGPHCEKSDGYGDSLTGTSSDCQPCPCPGSSCALVPKTEV 755  
DB 422 GACDPDGTDCYSGDENPDIECADCFIGFYNDP--HDPFRSCKPCPCCHNGFSCVIPETEEV 479  
QY 756 VCTHCTGTACKRCCLCDDGYGDPGLSGNVPRLCRPCQNDNIDPNAVGNCRNLITGEC 815  
DB 480 VCNCCPFGVTGARCELADGVFGPFGEHVPVRCPCQCNVNDPSPASGNCDELITGRCL 539  
QY 816 KCIYNTAGFYCDRCKEGFGNPLAPNPADKCKACACNYGTVQQOSSCNVPTGQCCLPHV 875  
DB 540 KCIHNTAGIYCDQCKAGYFGDPLAPNPADKCKACNEN----- 576  
QY 876 SGRDGTGCDPGYNNLSQGGCERCDCHALGSTNGQCDIRTGQCBCQPGITGHCERCETN 935  
DB 577 ----- 576  
QY 936 HFGFGPECKPCDCHHEGSLQCKDGRCEGREGVGNRCDOCEBENFYNRSPWQCQC 995  
DB 577 -----PMGSEP-----VGRSDGTCTVCKPFGFGPNCEH-----GAFSC 609  
QY 996 PACYFLVXDKAAHRVKLOELSLIANLGTGDDMVTDQAFEDRLKEAREVTDILBAQE 1055  
DB 610 PACYNQVXIQMDQFMQQLQRMALISKAGQGGGVVPTDEGRQCAEQALQILDRDAQI 669  
QY 1056 VKVDQNDMLDRLQVRNSSLHSQISRLQINRTIBETGILABRARSRVESTEQLIETASRE 1115

DB 670 SEGASRLGLQAKVRSQENSQSLDLKMTVERVRLGSGYQNRVDRTHRLITQMOLS 729  
QY 1116 LEKAKWA-ANVSITQPESTGPNNTLLAEARRLAERHKOEADDIVRVAKTANETSAA 1174  
DB 730 LAESEASLGNTNIPASDHVVGNGPKSLAQEATRLAESHVESASNMWQLTRETEDYSQA 789  
QY 1175 YNLLRLTL-----AGENQTALEIEELNRKVEQAKNITSQLEKQAAARVHEAKRAGDKA 1227  
DB 790 LSLVRKALHEGVGSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQHS 848  
QY 1228 VEIVASVAQLTPVDGEALE-NEANKIKKEAADLDRLIDQKLKDYEDLREDMRGKEHEVKN 1286  
DB 849 LRLDSVSPLOQVSDSQSPQVEAKIKQKADSLSLVTRHMDFKRTQKNLGNWKEEAQQ 908  
QY 1287 LLEKKAQQTADQLLARAADAALAEAAKKGSTLQEAINDILNLKDFRRVNDNKTA 1346  
DB 909 LLQNGKSGREKSDQLLSRANLAKSRAQEAALSGMNATFYVESILKNLREFDLQVDRKAE 968  
QY 1347 ABEALRRIPATNRTIAEANEKTRAEQAALGNAADATEAKNKAHEAERIAAGAAQKVNATST 1406  
DB 969 ABEAMKRLSYISQKVSDDSKTQQAERALGSAADAQAKNGAGALISSEIEIEIGSL 1028  
QY 1407 KADARTTGEVTDLDNEVNGMLRQLEEAENELKRRQDDADQDMMMAGMASQAQAEALNA 1466  
DB 1029 NLEANTADGALAMEKGLASLKSEMEVEGELERKELEFDTNMDAVQMVITEAQKVDTRA 1088  
QY 1467 RAKNSVSLLSQNLNLDQLDQGLDQTLNKLNETGSLNKAQKMDKASDLDRKVSDDLES 1526  
DB 1089 KNAGVTIQTLLTDLGLHMDPLUSVDEGLVLLEQKLSRAKTQIN-SQLRPMSELEE 1147  
QY 1527 EARKQEAAMIDYNRDIAEIIKDHNLEDIKKTLPTGCFNTPSIEK 1571  
DB 1148 RARQQRGHLLHLETSIDGLADVKULENIRDNLNLPFGCYNTQALEQ 1192

RESULT 15  
US-08-317-450B-15  
Sequence 15, Application US/08317450B  
Patent No. 5660982  
GENERAL INFORMATION:  
APPLICANT: Tytgvaeson, Karl  
APPLICANT: Kallunki, Pekka  
APPLICANT: Pyke, Charles  
TITLE OF INVENTION: Laminin Chains: Diagnostic and  
TITLE OF INVENTION: Therapeutic Use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,450B  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1111 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-317-450B-15

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Query Match      29.0%;    Score 2476.5;    DB 1;    Length 1111;

Query match	25.08%	SeqC	25.1%	Seqgen	11.1%
Best Local Similarity	39.4%	Pred. NO. 6.3e-140;			
Matches 481;	Conservative 215;	Mismatches 389;	Indels 137;	Gaps 12;	

QY 284 CLPFFNDRPWRRATAESAECPLPCDCNGRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAK 343

Db 9 CLCFSLLLPAARATSRRE---VDCNGKSRQCIFDRELHRQGTNGFRCLNCNDNTDGIH 64

QY 344 CERCENFFRLGNTEACSPCHCSPVGLSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLT 403

Db 65 CEKCKNGFYHRERDRCLPCNCNSKGSLSARCDNSGRCSCKPGVTGARCDRCLPGFHMILT 124

QY 404 EAGC-----RPCSCDPSPGSTDECNVETGRVCVCKDNVEGFNCERCCKPGFFFNLESSNPK 455

DB I25 DAGCIQDQRLLDSKDCDFPAGIAGFC--DAGRCLVCAPAVIGERCDCRSGIINLDGGNFE I82

[illegible][illegible]

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[illegible]

303 I C K T T I P C C L I T K T Y T E R I N E H P S N N W S P O I S V F E Y P R I I R N I T A I R I R A T Y G E Y S T G Y I D N 362

636 VTLOSARPGPGVPATWVESCTCPVGYGGOFCECTCLPGYRRETPTSLGPLYSPCVLCTCNHGS 695

D<sub>b</sub> 363 VTTLSARPVSGAPAPWVEQICIPVYGKQFCQDCASGYKRDSARLGPFGTICIPNCQG-G 421

QY 696 ETCDPETGVCDCRDNTAGPHCEKCSDDGYGDSLTGTSSDCQPCPCPGSSCAIVPKTKEV 755

Db 422 GACDPDTGDCYSGDENPDIECADCPIGFYNDP--HDP RCKPCPCHNGFSCSVIPETEEV 479

QY 756 VCTHCPTGTAGKRCELCDDGYFGDPLGSGNGPVRLCRPCQCNNDIDPNAVGNCNRLTGECL 815

Db 480 VCNCPGVTGARCELCA DGYFGDPFGEHGPVPCQPCQCNNSVDPASGNC DRLTG RCL 539

Qy 816 KCIYNTAGFYCDRCCKEGFFGNFLAPNPADCKKACACNYGTVQQQSSCNPTVGQCQCCLPHV 875

Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNFPADKCRACNCN----- 576

QY 876 SGRDCGTCDFGYYNLQSGQGCEKCDCHALGSLNGQCDIRTGQCECQPFGITGQHCEETN 935

377 ----- 378

[illegible][illegible][illegible]

QV 1056 VKDYDONI MDRI OEYVNSSI HSOI SPI ONI PNTI EETGIL AEPAPSPVESTEOL IETASPE 1115

670 SEGASRSLGLGLAKVRSOENSYOSRLDDPKMTVERVRLGSOYONRVDRTHRLITOMOLS 729

1116 LEKAKMA-ANVSITQPESTGEPNNMTLLAEFEARRLAEERHKQEADDIVRVAKTANETSAEA 1174 QY

Db 730 LAESEASLGNTNIPASDHYVGPNGFKSLAQEATRLAESHVESASNMEQLTRETEDYSKQA 789

QY 1175 YNLLRTL-----AGENQTALEIEELNRKYEAKNISQDLEKQARVHEEAKRAGDKA 1227

Db 790 LSLVRKALHEGVGSGSPDGAV-VQGLVEKLEKTSLAQQLTREATQAEIEADRSYQHS 848

Qy	1228	VEIYASVAOLTPPYDSALE-NEANKIKKEAADLRLIDOKLXDYEDLRDMRCGEHEVKN	1228
Db	849	LRLDVSPLQVSGDSQFVEEAKRIKQKADSLSSLVTRHMEFKRTQKNLGNWKEEAQQ	908
Qy	1287	LEFKGAEOCTDOLLARADAKALAEAAKGRSTLQANDTLNNLKOPDPREVNNDKTA	1346
Db	909	LLQNGSKREKSDQLLSRANLAKSRAQEAALSMGNATPYEVESLLKNLRFEDLQVDRKAE	968
Qy	1347	ABEALRRIPAINRTIAENEKTPREAOALGNARAADATEAKNAHEARTASAAQKATST	1406
Db	969	AEAMKRLSVISQKVSADSKTQOABRGLGSAADAQRAKNNGAGEALETISSETEQELGLS	1028
Qy	1407	KADAERTFGVETDLQNEVNGMLQLEBEANELKRRKODDADQDDMMGMAQSAQAQAEELNA	1466
Db	1029	NLEANYTADGALAMEGLASLAKSEMEVEGELEKSELEFDTNMDAVQMVITEAQKVDTRA	1088
Qy	1467	RKAKNSVSSLLSQNNLLDQLG	1488
Db	1089	KNAGVTIQDTNLTLDGLLLHMG	1110

Search completed: May 18, 2004, 15:02:47  
Job time : 18.8919 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 42.8441 Seconds

(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-20

Perfect score: 8527

Sequence: 1 AMDECADEGPRQRCMPFV.....EDIKTLPTGCTNPTSEKRP 1572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8527	100.0	1572	3 AAB19806	Aab19806 Mouse lam
2	8527	100.0	1572	3 AAB48455	Aab48455 Mouse lam
3	8527	100.0	1572	5 ABB81597	Abb81597 Mouse lam
4	8527	100.0	1605	3 AAB19805	Aab19805 Mouse lam
5	8527	100.0	1605	3 AAB48454	Aab48454 Mouse lam
6	8527	100.0	1605	5 ABB81596	Abb81596 Mouse lam
7	8446	99.1	1607	2 AAW50897	Aaw50897 Mouse lam
8	8038	94.3	1576	3 AAB19802	Aab19802 Human lam
9	8038	94.3	1576	3 AAB48453	Aab48453 Human lam
10	8038	94.3	1576	5 ABB81595	Abb81595 Human lam
11	8038	94.3	1584	3 AAB19804	Aab19804 Human lam
12	8038	94.3	1609	3 AAB19801	Aab19801 Human lam
13	8038	94.3	1609	3 AAB48452	Aab48452 Human lam
14	8038	94.3	1609	5 ABB81594	Abb81594 Human lam
15	8038	94.3	1609	7 ADC01887	Adc01887 Human lam
16	8038	94.3	1617	3 AAB19803	Aab19803 Human lam
17	8034	94.2	1609	2 AAW50898	Aaw50898 Human lam
18	3588	42.1	1587	3 AAB40917	Aab40917 Human ORF
19	3586	42.1	1587	5 AAM50361	Aam50361 Mouse lam
20	3586	42.1	1587	6 ABR58467	Abr58467 Human NOV
21	3583	42.0	1575	6 ABR58468	Abr58468 Human NOV
22	3476	40.8	1639	4 ABB59807	Abb59807 Drosophil
23	3445.5	40.4	1524	2 ABB59807	Aay15458 Human lam
24	2592	30.4	1193	5 AAE14712	Aae14712 Human lam
25	2592	30.4	1193	6 ABR48214	Abr48214 Human bla

#### ALIGNMENTS

##### RESULT 1

AAB19806

ID AAB19806 standard; protein; 1572 AA.

XX AC AAB19806;

XX DT 05-MAR-2001 (first entry)

XX DE Mouse laminin 2 mature gamma-1 chain.

XX KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;

XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX OS Mus musculus.

XX PN WO200066730-A2.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-US011378.

XX PR 30-APR-1999; 99US-0131720P.

XX PR 15-JUN-1999; 99US-0139198P.

XX PR 12-JUL-1999; 99US-0143289P.

XX PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI: 2000-687537/67.

XX N-PSDB; AAB89306.

XX Claim 5; Page 302-306; 305pp; English.

XX The present sequence is that of mouse laminin 2 gamma-1 chain mature

XX protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and

XX gamma-1 (100 kDa) chains. It is thought to be specifically required for

XX stabilizing myotubes during skeletal muscle development, and for

XX preventing apoptosis. Genetic defects in human laminin 2 structure or

XX expression are associated with a major type of congenital muscular

XX dystrophy. Laminin 2 is also thought to be important in Schwann

XX cell/basal lamina interactions. The invention provides laminin 2 alpha-2,

XX beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the

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CC polynucleotides encoding them (see AAA8891-906), methods for making  
CC recombinant laminin 2. Cells that express recombinant laminin 2, and  
CC methods for using purified laminin 2 for research and therapeutic  
CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX  
XX  
SQ Sequence 1572 AA;  
Query Match 100.0%; Score 8527; DB 3; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMDECADGGGPPQRCMPFVNAAFNVVAVNTCGTPPEEYCVGTGVTGKSHCLCDAG 60  
DB 1 AMDECADEGGPPQRCMPFVNAAFNVVAVNTCGTPPEEYCVGTGVTGKSHCLCDAG 60  
QY 61 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTGKAFDITYVRLKPHTS 120  
DB 61 QOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTGKAFDITYVRLKPHTS 120  
QY 121 RPESFAIYKRTREDDGFWIPYQYSGSCENTYSKANRGFIRTGGEQALCTDEFSI:SPL 180  
DB 121 RPESFAIYKRTREDDGFWIPYQYSGSCENTYSKANRGFIRTGGEQALCTDEFSI:SPL 180  
QY 181 TGGVAFSTLEGRPSAYNFDSNVLQEWVTATDIRVTNLRLNTGDEVFNDPKVLSYYY 240  
DB 181 TGGVAFSTLEGRPSAYNFDSNVLQEWVTATDIRVTNLRLNTGDEVFNDPKVLSYYY 240  
QY 241 AISDPAGGRCKNGHASECVNPFDKLMCKNKTGYVDCCKLPFNDPRPHRATAES 300  
DB 241 AISDPAGGRCKNGHASECVNPFDKLMCKNKTGYVDCCKLPFNDPRPHRATAES 300  
QY 301 ASECLPCDCNRSOBYDPELYSTGHGHCINCRDNTDCAKCRERENFFRLGNTEAC 360  
DB 301 ASECLPCDCNRSOBYDPELYSTGHGHCINCRDNTDCAKCRERENFFRLGNTEAC 360  
QY 361 SPCHSPVGSISTQCDSSVGRSCKPGVMDKCDRCQPGFHSLTAGRCPCSDPSGSTDE 420  
DB 361 SPCHSPVGSISTQCDSSVGRSCKPGVMDKCDRCQPGFHSLTAGRCPCSDPSGSTDE 420  
QY 421 CNVETGRCVKDNVEGFNCERCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSYVDI 480  
DB 421 CNVETGRCVKDNVEGFNCERCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSYVDI 480  
QY 481 SSTFQIDEDGWRVEQDGEASLEWSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQ 540  
DB 481 SSTFQIDEDGWRVEQDGEASLEWSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQ 540  
QY 541 NLSFPRVDRDRLSADLVLEGAGLRVSVPLTIAQNSYPSSETTVKVIPLHEATDYPW 600  
DB 541 NLSFPRVDRDRLSADLVLEGAGLRVSVPLTIAQNSYPSSETTVKVIPLHEATDYPW 600  
QY 601 RPALSPFFQKLNLTSTIKIRGTYSEASAGYLDVTLQASRPGPGVPATVWESCTCPVG 660  
DB 601 RPALSPFFQKLNLTSTIKIRGTYSEASAGYLDVTLQASRPGPGVPATVWESCTCPVG 660  
QY 661 YGGQFCETCLPGYRRETSFSLGYPSCVLCTCNHSETCDPETGVCDCRDNTAGHCKCS 720  
DB 661 YGGQFCETCLPGYRRETSFSLGYPSCVLCTCNHSETCDPETGVCDCRDNTAGHCKCS 720  
QY 721 DGYGDSITLGTSSDCQPCPGGSSCAIVPKTKVCTHCTGTAGKRCCLCDDGYFGDP 780  
DB 721 DGYGDSITLGTSSDCQPCPGGSSCAIVPKTKVCTHCTGTAGKRCCLCDDGYFGDP 780  
QY 781 LGSNGFVRLCRPCQNDNIDPNAVGNCRNLGTGECUKCIYNTAGFYCDRCCKGGFNLAP 840  
DB 781 LGSNGFVRLCRPCQNDNIDPNAVGNCRNLGTGECUKCIYNTAGFYCDRCCKGGFNLAP 840  
QY 841 NPADKCKACACNYGTVOQSSCNPTVGQCQLPHVSGRDCGTCDPGYTNLQSGGCRCD 900

DB 841 NPADKCKACACNYGTVOQSSCNPTVGQCQLPHVSGRDCGTCDPGYTNLQSGGCRCD 900  
QY 901 CHALGSTGQCQDIRTGQCECQCPGIGQHCCERCETHNFPGFPGCKPCDCHHEGSLSLOCK 960  
DB 901 CHALGSTGQCQDIRTGQCECQCPGIGQHCCERCETHNFPGFPGCKPCDCHHEGSLSLOCK 960  
QY 961 DDGRCECRGFGVGNRCDOCEENYFYNRSPWQCECPACVRLVKDAAAEHRVKQLESLLI 1020  
DB 961 DDGRCECRGFGVGNRCDOCEENYFYNRSPWQCECPACVRLVKDAAAEHRVKQLESLLI 1020  
QY 1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAOQVKDQVNDQNLMDRLQVNSLSHSQ:SR 1080  
DB 1021 ANLGTGDDMVTDQAFEDRLKEAREVTDLLREAOQVKDQVNDQNLMDRLQVNSLSHSQ:SR 1080  
QY 1081 LQNIQNTIBETGILAEARARSVESTEQIETIASRELEKAKMAANYSITQPESTGSPNMT 1140  
DB 1081 LQNIQNTIBETGILAEARARSVESTEQIETIASRELEKAKMAANYSITQPESTGSPNMT 1140  
QY 1141 LLAEEARRLAEHRKQEAADDIVRAKTANETSAAENLRLTLAGENQTALEIEELNRKYE 1200  
DB 1141 LLAEEARRLAEHRKQEAADDIVRAKTANETSAAENLRLTLAGENQTALEIEELNRKYE 1200  
QY 1201 QAKNISQDLEKQAARVHEEAKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
DB 1201 QAKNISQDLEKQAARVHEEAKAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
QY 1261 RLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEOQTADOLLARADAAKALAEBAKKGR 1320  
DB 1261 RLIDQKLDYEDLREDMRGKEHEVKNLLEKGAEOQTADOLLARADAAKALAEBAKKGR 1320  
QY 1321 STLQEAANDILNKLKDFDRRVNDNKTAAAEALRRIPAINRTTIAEAANEKTRQAALGNAAA 1380  
DB 1321 STLQEAANDILNKLKDFDRRVNDNKTAAAEALRRIPAINRTTIAEAANEKTRQAALGNAAA 1380  
QY 1381 DATEAKNAHAERIASAAQKNAATSTKADABERTFGEVTDLNEVNGMLRQLEAEENELKX 1440  
DB 1381 DATEAKNAHAERIASAAQKNAATSTKADABERTFGEVTDLNEVNGMLRQLEAEENELKX 1440  
QY 1441 KODDADQDDMMAGMASQAQAEALNARKNSVSSLLSOLNLLDQLGQDQDVTDLNKLNE 1500  
DB 1441 KODDADQDDMMAGMASQAQAEALNARKNSVSSLLSOLNLLDQLGQDQDVTDLNKLNE 1500  
QY 1501 IEGLSNKAKDEMKASDLDRKVSLESEARKQBAAMVYNDIAETIKDHNLEDIKKTLIP 1560  
DB 1501 IEGLSNKAKDEMKASDLDRKVSLESEARKQBAAMVYNDIAETIKDHNLEDIKKTLIP 1560  
QY 1561 TGCFTNTPSIEKP 1572  
DB 1561 TGCFTNTPSIEKP 1572  
RESULT 2  
AAB48455  
ID AAB48455 standard; protein; 1572 AA.  
XX  
AC AAB48455;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 28.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX  
OS Mus musculus.  
XX  
XX WO200066732-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX

PR 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
PA  
XX Kortessmaa J, Tryggvason K;  
PI  
XX WPI; 2000-687539/67.  
DR N-PSDB; AAC83716.  
DR  
XX  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
XX  
PS Claim 5; Page 240-245; 245pp; English.  
XX  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration  
XX  
XX Sequence 1572 AA;  
Query Match 100.0%; Score 8527; DB 3; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMDECADEGGRPQRCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTKSCHLCDAG 60  
DB 1 AMDECADEGGRPQRCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTKSCHLCDAG 60  
QY 61 QOHLQGAFLTDYNNQADTTWQSTMLAGVQYNSINLTLHGKAFDITVRLKFTS 120  
DB 61 QOHLQGAFLTDYNNQADTTWQSTMLAGVQYNSINLTLHGKAFDITVRLKFTS 120  
QY 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 180  
DB 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 180  
QY 181 TGGNVAFTLEGRPSAYNFDSFVLOEWYATDRTVTLNRLNTFGDEVNDPKVLKSYYY 240  
DB 181 TGGNVAFTLEGRPSAYNFDSFVLOEWYATDRTVTLNRLNTFGDEVNDPKVLKSYYY 240  
QY 241 AISDFAVGRCCKNGHASCVKNEFDFKLMCNCKNTYGVDCFKLPFFNDRPWRATAES 300  
DB 241 AISDFAVGRCCKNGHASCVKNEFDFKLMCNCKNTYGVDCFKLPFFNDRPWRATAES 300  
QY 301 ASBCLPCDNGRSQECYFDPFLYRSTGHHGHTNCRDNDTGAKRCRENPFRLGNTEAC 360  
DB 301 ASBCLPCDNGRSQECYFDPFLYRSTGHHGHTNCRDNDTGAKRCRENPFRLGNTEAC 360  
QY 361 SPCHCSFVGLSLTQCDYSYRCSCKPVGMDKCDRCQPGFHSLTEAGRCPSCDPSGSTDE 420  
DB 361 SPCHCSFVGLSLTQCDYSYRCSCKPVGMDKCDRCQPGFHSLTEAGRCPSCDPSGSTDE 420  
QY 421 CNVETGRVCVKDNEGFNCERCKPGFNFLESNPKGCTPCFCGHSSVCTNAGVSVDYI 480  
DB 421 CNVETGRVCVKDNEGFNCERCKPGFNFLESNPKGCTPCFCGHSSVCTNAGVSVDYI 480  
QY 481 SSTFOIDEGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGO 540  
DB 481 SSTFOIDEGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGO 540

DB 481 SSTFOIDEGWRVEQRDGSEASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYGO 540  
QY 541 NLSFSFVDRDRTRLSDAEDLVLSGAGLRVSVPLIAQGNYSFSETTKYKIFRLHEATDPW 600  
DB 541 NLSFSFVDRDRTRLSDAEDLVLSGAGLRVSVPLIAQGNYSFSETTKYKIFRLHEATDPW 600  
QY 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVLTQSAKPGVPAATWVESCTCPVG 660  
DB 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVLTQSAKPGVPAATWVESCTCPVG 660  
QY 661 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPBTGVCDCDRDNTAGPHCKSCS 720  
DB 661 YGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPBTGVCDCDRDNTAGPHCKSCS 720  
QY 721 DGYTGDSTLTGTSDDCPQCPGSSCAIVPKTKEVWCTHCTGTAGKRCCLCDDGYGDP 780  
DB 721 DGYTGDSTLTGTSDDCPQCPGSSCAIVPKTKEVWCTHCTGTAGKRCCLCDDGYGDP 780  
QY 781 LGSNGPVLRCPCQCNNDNIDPNAVGNCRNLTGCEKCIYNTAGFYCDRCHEGFGNPLAP 840  
DB 781 LGSNGPVLRCPCQCNNDNIDPNAVGNCRNLTGCEKCIYNTAGFYCDRCHEGFGNPLAP 840  
QY 841 NPADKCKACACNVTGVOQSSCNPTVTCOCCLPHVSRDCTGDPGYNNLQSGGCBRC 900  
DB 841 NPADKCKACACNVTGVOQSSCNPTVTCOCCLPHVSRDCTGDPGYNNLQSGGCBRC 900  
QY 901 CHALGSTNGQCDINTGQCECPGIGTQHCCERTNHFPGPECKPCDCHHEGSLSQCK 960  
DB 901 CHALGSTNGQCDINTGQCECPGIGTQHCCERTNHFPGPECKPCDCHHEGSLSQCK 960  
QY 961 DDGRCCEGFGVGNRCQCEENFYNNRSPGCEPCACVLEVKDKAAHRVKLQELSLI 1020  
DB 961 DDGRCCEGFGVGNRCQCEENFYNNRSPGCEPCACVLEVKDKAAHRVKLQELSLI 1020  
QY 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAEQVKVDQNDLMDRLQRYNSLSHSQIS 1080  
DB 1021 ANLGTGDDMVTDOAFEDRLKEAREVTDLLREAEQVKVDQNDLMDRLQRYNSLSHSQIS 1080  
QY 1081 LQNTNRTIETGILAEARSVESTEQLIBIASRELEKAKAAANVSITQESTGEPNMT 1140  
DB 1081 LQNTNRTIETGILAEARSVESTEQLIBIASRELEKAKAAANVSITQESTGEPNMT 1140  
QY 1141 LLAEEARLARERHKOADDIVRVAKTANETSAAEYNNLLTLAGENOTALIEBELNRKY 1200  
DB 1141 LLAEEARLARERHKOADDIVRVAKTANETSAAEYNNLLTLAGENOTALIEBELNRKY 1200  
QY 1201 QAKNISODLEKQARVHEEAKRAGDKAVETIYASVAQLTPVDSEALNEANKIKKEADLD 1260  
DB 1201 QAKNISODLEKQARVHEEAKRAGDKAVETIYASVAQLTPVDSEALNEANKIKKEADLD 1260  
QY 1261 RLIDQKLDYEDLEDMRGKEHEVKNLEKGAEQQTADQLLARADAALAEAAKGR 1320  
DB 1261 RLIDQKLDYEDLEDMRGKEHEVKNLEKGAEQQTADQLLARADAALAEAAKGR 1320  
QY 1321 STLQEAANDILNNLKDFORVNDKNTAAEALRRIPAINRTIABANEKTRTQAALGNAAA 1380  
DB 1321 STLQEAANDILNNLKDFORVNDKNTAAEALRRIPAINRTIABANEKTRTQAALGNAAA 1380  
QY 1381 DATEAKNAHEABERIASAAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEANELKR 1440  
DB 1381 DATEAKNAHEABERIASAAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEANELKR 1440  
QY 1441 KQDDADQDMWAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGQDQTDVLDNKLNE 1500  
DB 1441 KQDDADQDMWAGMASQAQAEALNARKAKNSVSSLLSOLNNLLDQLGQDQTDVLDNKLNE 1500  
QY 1501 IEGSLNKADEMKAASDLDRKVSLESEARKQEAAMINDYNDIAEIIKDIHNLEDIKKTLP 1560  
DB 1501 IEGSLNKADEMKAASDLDRKVSLESEARKQEAAMINDYNDIAEIIKDIHNLEDIKKTLP 1560  
QY 1561 TGCNTPTSIIEKP 1572  
DB 1561 TGCNTPTSIIEKP 1572

RESULT 3  
 ABB81597  
 ID ABB81597 standard; protein; 1572 AA.  
 AC ABB81597;  
 XX  
 DT 19-SEP-2002 (first entry)  
 XX  
 DE Mouse laminin 10 third chain protein sequence SEQ ID NO:20.  
 XX  
 KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
 KW tissue repair development; laminin; healing; vascular tissue;  
 KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
 KW proliferation; migration.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200250111-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 XX 21-DEC-2001; 2001WO-US051035.  
 XX  
 XX 21-DEC-2000; 2000US-0257449P.  
 PR 28-MAR-2001; 2001US-0279282P.  
 PR 13-NOV-2001; 2001US-00279282.  
 XX  
 PA (BIOS-) BIOSTRATUM INC.  
 XX  
 PI Tryggvason K, Doi M, Thyboll J;  
 XX  
 DR WPI; 2002-557650/59.  
 DR N-PSDB; ABQ72915.  
 XX  
 PT New human laminin-10 proteins, useful for accelerating the healing of  
 PT vascular tissue, improving the biocompatibility of grafts, or for  
 PT promoting re-endothelialization at the site of vascular injuries.  
 XX  
 PS Claim 9; Page 204-209; 231pp; English.  
 XX  
 CC The present invention describes human laminin alpha 5. Also described is  
 CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are  
 CC useful in maintaining cell/tissue phenotype as well as promoting cell  
 CC growth and differentiation in tissue repair development. Specifically,  
 CC laminin 10 can be used for accelerating the healing injuries of vascular  
 CC tissue, improving the biocompatibility of grafts useful for treating such  
 CC injuries, for promoting re-endothelialisation at the site of vascular  
 CC injuries, and promote cell attachment and subsequent cell stasis,  
 CC proliferation, differentiation, and/or migration. The present sequence  
 CC represents a third chain protein of laminin 10, from the present  
 CC invention  
 XX  
 SQ Sequence 1572 AA;  
 Query Match 100.0%; Score 8527; DB 5; Length 1572;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AMDECADEGGRRQRCMPBFVNAAFNVTVATNCTGTPPEEVCVOTGVTVTKSCHLCDAG 60  
 DB 1 AMDECADEGGRRQRCMPBFVNAAFNVTVATNCTGTPPEEVCVOTGVTVTKSCHLCDAG 60  
 QY 61 QOHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQVPNSINLTLHLGKAFDITVYRLKFTS 120  
 DB 61 QOHLQHGAAFLTDYNNQADTTWQSQOTMLAGVQVPNSINLTLHLGKAFDITVYRLKFTS 120  
 QY 121 RPESFAIYKRTEDGFWPIPYQYSSCENTYSKANRGFIRTCGDEQOALCTDESDISPL 180  
 DB 121 RPESFAIYKRTEDGFWPIPYQYSSCENTYSKANRGFIRTCGDEQOALCTDESDISPL 180  
 QY 181 TGGNVAFTLEGRPSAYNFDSPLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240

181 TGGNVAFTLEGRPSAYNFDSPLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240  
 QY 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRATAES 300  
 DB 241 AISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKCLPFFNDRPWRATAES 300  
 QY 301 ASECLPCDCNRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAACRCRNFRLGNTEAC 360  
 DB 301 ASECLPCDCNRSQECYFDPPELYRSTGHGGHCTNCRDNTDGAACRCRNFRLGNTEAC 360  
 QY 361 SPCHCSFVGLSTQCDSYGRCSCKPGWMDKDRCPQPGFHSLTEAGRCRSCDPSGSTDE 420  
 DB 361 SPCHCSFVGLSTQCDSYGRCSCKPGWMDKDRCPQPGFHSLTEAGRCRSCDPSGSTDE 420  
 QY 421 CNVETGRVCYKXNVEGFNCERCKPGFFNLESNPFGKCTPCFCFGHSSVCTNAGVGYVDI 480  
 DB 421 CNVETGRVCYKXNVEGFNCERCKPGFFNLESNPFGKCTPCFCFGHSSVCTNAGVGYVDI 480  
 QY 481 SSTFQIDEDGWRVEQRDSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYQG 540  
 DB 481 SSTFQIDEDGWRVEQRDSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYQG 540  
 QY 541 NLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
 DB 541 NLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
 QY 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLOSARPPGVPATWVESCTCPVG 660  
 DB 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLOSARPPGVPATWVESCTCPVG 660  
 QY 661 YGGQFCETCLPGYRRETPLSGYSPCVLCTCNHSETCDPETGVCDRCRNTAGPCEKCS 720  
 DB 661 YGGQFCETCLPGYRRETPLSGYSPCVLCTCNHSETCDPETGVCDRCRNTAGPCEKCS 720  
 QY 721 DGYGDSLTGSDQCPGSSCAIYVPTKVVVCTHCTGTAGKACELCDDGYFGDP 780  
 DB 721 DGYGDSLTGSDQCPGSSCAIYVPTKVVVCTHCTGTAGKACELCDDGYFGDP 780  
 QY 781 LGSNGVRLCRPCQNDNDPNAVNCNLTGECCLKIYNTAGFYCDRCCKEFGFNPLAP 840  
 DB 781 LGSNGVRLCRPCQNDNDPNAVNCNLTGECCLKIYNTAGFYCDRCCKEFGFNPLAP 840  
 QY 841 NPADKCKACACNYGTVOQSSCNPTVGOCCPLPHVSGRDCGTCDPGYVNLQSGQGCERD 900  
 DB 841 NPADKCKACACNYGTVOQSSCNPTVGOCCPLPHVSGRDCGTCDPGYVNLQSGQGCERD 900  
 QY 901 CHALGSTNGQCDIRTCQCEQPGITGQHCERTNHFPGPEGKPCDCHHSGSLQCK 960  
 DB 901 CHALGSTNGQCDIRTCQCEQPGITGQHCERTNHFPGPEGKPCDCHHSGSLQCK 960  
 QY 961 DGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCEPCACVRLVKDKAAEHRVKLQESLI 1020  
 DB 961 DGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCEPCACVRLVKDKAAEHRVKLQESLI 1020  
 QY 1021 ANLGTGDDMVTOAFEDRLKEAREVTDLLRAEQVKDQDNLMDRLQVNSSLSHSR 1080  
 DB 1021 ANLGTGDDMVTOAFEDRLKEAREVTDLLRAEQVKDQDNLMDRLQVNSSLSHSR 1080  
 QY 1081 LQNIQNTIBETGLAERARSVESTEQLEIEIASRELEKAKMAANVSIITQESTGEPNMT 1140  
 DB 1081 LQNIQNTIBETGLAERARSVESTEQLEIEIASRELEKAKMAANVSIITQESTGEPNMT 1140  
 QY 1141 LLAEEARRLAERHKQADDIRVAKTANETSABAYNLLRTLAGEQTALIEELNRKYE 1200  
 DB 1141 LLAEEARRLAERHKQADDIRVAKTANETSABAYNLLRTLAGEQTALIEELNRKYE 1200  
 QY 1201 QAKNIQDLEKQARVHEEAKKAGKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
 DB 1201 QAKNIQDLEKQARVHEEAKKAGKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
 QY 1261 RLTDQKLDYEDIREDMRGKEHVKNLEKGAQOOTADQOLLARADAAKALAEERAKKR 1320

Db 1261 RLIDQKLKDYEDREDMRGHEVKNLLEKGAEQQTADOLLARADAAKALAEBAKGR 1320  
QY 1321 STIQEANDILNNLKDFDRVNDNKNKTAAEALRRIPAINRTIABANKEKTREAOALGNAAA 1380  
Db 1321 STIQEANDILNNLKDFDRVNDNKNKTAAEALRRIPAINRTIABANKEKTREAOALGNAAA 1380  
QY 1381 DATEAKNKAHEABERIASAAOKNATSTKADAEFTFGEVTDLDNEVGMRLQLEAENELKR 1440  
Db 1381 DATEAKNKAHEABERIASAAOKNATSTKADAEFTFGEVTDLDNEVGMRLQLEAENELKR 1440  
QY 1441 KQDDADQMMWAGMASQAQAEALNARKAKNSVSSLLSQNLNLLDQGLDQDLDVLDLKNLE 1500  
Db 1441 KQDDADQMMWAGMASQAQAEALNARKAKNSVSSLLSQNLNLLDQGLDQDLDVLDLKNLE 1500  
QY 1501 IEGSLNKADEMKAASDLDRKVSLESEARKOEAAIMDYNRDIAEIIKDIHNLEDIKKTLF 1560  
Db 1501 IEGSLNKADEMKAASDLDRKVSLESEARKOEAAIMDYNRDIAEIIKDIHNLEDIKKTLF 1560  
QY 1561 TGCFTNPSIEKP 1572  
Db 1561 TGCFTNPSIEKP 1572

RESULT 4  
AAB19805  
ID AAB19805 standard; protein; 1605 AA.  
XX AC AAB19805;  
XX DT 05-MAR-2001 (first entry)  
XX DE Mouse laminin 2 gamma-1 chain.  
XX KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX OS Mus musculus.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..33  
XX FT /label= Signal\_peptide  
XX FT Protein 34..1605  
XX FT /label= Mature\_protein  
XX WC200066730-A2.  
XX PD 09-NOV-2000.  
XX PP 28-APR-2000; 2000WO-US011378.  
XX PR 30-APR-1999; 99US-01311720P.  
XX PR 15-JUN-1999; 99US-0139198P.  
XX PR 12-JUL-1999; 99US-0143289P.  
XX PR 24-SEP-1999; 99US-0155945P.  
XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX PI Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88905.  
XX PT Purified laminin 2 protein, useful for research and therapeutic purposes  
XX PT including peripheral nerve regeneration, treatment of degenerative muscle  
XX PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX PS Claim 5; Page 288-294; 305pp; English.  
XX CC The present sequence is that of the gamma-1 chain of mouse laminin 2.  
XX CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
XX CC (100 kDa) chains. It is thought to be specifically required for  
XX CC stabilizing myotubes during skeletal muscle development, and for  
XX CC preventing apoptosis. Genetic defects in human laminin 2 structure or

CC expression are associated with a major type of congenital muscular  
CC dystrophy. Laminin 2 is also thought to be important in Schwann  
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
CC polynucleotides encoding them (see AAA8891-906), methods for making  
CC recombinant laminin 2, cells that express recombinant laminin 2, and  
CC methods for using purified laminin 2 for research and therapeutic  
CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX  
SQ Sequence 1605 AA;  
Query Match 100.0%; Score 8527; DB 3; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMDECADEGGRPQRCMPFVNAAFNVTVATNTGCTPPEEYCVQTVGTGKSHCLDAG 60  
Db 34 AMDECADEGGRPQRCMPFVNAAFNVTVATNTGCTPPEEYCVQTVGTGKSHCLDAG 93  
QY 61 QOHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTILHKGAPDITYVRLKPHTS 120  
Db 94 QOHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSNINLTILHKGAPDITYVRLKPHTS 153  
QY 121 RPESPAIYKRTREDGPIWIPYQVYSGSCENTYSKANRGFIRGTGGDEQOALCTDEFSDISPL 180  
Db 154 RPESPAIYKRTREDGPIWIPYQVYSGSCENTYSKANRGFIRGTGGDEQOALCTDEFSDISPL 213  
QY 181 TGNVAFSTLEGSPSAYNFDNSPVLQEWVATDIRVTILNRLNTFGDEVNPKVLSYVY 240  
Db 214 TGNVAFSTLEGSPSAYNFDNSPVLQEWVATDIRVTILNRLNTFGDEVNPKVLSYVY 273  
QY 241 AISDFAVGGRCKNGHASECVKNBFDKLMCKNKTNTYGVDCCKCLPFNDPWRRAEAS 300  
Db 274 AISDFAVGGRCKNGHASECVKNBFDKLMCKNKTNTYGVDCCKCLPFNDPWRRAEAS 333  
QY 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKECRENFFRILNTEAC 360  
Db 334 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKECRENFFRILNTEAC 393  
QY 361 SPCHSPVGSLSSTQCDSYGRCSCKPGVNGDKDCRCQGFHSLTEAGRPCSCDPSGSTDE 420  
Db 394 SPCHSPVGSLSSTQCDSYGRCSCKPGVNGDKDCRCQGFHSLTEAGRPCSCDPSGSTDE 453  
QY 421 CNVETGRVCCKDNVEGFNCERCKPGFNLESNNPKGTCTPCFCFHHSSVCTNAVGSYVDI 480  
Db 454 CNVETGRVCCKDNVEGFNCERCKPGFNLESNNPKGTCTPCFCFHHSSVCTNAVGSYVDI 513  
QY 481 SSTFOIDEDGWRVQORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYGQ 540  
Db 514 SSTFOIDEDGWRVQORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYGQ 573  
QY 541 NLSFSFRVDRDTRLASADLVLEAGLRVSVPLAQGNSYPSSETTVKYIFRLHEATDPW 600  
Db 574 NLSFSFRVDRDTRLASADLVLEAGLRVSVPLAQGNSYPSSETTVKYIFRLHEATDPW 633  
QY 601 RPALSPFEFFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSGARPGVGPATVBSCTCPVG 660  
Db 634 RPALSPFEFFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSGARPGVGPATVBSCTCPVG 693  
QY 661 YGGQFCETCLPGYRRETPSLGIPSPCVLCTCNHSETCDPBTGVCDNRDNTAGHCBKCS 720  
Db 694 YGGQFCETCLPGYRRETPSLGIPSPCVLCTCNHSETCDPBTGVCDNRDNTAGHCBKCS 753  
QY 721 DGYVGDSTLTGSSDCQPCPCPGSSCAIVPKTKVWCTHCTPTGTAGKRCCLCDDGYFGDP 780  
Db 754 DGYVGDSTLTGSSDCQPCPCPGSSCAIVPKTKVWCTHCTPTGTAGKRCCLCDDGYFGDP 813  
QY 781 LGSNGPVLCPCCOONIDPNVAGNCNRLTGECLKCIYNTAGYCDRCKEGFFGNLAP 840





454 CNVETGRCVCKDNVGEFNCRCRKPFPNLESSNPKGCTPCFCGHSSVCTNAVGVSYDI 513  
481 SSTFQIDEDGWRVQZRGDSASLEWSSDRQYIAVISDSYPRYFIAPVKFLGNQVLSYGQ 540  
514 SSTFQIDEDGWRVQZRGDSASLEWSSDRQYIAVISDSYPRYFIAPVKFLGNQVLSYGQ 573  
541 NLSFSFRVDRDRRLSNEDLVLSGAGLRVSVPVLIAGNSYSPSETTKYIFRLHEATDYPW 600  
574 NLSFSFRVDRDRRLSNEDLVLSGAGLRVSVPVLIAGNSYSPSETTKYIFRLHEATDYPW 633  
601 RPALSPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCPCPVG 660  
634 RPALSPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSRPQPGVPATWVESCPCPVG 693  
661 YGQFCSTCLPGVRRTPSLGYPSPVCLTCNGHSETCDPBTGVCDCRONTAGPHCEKCS 720  
694 YGQFCSTCLPGVRRTPSLGYPSPVCLTCNGHSETCDPBTGVCDCRONTAGPHCEKCS 753  
721 DGYGDSSTLTSSDQPCPCPGSSCAIVPKTEVCTHCTGTAGKRCLELDDGDFGDP 780  
754 DGYGDSSTLTSSDQPCPCPGSSCAIVPKTEVCTHCTGTAGKRCLELDDGDFGDP 813  
781 LGSNGPVRLCRPCQNDNDPNVAGNCNRLTGELKCIYNTAGFYCDRCBGFPGNPLAP 840  
814 LGSNGPVRLCRPCQNDNDPNVAGNCNRLTGELKCIYNTAGFYCDRCBGFPGNPLAP 873  
841 NPADKCKACACNYTVOQSSCNPTVTCOCCLPHVSRDCTCDPGVYNLQSGGRCRD 900  
874 NPADKCKACACNYTVOQSSCNPTVTCOCCLPHVSRDCTCDPGVYNLQSGGRCRD 933  
901 CHALGSTNGOCDIRTGCEQCPGITGQHCERCETNHFGEPCGKPCDCHHEGSLQCK 960  
934 CHALGSTNGOCDIRTGCEQCPGITGQHCERCETNHFGEPCGKPCDCHHEGSLQCK 993  
961 DDRCCEBGFVGNRCDCENFYNRSWPCCECPACVRLVKDKAAEHRVKLOELESLL 1020  
994 DDRCCEBGFVGNRCDCENFYNRSWPCCECPACVRLVKDKAAEHRVKLOELESLL 1053  
1021 ANLTGDDMTVDQAFEDRLKEAREVTDLLREAEQEVKDVQNDLMDRLQVNSLSHQISR 1080  
1054 ANLTGDDMTVDQAFEDRLKEAREVTDLLREAEQEVKDVQNDLMDRLQVNSLSHQISR 1113  
1081 LQNRNTIETGILAEARSRVSTEQLIBIASRELEKAKMAANVSITOPESTGEFNNMT 1140  
1114 LQNRNTIETGILAEARSRVSTEQLIBIASRELEKAKMAANVSITOPESTGEFNNMT 1173  
1141 LLAEARLAEARKQAEADIVRVAKTANETSABAYNLLRTLAGENQTALEIEELNRKYE 1200  
1174 LLAEARLAEARKQAEADIVRVAKTANETSABAYNLLRTLAGENQTALEIEELNRKYE 1233  
1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
1234 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293  
1261 RLIDQKLDYEDLREDMRGKEHEVNLLKKGAEQQTADOLLARADAALAEAAKGR 1320  
1294 RLIDQKLDYEDLREDMRGKEHEVNLLKKGAEQQTADOLLARADAALAEAAKGR 1353  
1321 STLQEAANDILNNLKDFDRVNDNKTAAEALRIPAINRTIAEANKETREAQALGNAAA 1380  
1354 STLQEAANDILNNLKDFDRVNDNKTAAEALRIPAINRTIAEANKETREAQALGNAAA 1413  
1381 DATEAKNKAHEARLISAAQKATSTKADAEFTFGEVTDLDNEVNGMLQLEAEANELKR 1440  
1414 DATEAKNKAHEARLISAAQKATSTKADAEFTFGEVTDLDNEVNGMLQLEAEANELKR 1473  
1441 KQDDADQMMWAGWASQAQAEALNARKAKNSVSLLSQLNLLDQGLDQGLDQGLDQGLDQGLD 1500  
1474 KQDDADQMMWAGWASQAQAEALNARKAKNSVSLLSQLNLLDQGLDQGLDQGLDQGLDQGLD 1533  
1501 IEGSLNKAQEMKASDLDRKVSQLESPARKQEAAMIDYNRDIAEIIKIDHNLEDIKKTLPL 1560  
1534 IEGSLNKAQEMKASDLDRKVSQLESPARKQEAAMIDYNRDIAEIIKIDHNLEDIKKTLPL 1593

QY 1561 TGCFTNTPSIEKP 1572  
DB 1594 TGCFTNTPSIEKP 1605  
RESULT 6  
ABB81596  
ID ABB81596 standard; protein; 1605 AA.  
XX  
AC ABB81596;  
XX  
DT 19-SEP-2002 (first entry)  
XX  
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.  
XX  
KW Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..33  
FT /label= signal  
FT Protein 34..1605  
FT /label= laminin\_10\_third\_chain  
XX  
FN WO200250111-A2.  
XX  
PD 27-JUN-2002.  
XX  
PF 21-DEC-2001; 2001WO-US051035.  
XX  
PR 21-DEC-2000; 2000US-0257449P.  
PR 28-NAR-2001; 2001US-0279282P.  
PR 13-NOV-2001; 2001US-00279282.  
XX  
PA (BIOS-) BIOSTRATUM INC.  
XX  
PI Tryggvason K, Doi M, Thyboll J;  
XX  
DR WPI; 2002-557650/59.  
DR N-PSDB; ABQ72914.  
XX  
PT New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX  
PS Claim 9; Page 191-195; 231pp; English.  
XX  
XX The present invention describes human laminin alpha 5. Also described is  
XX an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are  
XX useful in maintaining cell/tissue phenotype as well as promoting cell  
XX growth and differentiation in tissue repair development. Specifically,  
XX laminin 10 can be used for accelerating the healing injuries of vascular  
XX tissue, improving the biocompatibility of grafts useful for treating such  
XX injuries, for promoting re-endothelialisation at the site of vascular  
XX injuries, and promote cell attachment and subsequent cell stasis,  
XX proliferation, differentiation, and/or migration. The present sequence  
XX represents a third chain protein of laminin 10, from the present  
XX invention.  
SQ Sequence 1605 AA;  
Query Match 100.0%; Score 8527; DB 5; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMDECADEGGPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSHCLDAG 60  
DB 34 AMDECADEGGPQRCMPFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKSHCLDAG 93

QY 61 QOHLQGAFLTDVNNQADTTWQSQTMLAGVQVPNSINLTLLHKGKAPDITVYRLKPHTS 120  
 Db 94 QOHLQGAFLTDVNNQADTTWQSQTMLAGVQVPNSINLTLLHKGKAPDITVYRLKPHTS 153  
 QY 121 RPESFAIYKRTREDGFWPIPYQYSGSCENTYKSKANRGFIIRTGDEBOQALCTDEFSDISPL 180  
 Db 154 RPESFAIYKRTREDGFWPIPYQYSGSCENTYKSKANRGFIIRTGDEBOQALCTDEFSDISPL 213  
 QY 181 TGGNVAFTLEGRPSAYNFDSNVPVLEQWVATDITRVTLNRLNTFGDEVFNDPKVLKGYYY 240  
 Db 214 TGGNVAFTLEGRPSAYNFDSNVPVLEQWVATDITRVTLNRLNTFGDEVFNDPKVLKGYYY 273  
 QY 241 AISDPAVGRCKNGHASECVKNBFDKLMCKNKNYGVDCCKLPFPNDRPWRATAES 300  
 Db 274 AISDPAVGRCKNGHASECVKNBFDKLMCKNKNYGVDCCKLPFPNDRPWRATAES 333  
 QY 301 ASECLPCDNGRSQBCYDPPELYRSTGHGGCTNCRDNTDGAKECERENFRLGNTBAC 360  
 Db 334 ASECLPCDNGRSQBCYDPPELYRSTGHGGCTNCRDNTDGAKECERENFRLGNTBAC 393  
 QY 361 SPCHSPVGSLSLTCDSYGRCSCKFPGVMDKCDRCQPGFHSLTBAGCRPCSCDPSGSTDE 420  
 Db 394 SPCHSPVGSLSLTCDSYGRCSCKFPGVMDKCDRCQPGFHSLTBAGCRPCSCDPSGSTDE 453  
 QY 421 CNVETGRVCVCKDNGVGFNCERCKPGFFNLSSNPKGCTPCFCGHSSVCTNAVGSYVDI 480  
 Db 454 CNVETGRVCVCKDNGVGFNCERCKPGFFNLSSNPKGCTPCFCGHSSVCTNAVGSYVDI 513  
 QY 481 SSTFOIDGMRVGEORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYGQ 540  
 Db 514 SSTFOIDGMRVGEORDGSEASLEWSSDRQYIAVISDSYFPFYPIAPVKFLGNQVLSYGQ 573  
 QY 541 NLSFVRDRDRTRLSAEDLVLEGAGLVSVPLIAQNSYSETVKXIFELHEATDYPW 600  
 Db 574 NLSFVRDRDRTRLSAEDLVLEGAGLVSVPLIAQNSYSETVKXIFELHEATDYPW 633  
 QY 601 RPALSPFFFOKLNNLTSLKIRGTYSERSAGYLDVTLQSAKPGPGVPATWVESCTCPVG 660  
 Db 634 RPALSPFFFOKLNNLTSLKIRGTYSERSAGYLDVTLQSAKPGPGVPATWVESCTCPVG 693  
 QY 661 YGGQFCETCLPGYRRETSPLGYSPCVLCTNGHSETCDPETGVDCDNDTAGHCEKCS 720  
 Db 694 YGGQFCETCLPGYRRETSPLGYSPCVLCTNGHSETCDPETGVDCDNDTAGHCEKCS 753  
 QY 721 DGYGDSLTGTSDDQCPGCGSSCAIVPKTKVWCTHPTGTAGKCELCDDGYFGDP 780  
 Db 754 DGYGDSLTGTSDDQCPGCGSSCAIVPKTKVWCTHPTGTAGKCELCDDGYFGDP 813  
 QY 781 LGSNGPVLRCPCQCNNDIDPNAVGNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAP 840  
 Db 814 LGSNGPVLRCPCQCNNDIDPNAVGNRLTGECLKCIYNTAGFYCDRCCKEGFFGNPLAP 873  
 QY 841 NPADKCKACACNGTVQOQSSCNVPTGOCCLPHVSGRDCGTCDPGYNLOSOGGECRCD 900  
 Db 874 NPADKCKACACNGTVQOQSSCNVPTGOCCLPHVSGRDCGTCDPGYNLOSOGGECRCD 933  
 QY 901 CHALGSTNGQCDIRTGQCECQFGITGQHCECETNHFGPGEGCKPCDCHEGSLSLQCK 960  
 Db 934 CHALGSTNGQCDIRTGQCECQFGITGQHCECETNHFGPGEGCKPCDCHEGSLSLQCK 993  
 QY 961 DGRCECRGFGVGNRCDCQCEENYFNRSWPGCGECPACVRLVKDAAHVRVKLQELSLI 1020  
 Db 994 DGRCECRGFGVGNRCDCQCEENYFNRSWPGCGECPACVRLVKDAAHVRVKLQELSLI 1053  
 QY 1021 ANLGTDDMVVTOAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSLSHSQISR 1080  
 Db 1054 ANLGTDDMVVTOAFEDRLKEAREVTDLLREAEQVKVDQNLMDRLQVNSLSHSQISR 1113  
 QY 1081 LQNIWNTIETGILAEARARSVESTEOILIEIASRELEKAKMAANSITQPESTCEPNMWT 1140  
 Db 1114 LQNIWNTIETGILAEARARSVESTEOILIEIASRELEKAKMAANSITQPESTCEPNMWT 1173

QY 1141 LLAEEARRLAERHKQEBADDIVRVAKTANETSABAYNNLLRLTAGENQTALEIEELNRKYE 1200  
 Db 1174 LLAEEARRLAERHKQEBADDIVRVAKTANETSABAYNNLLRLTAGENQTALEIEELNRKYE 1233  
 QY 1201 QAKNISODLEKQOARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
 Db 1234 QAKNISODLEKQOARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293  
 QY 1261 RLIDQKLDYEDLREDMRGKEHEVNKLEKGAEOQTADOLLARADAAKALAEAAKGR 1320  
 Db 1294 RLIDQKLDYEDLREDMRGKEHEVNKLEKGAEOQTADOLLARADAAKALAEAAKGR 1353  
 QY 1321 STLQEAENDILNNLKOPDREVNDKNTAAEALRRIIPAINRTIAEANEKTRQAOLALGNAAA 1380  
 Db 1354 STLQEAENDILNNLKOPDREVNDKNTAAEALRRIIPAINRTIAEANEKTRQAOLALGNAAA 1413  
 QY 1381 DATEAKNKAFAERIASAAQKNAATSTKADAERTFGEVTDLDNEVNGMLRQLEBEAENELKR 1440  
 Db 1414 DATEAKNKAFAERIASAAQKNAATSTKADAERTFGEVTDLDNEVNGMLRQLEBEAENELKR 1473  
 QY 1441 KQDDADODMMAGMASQAAQAEALNARKAKNSVSLLSQNLNLLDQLGQDVTVDLNKANE 1500  
 Db 1474 KQDDADODMMAGMASQAAQAEALNARKAKNSVSLLSQNLNLLDQLGQDVTVDLNKANE 1533  
 QY 1501 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAMDMYNRDIAEIKDIHNLEDIKKTL 1560  
 Db 1534 IEGSLNKAKDEMKAASDLDRKVSLESEARKQEAAMDMYNRDIAEIKDIHNLEDIKKTL 1593  
 QY 1561 TGCFTNTPSIEKP 1572  
 Db 1594 TGCFTNTPSIEKP 1605

RESULT 7  
 AAW50897  
 ID AAW50897 standard; protein; 1607 AA.  
 XX  
 AC AAW50897;  
 XX AC  
 XX XX  
 DT 07-DEC-1998 (first entry)  
 XX  
 DE Mouse laminin G1 chain.  
 XX  
 XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;  
 KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
 KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
 KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
 KW Garttmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
 KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
 KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
 KW therapy.  
 KW  
 XX Mus sp.  
 XX  
 XX WO9815179-A1.  
 XX  
 XX 16-APR-1998.  
 PD  
 XX 08-OCT-1997; 97WO-US018145.  
 PF  
 XX 08-OCT-1996; 96US-0027981P.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 XX  
 XX Castillo G, Snow AD;  
 XX  
 XX WPI; 1998-240534/21.  
 DR  
 XX Use of laminin and fragments - for developing products for use in the  
 PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
 PT CJD.  
 XX  
 XX Claim 15; Page 102-105; 132pp; English.  
 PS

XX This is the amino acid sequence of the mouse laminin G1 chain. The  
 CC primary object of the invention is to use laminin, laminin-derived  
 CC protein fragments and/or laminin-derived polypeptides as potent  
 CC inhibitors of amyloid formation, deposition, accumulation and/or  
 CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
 CC products (see AAWS0888-98) may include mouse or human laminin A or A1  
 CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
 CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
 CC binding domain of the laminin A chain. A claimed method for treating an  
 CC amyloid disease comprises administering a polypeptide having a  
 CC conformational similarity to a fragment of a laminin protein. A method  
 CC for diagnosing an amyloid disease involves determining levels of laminin  
 CC in a sample. Production of laminin or its fourth globular repeat *in vivo*  
 CC provides a method for *in vivo* inhibition of beta-amyloid amyloidosis. The  
 CC products and methods can be used for the diagnosis, prognosis, monitoring  
 CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
 CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
 CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
 CC associated with chronic inflammation, various forms of malignancy and  
 CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
 CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
 CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
 CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
 CC prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler  
 CC syndrome, Kuru and animal scrapie (PrP amyloid), the amyloidosis  
 CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
 CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
 CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or  
 CC transthyretin amyloid), and the amyloidosis associated with endocrine  
 CC tumours such as medullary carcinoma of the thyroid (variant of  
 CC procalcitonin)  
 XX  
 SQ Sequence 1607 AA;

Query Match 99.1%; Score 8446; DB 2; Length 1607;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1563; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 AMDECADEGGRPCRMPEFNAAFNVTVAINTCGTTPPEYCVOTGVTGKTSCHLCDAG 60  
 DB 34 AMDECADEGGRPCRMPEFNAAFNVTVAINTCGTTPPEYCVOTGVTGKTSCHLCDAG 93  
 QY 61 QQHLQGAALFDYNNQADTTWQSQTMLAGVQPNINSINTLHLGKAFDITYVRLKFTS 120  
 DB 94 QQHLQGAALFDYNNQADTTWQSQTMLAGVQPNINSINTLHLGKAFDITYVRLKFTS 153  
 QY 121 RPESFALYKRTREDDGPIPIQYVYSGSCENTYSKANGFIRTGDEBQALCTDEFSDISPL 180  
 DB 154 RPESFALYKRTREDDGPIPIQYVYSGSCENTYSKANGFIRTGDEBQALCTDEFSDISPL 213  
 QY 181 TGGNVAFSTLEGRPSAYFNPNFNSVLOEWVTATDIRVTNLRLNTFGDEVNDPKVLSYYY 240  
 DB 214 TGGNVAFSTLEGRPSAYFNPNFNSVLOEWVTATDIRVTNLRLNTFGDEVNEPKVLSYYY 273  
 QY 241 AISDFAVGRCCKNGHASECVKXNEFKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300  
 DB 274 AISDFAVGRCCKNGHASECVKXNEFKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 333  
 QY 301 ASBCLPCDCCNGRSGECYFDPFLYRSTGHGCHCTNCRDNTDGAKCERCERFRLGNTEAC 360  
 DB 334 ASBCLPCDCCNGRSGECYFDPFLYRSTGHGCHCTNCRDNTDGAKCERCERFRLGNTEAC 393  
 QY 361 SPCHSPVGLSTQCDYSYGRCSCKPGVMGDKDRCCQPGFHSLTEACRSCSDPSGSTDE 420  
 DB 394 SPCHSPVGLSTQCDYSYGRCSCKPGVMGDKDRCCQPGFHSLTEACRSCSDPSGSTDE 453  
 QY 421 CNVETGRVCVKNVEGNCRCRCKPGFNLESNNPKGCTPCFCGHSSVCTNAGVSVDYI 480  
 DB 454 CNVETGRVCVKNVEGNCRCRCKPGFNLESNNPKGCTPCFCGHSSVCTNAGVSVDYI 513  
 QY 481 SSTFQIDEDGWRVEQRDGSSEASLEWSSDRQDIAVISDSYFPRYFIAPVKFIGNQVLSYQG 540

DB 514 SSTFQIDEDGWRVEQRDGSSEASLEWSSDRQDIAVISDSYFPRYFIAPVKFIGNQVLSYQG 573  
 QY 541 NLSFSFRVDRDRTLRLSAEDLVLEGAGLRVSVPLLAQGNYSPESTTVKYIFRLHEATDYPW 600  
 DB 574 NLSFSFRVDRDRTLRLSAEDLVLEGAGLRVSVPLLAQGNYSPESTTVKYIFRLHEATDYPW 633  
 QY 601 RPALSPFPFQKLLNNLSIKIRGYYSRSAGYLDVDTLQSRPQPGVPATWVSCPTPVG 660  
 DB 634 RPALSPFPFQKLLNNLSIKIRGYYSRSAGYLDVDTLQSRPQPGVPATWVSCPTPVG 693  
 QY 661 YGGQFCETCLPGYRRETPSLGYPSPVCLCTCNHSECTDPTGVCDCRDNTAGPHECKS 720  
 DB 694 YGGQFCETCLPGYRRETPSLGYPSPVCLCTCNHSECTDPTGVCDCRDNTAGPHECKS 753  
 QY 721 DGYGDSLTGTSQCPQPCPGSSCAIVPKTKVWVCHTCTGTAGKRCCLCDDGYFDDP 780  
 DB 754 DGYGDSLTGTSQCPQPCPGSSCAIVPKTKVWVCHTCTGTAGKRCCLCDDGYFDDP 813  
 QY 781 LGSNGPVELCRPCQCNNDNIDPNAVGNCRNLGTECLKIYNTAGVFCORCKEGFGNPLAP 840  
 DB 814 LGSNGPVELCRPCQCNNDNIDPNAVGNCRNLGTECLKIYNTAGVFCORCKEGFGNPLAP 873  
 QY 841 NPADKCKACACN-YGTVQOQSSCNPTVTCQCCLPHVSGRDCGTCDPGYNNLQSGQGCERC 899  
 DB 874 NPADKCKACACNPTGTVQOQSSCNPTVTCQCCLPHVSGRDCGTCDPGYNNLQSGQGCERC 933  
 QY 900 DCHALGSTNGQCDITRGCEQCPGITGQHCERCETNHFGPECKPCDCHHESLSLQC 959  
 DB 934 DCHALGSTNGQCDITRGCEQCPGITGQHCERCETNHFGPECKPCDCHHESLSLQC 993  
 QY 960 KDDGRCECREGFGVGNRCDCENYFNRSWPGQCEPCACVRLVKDKAAEHVKLQLESL 1019  
 DB 994 KDDGRCECREGFGVGNRCDCENYFNRSWPGQCEPCACVRLVKDKAAEHVKLQLESL 1053  
 QY 1020 IANLGTGDDMTDOAFEDRLKEAREVTDLLREAEVQKVDQDNLMRLQVNSLSHQIS 1079  
 DB 1054 IANLGTGDDMTDOAFEDRLKEAREVTDLLREAEVQKVDQDNLMRLQVNSLSHQIS 1113  
 QY 1080 RLQNRNTIETGILAEARSVESTQLIEASRELEKAKN-AANYVSIQTPESTGPN 1138  
 DB 1114 RLQNRNTIETGILAEARSVESTQLIEASRELEKAKN-AANYVSIQTPESTGPN 1173  
 QY 1139 MTLAEARRLAEARHKQEADDIVRAKTANETSABAYNLLRLTAGNQTALEIEELNRK 1198  
 DB 1174 MTLAEARRLAEARHKQEADDIVRAKTANETSABAYNLLRLTAGNQTALEIEELNRK 1233  
 QY 1199 YEQAQNISODLEKQAARVHEEAKGADKAVEIYASVAQLTPVDSALEANEANKIKKEAAD 1258  
 DB 1234 YEQAQNISODLEKQAARVHEEAKGADKAVEIYASVAQLTPVDSALEANEANKIKKEAAD 1293  
 QY 1259 LDRLLDQKLDYEDLREDMRGKEHEVNKLEKGAEQQTADQLLARADAALAEAAKK 1318  
 DB 1294 LDRLLDQKLDYEDLREDMRGKEHEVNKLEKGAEQQTADQLLARADAALAEAAKK 1353  
 QY 1319 GRSTLOEANDILNLIKOPDRVNDKNTAAEALBRIIPAINRTIAEANEKTRQAOLAGNA 1378  
 DB 1354 GRSTLOEANDILNLIKOPDRVNDKNTAAEALBRIIPAINRTIAEANEKTRQAOLAGNA 1413  
 QY 1379 AADATEAKNKAHEARJASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1438  
 DB 1414 AADATEAKNKAHEARJASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1473  
 QY 1439 KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDQLGOLDTVLNLK 1498  
 DB 1474 KRKQDDADQDMMWAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDQLGOLDTVLNLK 1533  
 QY 1499 NEIEGSLNKADEKASDLDRKVSDFLESEARKQBAALMDYNRDIAEIIKDIHNEDEKKT 1558  
 DB 1534 NEIEGSLNKADEKASDLDRKVSDFLESEARKQBAALMDYNRDIAEIIKDIHNEDEKKT 1593  
 QY 1559 LPTGCFNTPTSEKP 1572  
 DB 1594 LPTGCFNTPTSEKP 1607



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Db 1203 YEQAQNIQSOLLEKQAAVHEBEAKRAGDKAVEIYASVAQLSPLOSETLENNIKWEAEN 1262
Qy 1259 LDRIDQKLDYEDLREDMGEKEHEVKNLLEKGAEOQTADQOLLARADAKALAEAAK 1318
Db 1263 LEQLIDQKLDYEDLREDMGEKEHEVKNLLEKGAEOQTADQOLLARADAKALAEAAK 1322
Qy 1319 GRSTLOQANDILNKKDFDRVNDNKTAAAEALRRIPAINRTIAEANEKTRQAQLGNA 1378
Db 1323 GRDTLOQANDILNKKDFDRVNDNKTAAAEALRKIPAINQTITEANEKTRQAQLGSA 1382
Qy 1379 AADATEAKNAKAHERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANEL 1438
Db 1383 AADATEAKNAKAHERIASAVQKNATSTKAEARTTFAEVTDLNEVNNMLKQLOEAEKEL 1442
Qy 1439 KRQDDADQDMMAGWASQAQAEALNARKAKSVSSLLSQNNLLDQLQDLDVLDNKL 1498
Db 1443 KRQDDADQDMMAGWASQAQAEALNARKAKSVTSLJSIINDLLEQLQDLDVLDNKL 1502
Qy 1499 NEIEGSLNKADEMKAQDLDRKVSLESEARKQEAAIMDYNRDIAIITKIDHNLDEIKKT 1558
Db 1503 NEIEGTLNKADEMKAQDLDRKVSLESEARKQEAAIMDYNRDIEIMKDINLEDIRKT 1562
Qy 1559 LPTGCFNTPSIEKP 1572
Db 1563 LPSGCFNTPSIEKP 1576

RESULT 9
ID AAB48453 standard; protein; 1576 AA.
AC AAB48453;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 8 polypeptide, SEQ ID NO: 24.
XX
KW Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
XX
PR 21-AUG-1999; 99US-0149738P.
XX
PR 24-SEP-1999; 99US-0155945P.
XX
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSSTRATUM INC.
XX
PI Kortessmaa J, Tryggvason K;
XX
DR WPI; 2000-687535/67.
XX
DR N-PSDB; AAC83714.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 214-218; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC functions. Laminin 8 is useful for treating injuries to tissue of
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CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1576 AA;
Query Match 94.3%; Score 8038; DB 3; Length 1576;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;
Qy 1 AMDECADGGGPORCMPEFVNAAFNVTVVANTGCTPPEEYCVQTVGTVTKSCHLDCAG 60
Db 3 AMDECTDGGGPORCMPEFVNAAFNVTVVANTGCTPPEEYCVQTVGTVTKSCHLDCAG 62
Qy 61 QOHLQHGAAFLTDYNNQADTTWQSOTMLAGVQVPSNINLTLLHCKAPDITVYRLKPHTS 120
Db 63 QPHLQHGAAFLTDYNNQADTTWQSOTMLAGVQVPSNINLTLLHCKAPDITVYRLKPHTS 122
Qy 121 RPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGPIRTGGDEQQAALCTDEFSDISPL 180
Db 123 RPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGPIRTGGDEQQAALCTDEFSDISPL 182
Qy 181 TGGNVAFSTLEGPSAYNFDSNVPVLOEWVTATDTRVTLNRLNTFGDEVNDPKVLSYY 240
Db 183 TGGNVAFSTLEGPSAYNFDSNVPVLOEWVTATDTRVTLNRLNTFGDEVNDPKVLSYY 242
Qy 241 AISDPAVGRCKNGHASECVKNEFDKLMCNKENTYGVDCCKLPFFNDRPWRATAES 300
Db 243 AISDPAVGRCKNGHASECMKNEFDKLVCKNKENTYGVDCCKLPFFNDRPWRATAES 302
Qy 301 ASECLPCDNGRSQECYFDPPELYRSTGGHCTCRDNTDGAECERENEFRLGNTEAC 360
Db 303 ASECLPCDNGRSQECYFDPPELYRSTGGHCTCRDNTDGAECERENEFRLGNTEAC 362
Qy 361 SPCHSPVGSLSSTQCDSYGRCSCKPGVMGDKDCRCQGFHSLTEAGRCPCSDPSGSTDE 420
Db 363 SSCHSPVGSLSSTQCDSYGRCSCKPGVMGDKDCRCQGFHSLTEAGRCPCSDPSGSTDE 422
Qy 421 CNVETGRVCVKNDVEGFNCERCKPGFFNLBNSSNPKGCTPCPCFGHSSVCTNAVGSYVDI 480
Db 423 CNVETGRVCVKNDVEGFNCERCKPGFFNLBNSSNPKGCTPCPCFGHSSVCTNAVGSYYSI 482
Qy 481 SSTFOIDEDGMRVQORDGSEASLEWSSDROVIAVISDYPPEYFIAPVKFIQNOVLVSYGQ 540
Db 483 SSTFOIDEDGMRVQORDGSEASLEWSSERQDIAVISDYPPEYFIAFVAKFLGKQVLVSYGQ 542
Qy 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNYSYPSSETTVKYIFRLHEATDYPW 600
Db 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNYSYPSSETTVKYVFLRHEATDYPW 602
Qy 601 RPALSPFEFOKLNNLTISKIRGTYSERSAGYLDVLTQSARPGVGPATWVECTCPVG 660
Db 603 RPALTFFEQKLLNNLTISKIRGTYSERSAGYLDVLTQSARPGVGPATWVECTCPVG 662
Qy 661 YGGQFCETCLPGRRETPESLGYPSPVLCNCGHSETCDPPTGVCDNRDNTAGPCEKCS 720
Db 663 YGGQFCMCLSGYARETENLGPSPVLCNCGHSETCDPPTGVCDNRDNTAGPCEKCS 722
Qy 721 DGYVGDSTLTGSSDCPCPCGGSSCAVPKTKVCTHCTCPTAGKRCCLCDDGYSGDP 780
Db 723 DGYVGDSTAGTSSDCPCPCGGSSCAVPKTKVCTHCTCPTAGKRCCLCDDGYSGDP 782
Qy 781 LGSNGFVRLCRPCQCNNDNDNNAVGNMNLGECCLKCIYNTAGFYCDRCKEGFFGNPLAP 840
Db 783 LGNGFVRLCRPCQCNNDNDNNAVGNMNLGECCLKCIYNTAGFYCDRCKEGFFGNPLAP 842
Qy 841 NPADKCKACACN-YGTVOQQSSCNVPTGQCQCLPHVSGRDCGTCDPGYVNLQSGGCERC 899
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Db 843 NPADKCKACNCPYGTWKQSSCNFVTGQCECLHVTGDCGACDPGFYNLSQGGCERC 902
Qy 900 DCHALGSTNGQCDIRITGQCECPQGITGOHCBRCSTNHFPGPECKPCDCHHBSLSLQC 959
Db 903 DCHALGSTNGQCDIRITGQCECPQGITGOHCBRCSTNHFPGPECKPCDCHHBSLSLQC 962
Qy 960 KDDGRCECEGFGVGNRCDCCEYFYNRSPGQCECPACVRLVKDKAAEHRVKLQELLES 1019
Db 963 KDDGRCECEGFGVGNRCDCCEYFYNRSPGQCECPACVRLVKDKADHRVKLQELLES 1022
Qy 1020 IANLGTGDMVTDOAFEDRLKEAREVTDLLREAEQVKVDQNDLMDRLQRVNSLSHSQIS 1079
Db 1023 IANLGTGDMVTDOAFEDRLKEAREVMDLLREAQVKVDQNDLMDRLQRVNNLTSSQIS 1082
Qy 1080 RLQINRTIETGTLAERARSRVSTEOLEIASRELEKAKM-AANYSITQPESTGPN 1138
Db 1083 RLQINRTIETGNLAERARHVENTERLEIASRELEKAKAAANYSITQPESTGPN 1142
Qy 1139 MTLAEEARRLAERHKQADDIRVAKTANETSABAYNLLRTLAGENQTALEIEELNRK 1198
Db 1143 MTLAEEARKLAERHKQADDIRVAKTANDTSTEAAYNLLRTLAGENQTAFAIEIEELNRK 1202
Qy 1199 YEQAKNISODLEKQAAVHEEAKRAGDKAVEIYASVACLTPVDSEALENEANKIKKEAD 1258
Db 1203 YEQAKNISODLEKQAAVHEEAKRAGDKAVEIYASVACLTPVDSEALENEANKIKKEAD 1262
Qy 1259 LDRITDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARADAAKALAEAAK 1318
Db 1263 LEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKGTQEQTDQLLARADAAKALAEAAK 1322
Qy 1319 GRSTLOEBANDILNNLKDFDRVNDKNTAAEALRIPAINRTIAEANEKTRAEQALAGNA 1378
Db 1323 GRDTLOEBANDILNNLKDFDRVNDKNTAAEALRIPAINRTIAEANEKTRAEQALGSA 1382
Qy 1379 AADATEAKNKAHEABRIASAKQKATSTKADAERTFGEVTDLDNEVNGMLRQLFEAEENEL 1438
Db 1383 AADATEAKNKAHEABRIASAKQKATSTKAEARTFAEVTDLDNEVNNMLKQLQEAKEKEL 1442
Qy 1439 KRKQDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSOLNNLLQGLDITVDLNLK 1498
Db 1443 KRKQDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSILINDLLEQLGLDITVDLNLK 1502
Qy 1499 NEIEGSLNKADEMKAASDLDRKVSLESEAKQBAALMDYNRDIAEIKDTHNLEDIKKT 1558
Db 1503 NEIEGTLNKADEMKAASDLDRKVSLENEAKQBAALMDYNRDIEEIKDTHNLEDIRKT 1562
Qy 1559 LPTGCFNTFSIEKP 1572
Db 1563 LPSGCFNTFSIEKP 1576
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RESULT 10  
ABB81595  
ID ABB81595 standard; protein; 1576 AA.

XX AC ABB81595;

XX DT 19-SEP-2002 (first entry)

XX DE Human laminin 10 third chain protein sequence SEQ ID NO:16.

XX KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
XX tissue repair development; laminin; healing; vascular tissue;  
XX re-endothelialisation; vascular injury; cell attachment; cell stasis;  
XX proliferation; migration.

XX OS Homo sapiens.

XX PN WO200250111-A2.

XX PD 27-JUN-2002.

XX

PF 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P.  
PR 28-MAR-2001; 2001US-0279282P.  
PR 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
PI WPI; 2002-557850/59.  
XX N-PSDB; ABQ72913.  
DR New human laminin-10 proteins, useful for accelerating the healing of  
XX vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX Claim 9; Page 177-182; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a third chain protein of laminin 10, from the present  
XX invention  
SQ Sequence 1576 AA;

Query Match 94.3%; Score 8038; DB 5; Length 1576;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 1 AMDECADEGRQRCMPPEFVNAFNVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 60  
Db 3 AMDECTDEGRQRCMPPEFVNAFNVVATNTCGTPPEEYCVQGTGVTKSCHLCDAG 62  
Qy 61 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVNSINLTHLGAFFDITVRLKFTS 120  
Db 63 QHQLHGAAFLTDYNNQADTTWQSQTMLAGVQYVSSINLTHLGAFFDITVRLKFTS 122  
Qy 121 RPESFAIYKTRTREDGFWIPYQYVSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDISPL 180  
Db 123 RPESFAIYKTRTREDGFWIPYQYVSGSCENTYSKANRGFIRTCGDEQQAALCTDEFSDISPL 182  
Qy 181 TGGNVAFTLEGPRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLSYYY 240  
Db 183 TGGNVAFTLEGPRPSAYNFDNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLSYYY 242  
Qy 241 AISDPAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATAS 300  
Db 243 AISDPAVGGRCCKNGHASECKNEFDKLVNCKHNTYGVDCBKCLPFFNDRPWRATAS 302  
Qy 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKCRCRENFRLGNTEAC 360  
Db 303 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCTNCRDNTDGAKCRCRENFRLGNNEAC 362  
Qy 361 SPCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSTD 420  
Db 363 SSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGRCPCSDPSGSTD 422  
Qy 421 CNVETGRVCYKDNVEGFCNCRCKPGFFNLESNPKGCTPCFCFGHSSVCTNAGVSVYDI 480  
Db 423 CNVETGRVCYKDNVEGFCNCRCKPGFFNLESNPRGCTPCFCFGHSSVCTNAGVSVYSI 482  
Qy 481 SSTFQIDEGWRVEQRDGSSEASLEWSSDRQYTAVIDSDSYFFPRYFTAPKVLGNVLSYQ 540  
Db 483 SSTFQIDEGWRVEQRDGSSEASLEWSSERQDIAVIDSDSYFFPRYFTAPKVLGNVLSYQ 542



541 NLSFSDVDRDRTRLSAEDLVLEGAGLRVSVPLIAAGNSYPSSETTVKVIIFRLHEATDYPW 600  
543 NLSFSDVDRDRTRLSAEDLVLEGAGLRVSVPLIAAGNSYPSSETTVKVIIFRLHEATDYPW 602  
601 RPLSPFQKLNLLNLSIKIGTYSERSAGYLDVDTLQSRAPGPGVPATWVESCTCPVG 660  
603 RPLTFPFQKLNLLNLSIKIGTYSERSAGYLDVDTLQSRAPGPGVPATWVESCTCPVG 662  
661 YGQFCETCLPGVRRTPSLGYSVPCVLTGNGHSETCDPFGVCDRCRNTAGPCEKCS 720  
663 YGQFCETCLPGVRRTPSLGYSVPCVLTGNGHSETCDPFGVCDRCRNTAGPCEKCS 722  
721 DGVYGDSTLGTSDCPCPCGSSCAIVPKTKVVCVCTGAGKRCCLCDDGFGDP 780  
723 DGVYGDSTLGTSDCPCPCGSSCAIVPKTKVVCVCTGAGKRCCLCDDGFGDP 782  
781 LGSNGPVLRCRQCQNDNDPNAVGNCLTGECLKIYNTAGFYCDRCBGFNPNLAP 840  
783 LGRNGPVLRCRQCQNDNDPNAVGNCLTGECLKIYNTAGFYCDRCBGFNPNLAP 842  
841 NPADKCAACN-YGVVQSSCNPTGQCCLPHVSGRDCGTCGPGYVNLQSGGCGERC 899  
843 NPADKCAACNPTGTMQSSCNPTGQCCLPHVSGRDCGTCGPGYVNLQSGGCGERC 902  
900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGCKPCDCHHEGSLSLQC 959  
903 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGCKPCDCHHEGSLSLQC 962  
960 KDGRCCEGFGVGNRCDCQCEYFNRSWPGQCEPCACRYLVKDKAAHVRKVLQELSL 1019  
963 KDGRCCEGFGVGNRCDCQCEYFNRSWPGQCEPCACRYLVKDKAAHVRKVLQELSL 1022  
1020 IANLGTGDMVTQDQAEFDRLEKEAREVTDLLREAEQVQDQNDLRLQVNSLSHSQIS 1079  
1023 IANLGTGDMVTQDQAEFDRLEKEAREVTDLLREAEQVQDQNDLRLQVNSLSHSQIS 1082  
1080 RLQNIINTIETGILAEARARSVESTQIEIETASRELEKAM-AANVSITQESTGEPPN 1138  
1083 RLQNIINTIETGILAEARARSVESTQIEIETASRELEKAM-AANVSITQESTGEPPN 1142  
1139 MTLAEARLARHKEADDDIVRVAKTANETSAEAYNLLRLTAGENCTAEIEBELNRK 1198  
1143 MTLAEARLARHKEADDDIVRVAKTANETSAEAYNLLRLTAGENCTAEIEBELNRK 1202  
1199 YEOAKNISQLEKQAAVHEAKRAGDKAVEIYASVAQLTFVDSEALEANEAKIKERAD 1258  
1203 YEOAKNISQLEKQAAVHEAKRAGDKAVEIYASVAQLTFVDSEALEANEAKIKERAD 1262  
1259 LDRLIDOKLYEDLREDYRGKEHEVKNLLEKGAQEQOTADQALLARADAAKALAEAAK 1318  
1263 LEQLIDOKLYEDLREDYRGKEHEVKNLLEKGAQEQOTADQALLARADAAKALAEAAK 1322  
1319 GRSTQEAANDILNNLKDFFRRVNDNKTAAEALRLRIPAINRTIAEANEKTRQAALGNA 1378  
1323 GRSTQEAANDILNNLKDFFRRVNDNKTAAEALRLRIPAINRTIAEANEKTRQAALGNA 1382  
1379 AADATEAKNAHAERIASAQAQNAATSTKADAEETGEVTDLDNENGMRLQLEAEANEL 1438  
1383 AADATEAKNAHAERIASAQAQNAATSTKADAEETGEVTDLDNENGMRLQLEAEANEL 1442  
1439 KRQDDADQDDMMWAGMASQAQAEALNARKAKNSVSLLSQANLLDQLGQDITVDLNLK 1498  
1443 KRQDDADQDDMMWAGMASQAQAEALNARKAKNSVSLLSQANLLDQLGQDITVDLNLK 1502  
1499 NEIEGSLINKAKDEMKASDLDKRVSDLESEARKQEAAMIDNRYDIAIHKDHNLEDIKKT 1558  
1503 NEIEGSLINKAKDEMKASDLDKRVSDLESEARKQEAAMIDNRYDIAIHKDHNLEDIKKT 1562  
1559 LPTGCFNTPSIEKP 1572  
1563 LPTGCFNTPSIEKP 1576

RESULT 11  
AAB19804  
ID AAB19804 standard; protein; 1584 AA.  
XX  
AC AAB19804;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.  
XX  
Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..33  
FT Protein 34..1609  
FT Peptide /label= Mature\_protein  
FT Peptide 1610..1617  
FT Peptide /label= FLAG  
XX  
FN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
DR WPI; 2000-687537/67.  
DR N-PSDB; AAA88904.  
XX  
PT Purified laminin 2 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 275-280; 305pp; English.  
XX  
CC The present sequence is that of the mature gamma-1 chain of human laminin  
CC 2, with an additional C-terminal FLAG epitope, resulting from expression  
CC in transfected cells from mammalian expression vectors. Laminin 2 is  
CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)  
CC chains. It is thought to be specifically required for stabilizing  
CC myotubes during skeletal muscle development, and for preventing  
CC apoptosis. Genetic defects in its structure or expression are associated  
CC with a major type of congenital muscular dystrophy. Laminin 2 is also  
CC thought to be important in Schwann cell/basal lamina interactions. The  
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain  
CC polypeptides (see AAB1971-806) and the polynucleotides encoding them  
CC (see AAA8891-906), methods for making recombinant laminin 2, cells that  
CC express recombinant laminin 2, and methods for using purified laminin 2  
CC for research and therapeutic purposes including peripheral nerve  
CC regeneration, treatment of degenerative muscle disorders, angiogenesis  
CC regulation, promoting cell attachment and migration, ex vivo cell  
CC therapy, improving the take of grafts, improving the biocompatibility of  
CC medical devices and preparing improved culture devices and media  
XX  
SQ Sequence 1584 AA;  
Query Match 94.3%; Score 8038; DB 3; Length 1584;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
QY 1 AMDECAEGGRQRCMPEFVNAENVTATNTCGTPEEYCVQTVGTGKSHCLDAG 60

Db 3 AMDECTDEGGRPORCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTGKSCHLCDAG 62  
QY 61 QOHLQHGAAFLTDVNNQADTTWQSQMLAGVOYPSINLTLLHGAFAFDITYVRLKPHTS 120  
Db 63 QPHLOHGAAFLTDVNNQADTTWQSQMLAGVOYPSINLTLLHGAFAFDITYVRLKPHTS 122  
QY 121 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIIRTGDEQOALCTDFSFISPL 180  
Db 123 RPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIIRTGDEQOALCTDFSFISPL 182  
QY 181 TGGNVAESTLEGPSAYNFENSPVLQEWVATATDIRVTLNRLNTFGDEVNDPVKLSYYY 240  
Db 183 TGGNVAESTLEGPSAYNFENSPVLQEWVATATDIRVTLNRLNTFGDEVNDPVKLSYYY 242  
QY 241 AISDFAYGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300  
Db 243 AISDFAYGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 302  
QY 301 ASECLPCDCNCRSGOECYFDPBELYSTGHGHCTNCRDNTDGAKCERENFFLGNTEAC 360  
Db 303 ASECLPCDCNCRSGOECYFDPBELYSTGHGHCTNCRDNTDGAKCERENFFLGNTEAC 362  
QY 361 SPCHSPVGSLSITQCDSYGRCSCKPGVWGDKDRCPGFHSLTEAGRCPCSDPSSGSTE 420  
Db 363 SSCHSPVGSLSITQCDSYGRCSCKPGVWGDKDRCPGFHSLTEAGRCPCSDPSSGSTE 422  
QY 421 CNVETGRVCVKNDVEGNCERCKPGFNLBNSSPKGCTPCFCGHSVCTNNAVGYVYDI 480  
Db 423 CNVETGRVCVKNDVEGNCERCKPGFNLBNSSPKGCTPCFCGHSVCTNNAVGYVYDI 482  
QY 481 SSTQIODEDGNRVEOROGSEASLEWSSDROVIAVISDSYFPRFIAPVKFLGNQVLSYGQ 540  
Db 483 SSTQIODEDGNRVEOROGSEASLEWSSDROVIAVISDSYFPRFIAPVKFLGNQVLSYGQ 542  
QY 541 NLSFSFRVDRDRTLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
Db 543 NLSFSFRVDRDRTLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 602  
QY 601 RPALSPFEQKLLNLSIKIRGYTSERSAGYLDVLTQSGARPQGPVPATWVESCPCPVG 660  
Db 603 RPALTPFEQKLLNLSIKIRGYTSERSAGYLDVLTQSGARPQGPVPATWVESCPCPVG 662  
QY 661 YGGQFCETCLPGYRRETPSLGYPSPVCLTCNGHSETCDPETGVCDORDNTAGPHCEKCS 720  
Db 663 YGGQFCETCLPGYRRETPSLGYPSPVCLTCNGHSETCDPETGVCDORDNTAGPHCEKCS 722  
QY 721 DGYGDSITLGTSSDCQPCPCPGSSCAIVPKTKWVCTHCTGTAGKRCCLDDGYGDP 780  
Db 723 DGYGDSITLGTSSDCQPCPCPGSSCAIVPKTKWVCTHCTGTAGKRCCLDDGYGDP 782  
QY 781 LGSNGPVLRCRQCQCNNDIDNAVGNCRNLGTGECLKICYNTAGFYCDRCCKEGFNGPLAP 840  
Db 783 LGRNGPVLRCRQCQCNNDIDNAVGNCRNLGTGECLKICYNTAGFYCDRCCKEGFNGPLAP 842  
QY 841 NPAOKCKACAN-VGTVOQQSCNHPVTGQOCLPHVSGRDCGTCDPGYNNLQSGQCERC 899  
Db 843 NPAOKCKACAN-VGTVOQQSCNHPVTGQOCLPHVSGRDCGTCDPGYNNLQSGQCERC 902  
QY 900 DCHALGSTNGQCDIRTGQCEQPGITGQHCBERTNHFQGECKPCDCHHEGSLSLQC 959  
Db 903 DCHALGSTNGQCDIRTGQCEQPGITGQHCBERTNHFQGECKPCDCHHEGSLSLQC 962  
QY 960 KDDGRCECREGFGVNRCDQCEBENTFYNRSPGQCECPACVRLVYKDKAAEHRVKLQELLES 1019  
Db 963 KDDGRCECREGFGVNRCDQCEBENTFYNRSPGQCECPACVRLVYKDKAAEHRVKLQELLES 1022  
QY 1020 TANLGTGDMVTDQAFEDRLKEAREVTDLLREAEQVVDQNDLMDRLQRVNSLSHQIS 1079  
Db 1023 TANLGTGDMVTDQAFEDRLKEAREVTDLLREAEQVVDQNDLMDRLQRVNSLSHQIS 1082  
QY 1080 RLQNTIRNTIETGLAEARSRVSTEQLEIFIASRELEKAKV-AANYSIITQPESTGDPNN 1138

Db 1083 RLQNTIRNTIETGLAEQARAHVENTERLEIFIASRELEKAKVAAANYSVTQPESTGDPNN 1142  
QY 1139 MTLAAEEARRLAERHKQEADDIVRVAKTANETSABEYNNLLRTLAGENQTLAEIEELNRK 1198  
Db 1143 MTLAAEEARRLAERHKQEADDIVRVAKTANDTSTAEYNNLLRTLAGENQTLAEIEELNRK 1202  
QY 1199 YEQAQNIISODLEKQAAARVHBEAKRAGDKAVEIYASVAQLTVPDSEALENEANKIKKEAAD 1258  
Db 1203 YEQAQNIISODLEKQAAARVHBEAKRAGDKAVEIYASVAQLTVPDSEALENEANKIKKEAAD 1262  
QY 1259 LDRLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEOQTADQOLLARADAALAEAEAAK 1318  
Db 1263 LEQLIDQKLKDYEDLREDMRGKEHEVKNLLEKGTQEQOTADQOLLARADAALAEAEAAK 1322  
QY 1319 GRSTLOEANDILNLLKOPDRVNDKNTAAEALARRIPAINETIABANEKTRAEQALALGNA 1378  
Db 1323 GRDTLOEANDILNLLKOPDRVNDKNTAAEALARRIPAINETIABANEKTRAEQALALGNA 1382  
QY 1379 AADATEAKNKAHEABERIASAAQKATSTKADAERTFGVETDLDNEVNGMLQLEBAENEL 1438  
Db 1383 AADATEAKNKAHEABERIASAAQKATSTKADAERTFGVETDLDNEVNGMLQLEBAENEL 1442  
QY 1439 KKQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDOLGOLDVTDVLANKL 1498  
Db 1443 KKQDDADQDMMAGMASQAAQAEALNARKAKNSVSSLLSQNLNLLDOLGOLDVTDVLANKL 1502  
QY 1499 NEIEGSLNKAQDEKMAKSDLRKVSLESEARKQAAIMDYNRDAEIIKDIHNLEDIKKT 1558  
Db 1503 NEIEGSLNKAQDEKMAKSDLRKVSLESEARKQAAIMDYNRDAEIIKDIHNLEDIKKT 1562  
QY 1559 LPTGCFNTPSIEKP 1572  
Db 1563 LPSGCFNTPSIEKP 1576

RESULT 12  
AAB19801  
ID AAB19801 standard; protein; 1609 AA.  
XX  
AC AAB19801;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Human laminin 2 gamma-1 chain.  
XX  
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..33  
FT Protein /label= signal\_peptide  
FT /label= Mature\_protein 34..1609  
XX  
PN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
DR WPI; 2000-687537/67.  
DR N-PSDB; AAA88901.



DT	02-MAR-2001	(first entry)	Db	276	AI	SDFAVGGRCKNGHASECMNEFDFKLVNCNKHNTYGVDCCKLPFFNDRPMRATAES	335
XX							
DE							
XX							
XX							
KW	Human laminin 8	polypeptide, SEQ ID NO: 22.	Qy	301	ASECLPCDCNGRSOEYFDPBELYSTGHGHTNCRDNTGAKCERENFFRLNGTEAC		360
KW	Human; laminin 8; neuroprotective; angiogenic; osteopathic;						
KW	antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;						
KW	vascular tissue injury; neural injury; angiogenesis regulation.		Db	336	ASECLPCDCNGRSOEYFDPBELYSTGHGHTNCRDNTGAKCERENFFRLNGNEAC		395
XX							
OS	Homo sapiens.		Qy	361	SPCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSHTBAGCRPSCDPSGSDTE		420
XX							
XX			Db	396	SSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCQPGFHSHTBAGCRPSCDPSGSDTE		455
XX							
PN	WO200066732-A2.		Qy	421	CNVTGRCVCKDNVEGFNCERCKPGFENLSSNPKGTGTCFCFGHSSVCTNAVGSYVVDI		480
XX							
PN	09-NOV-2000.		Db	456	CNVTGRCVCKDNVEGFNCERCKPGFENLSSNPKGTGTCFCFGHSSVCTNAVGSYVSI		515
XX							
XX	28-APR-2000; 2000WO-US011543.		Qy	481	SSTFQIDEDGWRVQRDGEASLEWSSDRQYIAVISDSYPPRYFIAPVKFIGNOVLSYQG		540
XX							
XX	30-APR-1999; 99US-01311720P.		Db	516	SSTFQIDEDGWRVQRDGEASLEWSSDRQYIAVISDSYPPRYFIAPVKFIGNOVLSYQG		575
PR	21-AUG-1999; 99US-0149738P.		Qy	541	NLSFSFRVDRDTRLSAEDLVLEGAGLRVSVPLTAQNSYSPSETTVKIFRLHEATYPM		600
PR	24-SEP-1999; 99US-0155945P.						
PR	11-FEB-2000; 2000US-0182012P.		Db	576	NLSFSFRVDRDTRLSAEDLVLEGAGLRVSVPLTAQNSYSPSETTVKIFRLHEATYPM		635
XX							
PA	(BIOS-) BIOSTRATUM INC.		Qy	601	RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSGARPQGPVATWVESCPCPVG		660
XX							
XX	Kortessmaa J, Tryggvason K;		Db	636	RPALTPEEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSGARPQGPVATWVESCPCPVG		695
XX							
DR	WPI; 2000-687539/67.		Qy	661	YGGQFCETCLPGYRRETPSLGYPSPCVLCTGNHSETCDPBTGVCDCEDNTAGPHCKCS		720
DR	N-PSDB; AAC83713.						
XX			Db	696	YGGQFCETCLPGYRRETPSLGYPSPCVLCTGNHSETCDPBTGVCDCEDNTAGPHCKCS		755
XX							
PT	Purified laminin 8 protein, useful for research and therapeutic purposes		Qy	721	DGYGDSLTGTSDDCQPCPCPGSSSCAIVPKTKVWCTHCTPTGTAGKRCCLDDGYGDP		780
PT	including peripheral nerve regeneration, treatment of degenerative muscle						
PT	disorders, angiogenesis regulation, and ex vivo cell therapy.		Db	756	DGYGDSLTGTSDDCQPCPCPGSSSCAIVPKTKVWCTHCTPTGTAGKRCCLDDGYGDP		815
XX							
PS	Claim 5; Page 202-207; 245pp; English.		Qy	781	LGSGNVPVLCRPPCCQNDNIDPNAVGNMRLTGECCLKIYNTAGYCDRCCKEFGNPLAP		840
XX							
XX	The present sequence is a laminin 8 polypeptide chain. Laminins are a		Db	816	LGRNGFVRLCLQCQSDNIDPNAVGNMRLTGECCLKIYNTAGYCDRCCKEFGNPLAP		875
CC	family of heterotrimeric glycoproteins that function via binding						
CC	interactions with neighbouring cell receptors and by forming laminin		Qy	841	NPADKCKACACN-VGTVOQSSCNPTVTCQCLPHVSGRDCGTCDPGYNNLQSGQGCERC		899
CC	networks. They are signalling molecules which influence cellular						
CC	function. Laminin 8 is useful for treating injuries to tissue of		Db	876	NPADKCKACACNPGYTMKQSSCNPTVTCQCLPHVSGRDCGTCDPGYNNLQSGQGCERC		935
CC	mesenchymal origin, such as bone, cartilage, tendon, and ligament,						
CC	treating injuries to vascular tissue, promoting cell attachment and		Qy	900	DCHALGSTNGQCDINTGQCECQPGITGQCHRCERTNHFQPGCECKDCCHESLSLQC		959
CC	migration, ex vivo cell therapy, improving the biocompatibility of						
CC	medical devices, and preparing improved cell culture devices and media.		Db	936	DCHALGSTNGQCDINTGQCECQPGITGQCHRCERTNHFQPGCECKDCCHESLSLQC		995
CC	Laminin 8 is also useful for promoting re-endothelialisation at the site						
CC	of vascular injuries, improving the take of grafts, improving the		Qy	960	KDGRCECREGFGVNRCDQCEENFYNRSWPGCECPACYRLVKDKAAEHVRLKLESL		1019
CC	biocompatibility of medical devices, treating neural injuries (neural						
CC	regeneration), regulating angiogenesis, and promoting cell attachment and		Db	996	KDGRCECREGFGVNRCDQCEENFYNRSWPGCECPACYRLVKDKAAEHVRLKLESL		1055
CC	migration						
XX			Qy	1020	IANLGTGDDMTDQAFEDRLKEAREVTDLLREAGQVQVNDQNLMDRLQVNSLSHSOIS		1079
SQ	Sequence 1609 AA;						
	Query Match 94.3%; Score 8038; DB 3; Length 1609;		Db	1056	IANLGTGDDMTDQAFEDRLKEAREVMDLLREAGQVQVNDQNLMDRLQVNSLSHSOIS		1115
	Best Local Similarity 93.3%; Pred. No. 0;						
	Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;		Qy	1080	RLQNTINTIETGIIAERARSVESTEOLEIETASRELEKAM-AANVSITPESTGEPNN		1138
Qy	1 AMDECADEGGRPQRCMPFVNAAFNVTVAINTCGTPPEYCVQGTGVTGKSCHLCDAG		Db	1116	RLQNTINTIETGIIAERARSVESTEOLEIETASRELEKAM-AANVSITPESTGEPNN		1175
Db	36 AMDECTDGGRPQRCMPFVNAAFNVTVAINTCGTPPEYCVQGTGVTGKSCHLCDAG		Qy	1139	MTLLAEARLAEHRKQADDIRVAKTANETSAEYNNLLRTLAGENQTALEIEELNRK		1198
Qy	61 QOHLQGAFLTDVNNQADTTWQSQOTMLAGVQYPSNINLTLHGKAFDITYVRLKPHTS		Db	1176	MTLLAEARLAEHRKQADDIRVAKTANETSAEYNNLLRTLAGENQTALEIEELNRK		1235
Db	96 QPHLQGAFLTDVNNQADTTWQSQOTMLAGVQYPSNINLTLHGKAFDITYVRLKPHTS		Qy	1199	YFOAKNIISDLLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSALENEANKIKKEAD		1258
Qy	121 RPESFALKYRTREDGPMTPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDFPSDISPL		Db	1236	YFOAKNIISDLLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSALENEANKIKKEAD		1295
Db	156 RPESFALKYRTREDGPMTPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDFPSDISPL		Qy	1259	LORLIDQKLKYDEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARAADAALAEAAK		1318
Qy	181 TGGNVAFTLGRFSAYNFDNSPLQEWVTATDIRVTLNRLNTFGDEVNDPKVLSYYY		Db	1296	LORLIDQKLKYDEDLREDMRGKEHEVKNLLEKGAEQQTADQLLARAADAALAEAAK		1355
Db	216 TGGNVAFTLGRFSAYNFDNSPLQEWVTATDIRVTLNRLNTFGDEVNDPKVLSYYY		Qy	1319	GRSTTQAEANDILNLUKDFRRVNDKTAABEALRIPAINRTIAENKTEBAQALGNA		1378
Qy	241 AISDFAVGGRCKNGHASECMNEFDFKLVNCNKHNTYGVDCCKLPFFNDRPMRATAES		Db	1356	GRDTTQAEANDILNLUKDFRRVNDKTAABEALRIPAINRTIAENKTEBAQALGNA		1415

QY 1379 AADATEAKNAHEAERTASAAQKATSTKADAERTFGEVTDLDNEVNGMLRQLEAEENEL 1438  
DB 1416 AADATEAKNAHEAERTASAVQKATSTKAAEERTFAEVTDLONEVNNMLKQLQAEAKEL 1475  
QY 1439 KRKODDADODMMAGMASQAQAQAEELNARKAKNSVSSLLSQLNLLDQLQOLDVLDNKL 1498  
DB 1476 KRKODDADODMMAGMASQAQAQAEELNARKAKNSVSSLLSIINDLLEQLQOLDVLDNKL 1535  
QY 1499 NEIEGSLINKAKDENKASDLDRKVSDESEARKQOAAIMDYNRDIAEIIKDIHNLDEIKKT 1558  
DB 1536 NEIEGSLINKAKDENKVSDDLDRKVSDELEAKQOAAIMDYNRDIEELIMKDIRNLEDIRKT 1595  
QY 1559 LPTGCFNTPSIEKP 1572  
DB 1596 LPSCGFNTPSIEKP 1609

RESULT 14  
ABB81594  
ID ABB81594 standard; protein; 1609 AA.  
AC ABB81594;  
DT 19-SEP-2002 (first entry)  
XX Human laminin 10 third chain protein sequence SEQ ID NO:14.  
XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX Homo sapiens.

Key Location/Qualifiers  
FH Peptide 1..33  
FT /label= signal  
ET Protein 34..1609  
FT /label= laminin\_10\_third\_chain

WO200250111-A2.  
27-JUN-2002.  
21-DEC-2001; 2001WO-US051035.  
21-DEC-2000; 2000US-0257449P.  
28-MAR-2001; 2001US-0279282P.  
13-NOV-2001; 2001US-00279282.  
(BIOS-) BIOSTRATUM INC.  
Tryggvason K, Doi M, Thyboll J;  
WPI; 2002-557650/59.  
DR N-ESDB; ABQ72912.

New human laminin-10 proteins, useful for accelerating the healing of  
vascular tissue, improving the biocompatibility of grafts, or for  
promoting re-endothelialization at the site of vascular injuries.  
Claim 9; Page 165-170; 231pp; English.

The present invention describes human laminin alpha 5. Also described is  
an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
useful in maintaining cell/tissue phenotype as well as promoting cell  
growth and differentiation in tissue repair development. Specifically,  
laminin 10 can be used for accelerating the healing injuries of vascular  
tissue, improving the biocompatibility of grafts useful for treating such  
injuries, for promoting re-endothelialisation at the site of vascular  
injuries, and promote cell attachment and subsequent cell stasis,  
proliferation, differentiation, and/or migration. The present sequence

CC represents a third chain protein of laminin 10, from the present  
invention  
XX  
SQ Sequence 1609 AA;  
Query Match 94.3%; Score 8038; DB 5; Length 1609;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
QY 1 AMDECADGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGVTKSHCLDAG 60  
DB 36 AMDECTDEGGRPQRCMPFVNAAFNVTVVATNTCGTPPEEYCVQTVGTGVTKSHCLDAG 95  
QY 61 QOHLOHGAFLTDYNNQADTTWQSQTMLAGVOYVNSINLTLHLKAFDITVRLKFTS 120  
DB 96 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVOYVNSINLTLHLKAFDITVRLKFTS 155  
QY 121 RPESFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTCGGDEQQALCTDEFSDISPL 180  
DB 156 RPESFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTCGGDEQQALCTDEFSDISPL 215  
QY 181 TCGNVAFTLEGRPSAYNPDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYIY 240  
DB 216 TCGNVAFTLEGRPSAYNPDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSYIY 275  
QY 241 AISDFAVGGRCKNGHASECVKNBFKLMCKNHTYGVDCCKLPFFNDPWRATAES 300  
DB 276 AISDFAVGGRCKNGHASECVKNBFKLMCKNHTYGVDCCKLPFFNDPWRATAES 335  
QY 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHTNCRDNTDGAKCRCRNFRLGNTRAC 360  
DB 336 ASECLPCDCNGRSQECYFDPPELYRSTGHGHTNCRDNTDGAKCRCRNFRLGNTRAC 395  
QY 361 SPCHSPVGSLSSTOCDYSGRCCKPGVMGDKDRCPGFHSLTEAGRCPCSDPSGSTDE 420  
DB 396 SSCHSPVGSLSSTOCDYSGRCCKPGVMGDKDRCPGFHSLTEAGRCPCSDPSGSTDE 455  
QY 421 CNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPKGTCFCFGHSSVYCTNAVGSYDI 480  
DB 456 CNVETGRVCCKDNVEGFNCERCKPGFFNLESSNPKGTCFCFGHSSVYCTNAVGSYDI 515  
QY 481 SSTFQIDEDGWRVEORDGSEASLEWSDROVIAVSDSYFFRYFIAPVKFLGNQVLSGQ 540  
DB 516 SSTFQIDEDGWRVEORDGSEASLEWSDROVIAVSDSYFFRYFIAPVKFLGNQVLSGQ 575  
QY 541 NLSFSFRVDRDRLSADLVLEGAGLRSVPLIAQNSYPSSETTVKIFRHEATDTPW 600  
DB 576 NLSFSFRVDRDRLSADLVLEGAGLRSVPLIAQNSYPSSETTVKIFRHEATDTPW 635  
QY 601 RPALSPFQKLLNNLTISIKRTGYTSERSAGYLDVTLQSRAPGPGVPATVWESCTCPVG 660  
DB 636 RPALTPFQKLLNNLTISIKRTGYTSERSAGYLDVTLQSRAPGPGVPATVWESCTCPVG 695  
QY 661 YGQFCETCLPGYRRETPSLGYPSPVLCNCGHSETCDPETGVCDRDNTAGPCEKCS 720  
DB 696 YGQFCETCLPGYRRETPSLGYPSPVLCNCGHSETCDPETGVCDRDNTAGPCEKCS 755  
QY 721 DGYGDSLTGSSDCQPCPCPGSSCAIYVPKTKVYVTHCTPTAGKCELCDDGYFGDP 780  
DB 756 DGYGDSLTGSSDCQPCPCPGSSCAIYVPKTKVYVTHCTPTAGKCELCDDGYFGDP 815  
QY 781 LGSNGPVLRCPCQCNMDIDNNAVCNRLTGECLKCIYNTAGFYCDCKEKGFFGNPLAP 840  
DB 816 LGRNPVRLCRUCQCNMDIDNNAVCNRLTGECLKCIYNTAGFYCDCKEKGFFGNPLAP 875  
QY 841 NPADKCKACACN- YGTVOQQSSCNFVTGQCCLCPHVSQRDQCTCDPGYNNYQSGQGCERC 899  
DB 876 NPADKCKACACNPGYTMQSSCNFVTGQCCLCPHVTGQDCGACDPGFYNNYQSGQGCERC 935  
QY 900 DCHALGSTNGQCDIRTGQCBQPGITGOHCRCERTNHFPGPEGCKPCDCHHESLSLQOC 959  
DB 936 DCHALGSTNGQCDIRTGQCBQPGITGOHCRCERTNHFPGPEGCKPCDCHHESLSLQOC 995

Qy	960	KDGRCECRREGFVGNRCQCQCENTFYNRSWPGCECPACVSLVKDQAABHRVTKLQEELESL	1019
Db	996	KDGRCECRREGFVGNRCQCQCENTFYNRSWPGCECPACVSLVKDQVADHRVTKLQEELESL	1055
Qy	1020	IANLGTGDMVTDQAFEDRLKEARESEVTDLLREAEQVKVDQDNLMDRLQRVNSLSHSQIS	1079
Db	1056	IANLGTGDMVTDQAFEDRLKEARESEVMDLLREAEQVKVDQDNLMDRLQRVNTLSQIS	1115
Qy	1080	RLOINRNTIETGILAEARSRVSTEQILBIASRELEKAKM-AANYVSIQTPESTGSPNN	1138
Db	1116	RLOINRNTIETGTLAEQARAHVENTERLBIASRELEKAKVAANYSVTQPESTGSPNN	1175
Qy	1139	MTLLAEARRLAERHKQBADDIVRVAKTANETSAEAYNLLRLTLAGEHOTALEEELNRK	1198
Db	1176	MTLLAEARKLAERHKQEADDIVRVAKTANDTSTEAYNLLRLTLAGEHOTAFIEELNRK	1235
Qy	1199	YEQAKNISODLEKQAARVHEEAKGADKAVEIYASVAQLTPVDSSEALENEANKIKKEAAD	1258
Db	1236	YEQAKNISODLEKQAARVHEEAKGADKAVEIYASVAQLSPLDSETLLENEANNIKKEAEN	1295
Qy	1259	LDRLIDQKLKDYEDLRDMDRGKEHEVKNLLEKGAEOQTADQLIARADAAKALAEAAKK	1318
Db	1296	LEQLIDQKLKDYEDLRDMDRGKELEVKNLLEKGTQEQTADQLLARADAAKALAEAAKK	1355
Qy	1319	GRSTLQEQANDILANNKQDFDRVNDNKTAAEEALRRIPAINRTTAEANEKTRERQALGNA	1378
Db	1356	GRDTLQEQANDILNNLKQDFDRVNDNKTAAEEALRKIPAINQTTAEANEKTRERQOALGSA	1415
Qy	1379	AADATEAKNKAHEAERIASAAQKNATSTKADAERTFGEVTDLDNEVNGMLRQLEEAENEL	1438
Db	1416	AADATEAKNKAHEAERIASAVQKNATSTKAEARTFAEVTDLDDNEVNNMLKQLQEAKEKL	1475
Qy	1439	KRKQDDADQDMMWAGMASQAQAEALNARKAKNSVSLLSQLNNLLDQLDQDVTDLNKL	1498
Db	1476	KRKQDDADQDMMWAGMASQAQAEABINARKAKNSVLSLSIINDLLEQLGQLDVTDLNKL	1535
Qy	1499	NEIEGSLNKADEMKAESDLDRKVSDDLSEARKQEEAAMDYNRDIAETIKDIHNLEDIKKT	1558
Db	1536	NEISGTLNKADEMKMVSDDLDRKVSDDLSEAKQEEAAMDYNRDIEEIMKDINLEDIRKT	1595
Qy	1559	LPTGCFTNPSTIEKP	1572
Db	1596	LPSCGFTNPSTIEKP	1609
RESULT	15		
ADCO1887			
ID	ADCO1887	standard; protein; 1609 AA.	
XX	AC	ADCO1887;	
XX	AC	ADCO1887;	
XX	XX		
DT	18-DEC-2003	(first entry)	
XX			
DE	Human laminin gamma 1 subunit.		
XX			
KW	Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;		
KW	gammal subunit; alpha4 subunit; angiogenesis.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003103975-A1.		
XX			
PD	05-JUN-2003.		
XX			
PF	18-NOV-2002; 2002US-00299058.		
XX			
PR	03-NOV-1999; 99US-0163199P.		
ER	23-NOV-2000; 2000US-00706235.		
XX			
XX	(JONE/) JONES J C R.		
PA	(GONZ/) GONZALES M.		
XX			
PI	Jones JCR, Gonzales M;		





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 43.5393 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-18

Perfect score: 8694

Sequence: 1 MTGGGSAALALQGRGLNPL.....EDIKTLPTGCPNTPSIEKP 1605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_arChaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6159	70.8	1593	13 Q8JHV8	Q8jnv8 brachydanio
2	4704	54.1	1007	13 Q90ZN3	Q90zn3 gallus gall
3	3538.5	40.7	1623	5 Q9UJN3	Q9u3u7 anopheles g
4	2583.5	29.7	1196	6 Q867A2	Q867a2 canis faml
5	2579.5	29.7	1190	6 Q8HZI9	Q8hzi9 equus cabal
6	1719.5	19.8	1785	13 Q8JHV7	Q8jnv7 brachydanio
7	1697.5	19.5	529	4 Q8N2D6	Q8n2d6 homo sapien
8	1669.5	19.2	1792	13 Q57484	O57484 gallus gall
9	1638	18.8	351	11 P97552	P97552 rattus norv
10	1632	18.8	3102	5 Q45614	Q45614 caenorhabdi
11	1630	18.7	1761	4 Q86XN2	Q86xn2 homo sapien
12	1549	17.8	1799	11 Q8R0Y0	Q8r0y0 homo sapien
13	1502.5	17.3	2731	5 Q9VJTS	Q9vjts drosophila
14	1502.5	17.3	3367	5 Q9XZC9	Q9xzc9 drosophila
15	1502.5	17.3	3375	5 Q8IP51	Q8ip51 drosophila
16	1482.5	17.1	1827	13 Q8JHV6	Q8jnv6 brachydanio

17	1464	16.8	1631	4 Q9Y6U6	Q9y6u6 homo sapien
18	1458	16.8	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1415	16.3	319	4 Q96BH6	Q96bh6 homo sapien
20	1384	15.9	3704	5 Q91904	Q91904 caenorhabdi
21	1358.5	15.6	3695	4 Q8TD88	Q8tdf8 homo sapien
22	1173	13.5	1168	5 Q967S8	Q967s8 schistocarc
23	1164.5	13.4	604	11 Q924Z9	Q924z9 rattus norv
24	1139.5	13.1	603	13 Q42140	Q42140 brachydanio
25	1135.5	13.1	569	13 Q57339	Q57339 xenopus lae
26	1129.5	13.0	602	13 Q42203	Q42203 brachydanio
27	1127.5	13.0	1026	5 Q8SWY0	Q8swy0 drosophila
28	1116.5	12.8	464	11 Q61985	Q61985 mus musculu
29	1107.5	12.7	1069	5 Q9BPS2	Q9bps2 bombyx mori
30	1081.5	12.4	1086	4 Q8TAS6	Q8tas6 homo sapien
31	1078.5	12.4	1067	5 Q44565	Q44565 caenorhabdi
32	1073.5	12.3	555	5 Q9NFW6	Q9nfw6 brachioisto
33	1041.5	12.0	1546	4 Q9NS27	Q9ns27 homo sapien
34	1037.5	11.9	1546	4 Q75445	Q75445 homo sapien
35	1029	11.8	610	5 Q96659	Q96659 hirudo medi
36	1003.5	11.5	1461	11 Q9JLP3	Q9jlp3 mus musculu
37	977.5	11.2	984	11 Q8K271	Q8k271 mus musculu
38	970.5	11.2	1512	11 Q8K3K1	Q8k3k1 rattus norv
39	950.5	10.9	1486	4 Q14637	Q14637 homo sapien
40	926.5	10.7	695	11 Q8C9J2	Q8c9j2 mus musculu
41	924	10.6	1168	11 Q91V90	Q91v90 mus musculu
42	903	10.4	911	11 Q9CRX6	Q9crx6 mus musculu
43	871	10.0	667	5 Q9VY25	Q9vy25 drosophila
44	858	9.9	580	4 Q00634	Q00634 homo sapien
45	858	9.9	580	11 Q9RIA3	Q9ria3 mus musculu

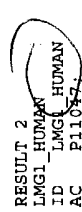
#### ALIGNMENTS

#### RESULT 1

Q8JHV8	PRELIMINARY;	PRT; 1593 AA.
ID Q8JHV8		
AC Q8JHV8		
DT 01-OCT-2002 (TRENBLrel. 22, Created)		
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)		
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)		
DE Laminin gamma 1.		
GN LAMC1.		
OS Brachydanio rerio (Zebrafish) (Danio rerio).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;		
OC Cyprinidae; Danio.		
OX NCBI_taxid=7955;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=22065263; PubMed=12070089;		
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,		
RA Hirst E.M., Stemple D.L.		
RT "zebrafish mutants identify an essential role for laminins in		
RT notochord formation."		
RL Development 129:3137-3146(2002).		
DR EMBL; AF468048; AAMG1766.1; -		
DR GO; GO:0005578; C:extracellular matrix; IEA.		
DR GO; GO:0005198; F:structural molecule activity; IEA.		
DR InterPro; IPR006209; EGF like.		
DR InterPro; IPR000034; Laminin_B.		
DR InterPro; IPR002049; Laminin_EGF.		
DR InterPro; IPR008211; LamNT.		
DR InterPro; IPR008212; Lam_N2.		
DR Pfam; PF00053; laminin_EGF; 10.		
DR Pfam; PF00052; laminin_B; 1.		
DR Pfam; PF00055; laminin_Nterm; 1.		
DR PRINTS; PR00011; EGF_LAMININ.		
DR ProDom; PD002082; Lam_N2; 1.		
DR SMART; SM00180; EGF_Lam; 1.		
DR SMART; SM00281; LamB; 1.		
DR SMART; SM00136; LamNT; 1.		
DR PROSITE; PS00022; EGF_1; 7.		

[illegible]

Query Match		99.2%;	Score 8627;	DB 1;	Length 1607;	
Best Local Similarity		99.4%;	Pred. No. 7.6e-318;			
Matches 1598;		Conservative	99.4%;	2;	Mismatches 5;	Indels 2;
						Gaps 2;
QY	1	MTGGRAALALQPRGLWPLAVLAAGVAVRAAMDECADEGRPORCPORCPPEFNAFNT	60			
DB	1	MTGGRAALALQPRGLWPLAVLAAGVAVRAAMDECADEGRPORCPORCPPEFNAFNT	60			
QY	61	VVATNTCGTTPPEYCYVQTVGTVKSCHLCDAGQOHLQGAFLTDYNNQADTTWQSQ	120			
DB	61	VVATNTCGTTPPEYCYVQTVGTVKSCHLCDAGQOHLQGAFLTDYNNQADTTWQSQ	120			
QY	121	MLAGVQVPSNINLTLHGKAFDITYYRLKPHTSRPSFAIYKRTREDGPMIPIYQYVSGS	180			
DB	121	MLAGVQVPSNINLTLHGKAFDITYYRLKPHTSRPSFAIYKRTREDGPMIPIYQYVSGS	180			
QY	181	ENTYSKANRGFIITGDEQOALCTDFSDISPLTGNVAFSTLLEGSPSAYNFDSVLOE	240			
DB	181	ENTYSKANRGFIITGDEQOALCTDFSDISPLTGNVAFSTLLEGSPSAYNFDSVLOE	240			
QY	241	WVTATDIRVTLNLTNLTGDEQOALCTDFSDISPLTGNVAFSTLLEGSPSAYNFDSVLOE	300			
DB	241	WVTATDIRVTLNLTNLTGDEQOALCTDFSDISPLTGNVAFSTLLEGSPSAYNFDSVLOE	300			
QY	301	LMCNCKHNTYGVDCERKLPFFNDPWRRAATASASECLPCDNCGRSQEYCFDPPELYRSTG	360			
DB	301	LMCNCKHNTYGVDCERKLPFFNDPWRRAATASASECLPCDNCGRSQEYCFDPPELYRSTG	360			
QY	361	HGHCNCRDNTDGAKCERENFFRLGNTACSPCHSPVGSLSQDCSYGRCSCKPGV	420			
DB	361	HGHCNCRDNTDGAKCERENFFRLGNTACSPCHSPVGSLSQDCSYGRCSCKPGV	420			
QY	421	MGKDCRCQPFHSLTEAGRCPCSDPSGSTDECNVETGRCVKONVEGFCNRCCKPGFF	480			
DB	421	MGKDCRCQPFHSLTEAGRCPCSDPSGSTDECNVETGRCVKONVEGFCNRCCKPGFF	480			
QY	481	NLESSNPKGCTPCFCFHSHSVCTNAVGSYVDISSTFQIDEGWRVEQDGSSEASLEWSS	540			
DB	481	NLESSNPKGCTPCFCFHSHSVCTNAVGSYVDISSTFQIDEGWRVEQDGSSEASLEWSS	540			
QY	541	DRQYIAVSDSYPRYFIAPVKFLGNQVLSYGNLSFSPFRVDRDRTRLSAEDLVLEGAGL	600			
DB	541	DRQYIAVSDSYPRYFIAPVKFLGNQVLSYGNLSFSPFRVDRDRTRLSAEDLVLEGAGL	600			
QY	601	RVSVPILIAAGNSYPSSETTKYIFRLHEATDYPWRPALSPFEQKLLNLTSTIKIRGTYS	660			
DB	601	RVSVPILIAAGNSYPSSETTKYIFRLHEATDYPWRPALSPFEQKLLNLTSTIKIRGTYS	660			
QY	661	RSAGYLDVTLQARPGPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSLGYPSPCV	720			
DB	661	RTAGYLDVTLQARPGPGVPATWVESCTCPVGYGGQFCETCLPGYRRETSLGYPSPCV	720			
QY	721	LCTCNHSETCDBETGVCDRCNTAGPHCEKSDGYGDSITLGTSDCQPCPCPGSSCA	780			
DB	721	LCTCNHSETCDBETGVCDRCNTAGPHCEKSDGYGDSITLGTSDCQPCPCPGSSCA	780			
QY	781	IVPKTEVVTCHTCTAGKRCLELDDGYFGDPLGNSGVPVLCRQCQNDNDPNAVNC	840			
DB	781	IVPKTEVVTCHTCTAGKRCLELDDGYFGDPLGNSGVPVLCRQCQNDNDPNAVNC	840			
QY	841	NRLTGCLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACN-YGTVOQQSSCNPNV	899			
DB	841	NRLTGCLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACN-YGTVOQQSSCNPNV	900			
QY	900	GQCQCLPHVSGRDCGTCDFGYNLQSGQCCERCDCHALGSTNGQCDIRTGQCECPGLITG	959			
DB	901	GQCQCLPHVSGRDCGTCDFGYNLQSGQCCERCDCHALGSTNGQCDIRTGQCECPGLITG	960			
QY	960	QHCERCETHNFGPGGCKPCDCHHSGSLQCKDDGRCEGFGVGNRCDOCEENFYFN	1019			
DB	961	QHCERCETHNFGPGGCKPCDCHHSGSLQCKDDGRCEGFGVGNRCDOCEENFYFN	1020			



RESULT 2  
LMG1 HUMAN  
ID HUMAN  
AC P11074  
STANDARD; PRT; 1609 AA.  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin gamma-1 chain precursor (Laminin B2 chain).  
GN LAMC1 OR LAMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=91093126; PubMed=1985895;  
RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;  
RT "Structure of the human laminin B2 chain gene reveals extensive  
RT divergence from the laminin B1 chain gene.";  
RN J. Biol. Chem. 266:221-228 (1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=88198245; PubMed=3360804;  
RA Pikkariainen T., Kallunki T., Tryggvason K.;  
RT "Human laminin B2 chain. Comparison of the complete amino acid  
RT sequence with the B1 chain reveals variability in sequence homology  
RT between different structural domains.";  
RN J. Biol. Chem. 263:6751-6758 (1988).  
RN [3]  
RP SEQUENCE OF 1393-1609 FROM N.A.  
RA MEDLINE=99169663; PubMed=3234037;  
RA Fukushima Y., Pikkariainen T., Kallunki T., Eddy R.L., Byers M.G.,

RA HALEY L.L., Henry W.M., Tryggvason K., Shows T.B.;  
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of  
RT the gene to chromosome region 1q25-->q31";  
RL Cytogenet. Cell Genet. 48:137-141(1988).  
RN [4]  
RP SEQUENCE OF 1282-1609 FROM N.A.  
RC TISSUE-Endothelial cells;  
RX MEDLINE=22660472; PubMed=1806043;  
RA Santos C.L.S., Sabbaga J., Brenzani R.;  
RT "Differences in human laminin B2 sequences.";  
RN DNA Seq. 1:275-277(1991).  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITE ASN-650.  
RX MEDLINE=22660472; PubMed=12754519;  
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;  
RT "Identification and quantification of N-linked glycoproteins using  
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";  
RL Nat. Biotechnol. 21:660-666(2003).  
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The gamma-1 chain is a subunit of laminin-1 (BS laminin),  
CC laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),  
CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).  
CC -1- SUBCELLULAR LOCATION: Extracellular.  
CC -1- TISSUE SPECIFICITY: Found in the basement membranes (major  
CC component).  
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact  
CC with other laminin chains to form a coiled coil structure.  
CC -1- DOMAIN: Domains VI and IV are globular.  
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -1- SIMILARITY: Contains 1 laminin EGF-like domains.  
CC -1- SIMILARITY: Contains 1 laminin IV domain.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M55210; AAA59492.1; JOINED.  
CC EMBL; M55217; AAA59492.1; JOINED.  
CC EMBL; M55201; AAA59492.1; JOINED.  
CC EMBL; M55211; AAA59492.1; JOINED.  
CC EMBL; M55212; AAA59492.1; JOINED.  
CC EMBL; M55213; AAA59492.1; JOINED.  
CC EMBL; M55214; AAA59492.1; JOINED.  
CC EMBL; M55215; AAA59492.1; JOINED.  
CC EMBL; M55216; AAA59492.1; JOINED.  
CC EMBL; M55192; AAA59492.1; JOINED.  
CC EMBL; M55193; AAA59492.1; JOINED.  
CC EMBL; M55194; AAA59492.1; JOINED.  
CC EMBL; M55195; AAA59492.1; JOINED.  
CC EMBL; M55196; AAA59492.1; JOINED.  
CC EMBL; M55197; AAA59492.1; JOINED.  
CC EMBL; M55198; AAA59492.1; JOINED.  
CC EMBL; M55199; AAA59492.1; JOINED.  
CC EMBL; M55200; AAA59492.1; JOINED.  
CC EMBL; M55202; AAA59492.1; JOINED.  
CC EMBL; M55203; AAA59492.1; JOINED.  
CC EMBL; M55204; AAA59492.1; JOINED.  
CC EMBL; M55205; AAA59492.1; JOINED.  
CC EMBL; M55206; AAA59492.1; JOINED.  
CC EMBL; M55207; AAA59492.1; JOINED.  
CC EMBL; M55208; AAA59492.1; JOINED.  
CC EMBL; M55209; AAA59492.1; JOINED.

DR EMBL; J03202; AAA59488.1; -;  
DR EMBL; M27554; AAA59489.1; -;  
DR EMBL; X13939; CAA32122.1; -;  
DR PIR; S13548; MMHUB2.  
DR HSSP; P02468; 1TLE.  
DR Genew; HGNC:6492; LAMC1.  
DR MIM; 150290; -;  
DR GO; GO:0005604; C:basement membrane; TAS.  
DR GO; GO:0007492; P:endoderm development; TAS.  
DR GO; GO:0006461; P:protein complex assembly; TAS.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR008212; Lam\_N2.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin\_B\_1.  
DR Pfam; PF00053; laminin\_EGF\_9.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 8.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 11.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.  
FT SIGNAL 1 33  
FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.  
FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 286 341 LAMININ EGF-LIKE 1.  
FT DOMAIN 342 397 LAMININ EGF-LIKE 2.  
FT DOMAIN 338 444 LAMININ EGF-LIKE 3.  
FT DOMAIN 445 494 LAMININ EGF-LIKE 4.  
FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 505 689 LAMININ DOMAIN IV.  
FT DOMAIN 690 723 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 724 772 LAMININ EGF-LIKE 6.  
FT DOMAIN 773 827 LAMININ EGF-LIKE 7.  
FT DOMAIN 828 883 LAMININ EGF-LIKE 8.  
FT DOMAIN 884 934 LAMININ EGF-LIKE 9.  
FT DOMAIN 935 982 LAMININ EGF-LIKE 10.  
FT DOMAIN 983 1030 LAMININ EGF-LIKE 11.  
FT DOMAIN 1030 1609 DOMAIN II AND I.  
FT DOMAIN 1038 1609 COILED COIL (POTENTIAL).  
FT DISULFID 286 295 BY SIMILARITY.  
FT DISULFID 288 305 BY SIMILARITY.  
FT DISULFID 307 316 BY SIMILARITY.  
FT DISULFID 319 339 BY SIMILARITY.  
FT DISULFID 342 351 BY SIMILARITY.  
FT DISULFID 344 367 BY SIMILARITY.  
FT DISULFID 370 379 BY SIMILARITY.  
FT DISULFID 382 395 BY SIMILARITY.  
FT DISULFID 398 410 BY SIMILARITY.  
FT DISULFID 400 416 BY SIMILARITY.  
FT DISULFID 418 427 BY SIMILARITY.  
FT DISULFID 430 442 BY SIMILARITY.  
FT DISULFID 445 456 BY SIMILARITY.  
FT DISULFID 447 463 BY SIMILARITY.  
FT DISULFID 465 474 BY SIMILARITY.  
FT DISULFID 477 492 BY SIMILARITY.  
FT DISULFID 724 733 BY SIMILARITY.  
FT DISULFID 726 740 BY SIMILARITY.  
FT DISULFID 742 751 BY SIMILARITY.  
FT DISULFID 754 770 BY SIMILARITY.  
FT DISULFID 773 781 BY SIMILARITY.  
FT DISULFID 775 792 BY SIMILARITY.  
FT DISULFID 795 804 BY SIMILARITY.  
FT DISULFID 807 825 BY SIMILARITY.  
FT DISULFID 828 842 BY SIMILARITY.  
FT DISULFID 830 849 BY SIMILARITY.  
FT DISULFID 852 861 BY SIMILARITY.

FT	DISULFID	864	881	BY SIMILARITY.	
FT	DISULFID	884	898	BY SIMILARITY.	
FT	DISULFID	886	905	BY SIMILARITY.	
FT	DISULFID	907	916	BY SIMILARITY.	
FT	DISULFID	919	932	BY SIMILARITY.	
FT	DISULFID	935	947	BY SIMILARITY.	
FT	DISULFID	937	954	BY SIMILARITY.	
FT	DISULFID	956	965	BY SIMILARITY.	
FT	DISULFID	968	980	BY SIMILARITY.	
FT	DISULFID	983	995	BY SIMILARITY.	
FT	DISULFID	985	1001	BY SIMILARITY.	
FT	DISULFID	1003	1012	BY SIMILARITY.	
FT	DISULFID	1015	1028	BY SIMILARITY.	
FT	DISULFID	1031	1031	INTERCHAIN (PROBABLE).	
FT	DISULFID	1034	1034	INTERCHAIN (PROBABLE).	
FT	DISULFID	1600	1600	INTERCHAIN (PROBABLE).	
FT	CARBOHYD	60	60	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	576	576	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	650	650	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1161	1161	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1175	1175	N-LINKED (GLCNAC. . .)	(POTENTIAL).

Query Match 93.7%; Score 8144; DB 1; Length 1609;  
 Best Local Similarity 92.7%; Pred. No. 1.2e-299;  
 Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;

QY	1	MTGGRAALALQGRRLWPLAVL--AAVAGCVRAAWECADEGGRRPQCMPEFVNAAFN	58
DB	1	MRGSHRAAPALRFRRLWPLVLAIAAAAGCAQAAMDECTDEGGRRPQCMPEFVNAAFN	60
QY	59	VTVAATTCGTPPEEYCVQGTGVTGKCHLDCAGQOHQGAFTDYNNQADTTWQS	118
DB	61	VTVAATTCGTPPEEYCVQGTGVTGKCHLDCAGQPHLQGAFTDYNNQADTTWQS	120
QY	119	QWLAGVOVNSNLTLLHLCAPDIIVRLKFTSRPESFAYIKRTREDGPMIPYQYSG	178
DB	121	QWLAGVOYSSNLTLLHLCAPDIIVRLKFTSRPESFAYIKRTREDGPMIPYQYSG	180
QY	179	SCENTYSKANRGFIRTGDDSQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL	238
DB	181	SCENTYSKANRGFIRTGDDSQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL	240
QY	239	QEWYATDITVTLNLTGDFVNDPKVLKSYYYAISDFAVGCRCKNGHASECKNEF	298
DB	241	QEWYATDITVTLNLTGDFVNDPKVLKSYYYAISDFAVGCRCKNGHASECKNEF	300
QY	299	DKLMCKNHTYGVDCCKLPFFNDPRWRATAESASECLPCDCNGRSQECYFDPPELYRS	358
DB	301	DKLVCKNHTYGVDCCKLPFFNDPRWRATAESASECLPCDCNGRSQECYFDPPELYRS	360
QY	359	TGHHGHTNCRNDTDAKCHRENTFRNLNTEACSPCHCSPVGSLSTQCDYGRCSCKP	418
DB	361	TGHHGHTNCRNDTDAKCHRENTFRNLNTEACSPCHCSPVGSLSTQCDYGRCSCKP	420
QY	419	GVMGDKCDRCQPFHSLTEAGRCPCSDPSGSTDECNVETGRVCCKDNVEGFCNCRCKP	478
DB	421	GVMGDKCDRCQPFHSLTEAGRCPCSDPSGSTDECNVETGRVCCKDNVEGFCNCRCKP	480
QY	479	FFNLESSNPKGCTPCFCFHHSSVCTNAVGVSVYDISSTFQIDEDGWRVQRDCGSASLEW	538
DB	481	FFNLESSNPKGCTPCFCFHHSSVCTNAVGVSVYDISSTFQIDEDGWRVQRDCGSASLEW	540
QY	539	SSDRQYIAVLSDSYFPRYFTAPVKELGNQVLSYGNLSPFSRVDREDTRLSAEDLVLEGA	598
DB	541	SSERQYIAVLSDSYFPRYFTAPVKELGNQVLSYGNLSPFSRVDREDTRLSAEDLVLEGA	600
QY	599	GLRVSVPLIAQGNYSSETTKYIFRLHEATDYPWRPALSPFEFQKLLNLTSLIKIRGY	658
DB	601	GLRVSVPLIAQGNYSSETTKYIFRLHEATDYPWRPALTPFEFQKLLNLTSLIKIRGY	660

QY	659	SERSAGYLDVDTLOSARPGVPATWBSCTCPVGYGGQFCETCLPGYRRRETSPSLGPYSP	718
DB	661	SERSAGYLDVDTLASARPGVPATWBSCTCPVGYGGQFCETCLPGYRRRETSPSLGPYSP	720
QY	719	CVLCTCNHSETCDPETGVCDNRNTAGPHCEKSDGYGISTLTSSDCQPCPCPGSS	778
DB	721	CVLCAHNSHSETCDPETGVCDNRNTAGPHCEKSDGYGISTLTSSDCQPCPCPGSS	780
QY	779	CAIVPKTEVVCTHCTAGKRCBCLDDGVFGPLSGNGPVRCLPCQCNNDNDPNAVG	838
DB	781	CAVWPKTEVVCTHCTAGKRCBCLDDGVFGPLSGNGPVRCLPCQCNNDNDPNAVG	840
QY	839	NCNRLTGECLKIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACN-YGTVQOQSSCNP	897
DB	841	NCNRLTGECLKIYNTAGFYCDRCKEGFFGNPLAPNPADKCKACACNPGYTMKQOQSSCNP	900
QY	898	VTGQCCCLPHVSGRCDCGTDPGVNLSQGCRCRCDCHALGSTNGCCDRTGQCECQPGI	957
DB	901	VTGQCCCLPHVSGRCDCGTDPGVNLSQGCRCRCDCHALGSTNGCCDRTGQCECQPGI	960
QY	958	TGQHCERCETNHFHFGPPEGKPCDCHHBSLSLQCKDDGRCCEGFGVGNRCDCQENYF	1017
DB	961	TGQHCERCENHFGPPEGKPCDCHHBSLSLQCKDDGRCCEGFGVGNRCDCQENYF	1020
QY	1018	YNSWPGQCEPCACVRLVKDAAEHRYKLBELSLIANLGTGDDMTDQAFEDLKEAER	1077
DB	1021	YNSWPGQCEPCACVRLVKDAAEHRYKLBELSLIANLGTGDDMTDQAFEDLKEAER	1080
QY	1078	EVTDLRLRAQVQVDQNLMDRLQVNSLSHSQISRLQNTIRNTIETEGILAEARSRVES	1137
DB	1081	EWDLRLRAQVQVDQNLMDRLQVNSLSHSQISRLQNTIRNTIETEGILAEARSRVES	1140
QY	1138	TEQLIEIASRELEKAKM-AANVSTQPESTGEPNNMTLLAEARLAEHKEADDIRV	1196
DB	1141	TERLIEIASRELEKAKVAAANVSTQPESTGEPNNMTLLAEARLAEHKEADDIRV	1200
QY	1197	AKTANETSABAYNLLRLTAGENQTALEIPELNKRYEQAKNISDLKQAAARVHEEAKRA	1256
DB	1201	AKTANDTSABAYNLLRLTAGENQTALEIPELNKRYEQAKNISDLKQAAARVHEEAKRA	1260
QY	1257	GDKAVEIYASVAQITPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE	1316
DB	1261	GDKAVEIYASVAQISPLDSETLENEANNIKKEAADLRLIDQKLKDYEDLREDMRGKEHE	1320
QY	1317	VKNLLEKGAQOQTADQILARADAALAEAAKKGSTLOEANDIILNNLKDPDRVNDN	1376
DB	1321	VKNLLEKGTQOQTADQILARADAALAEAAKKGSTLOEANDIILNNLKDPDRVNDN	1380
QY	1377	KTAABEALRRIPAINRTIAEANEKTRBAQALGNAADATEAKNKAHEABRIASAAQNA	1436
DB	1381	KTAABEALRKIPAINQITIAEANEKTRBAQALGNAADATEAKNKAHEABRIASAAQNA	1440
QY	1437	TSTKADAEARTFGEVTDLDNEVNGMLRQLEBAENELKQKQDADODMMAGASQAQAE	1496
DB	1441	TSTKABAEARTFAEYTDLDNEVNNMLKQLEBAEKELKQKQDADODMMAGASQAQAE	1500
QY	1497	LNARKAKNSVSSLSQLNNLLDQGLDQTDVLDNKLNEIEGSLNKADEMKAESDLDRKVD	1556
DB	1501	INARKAKNSVTSLSLSIINDLLEQLQGLDQTDVLDNKLNEIEGTLNKADEMKAESDLDRKVD	1560
QY	1557	LESBAKQEAAMQYNDRIAEIINKHNLBEDIKTLPTGCFNTPSIEKP	1605
DB	1561	LENBAKQEAAMQYNDRIAEIINKHNLBEDIKTLPTGCFNTPSIEKP	1609

RESULT 3  
 LMG3\_HUMAN  
 ID LMG3\_HUMAN STANDARD; PRT; 1587 AA.  
 AC Q9Y6N6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

GN LAMC3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=92242614; PubMed=10225960;  
RA Koch M., Olson F.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,  
RA Burgeson R.E., Champlaud M.F.;  
RT "Characterization and expression of the laminin gamma3 chain: a novel,  
RT non-basement membrane-associated, laminin chain.";  
RL J. Cell Biol. 145:605-618(1999).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The gamma-3 chain is a subunit of laminin-12.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and  
CC the reproductive tracts.  
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact  
CC with other laminin chains to form a coiled coil structure.  
CC -!- DOMAIN: Domain IV is globular.  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 1 laminin IV domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMIL; AF041835; AAD36991.1; -  
CC HSSP; P02468; 1TLE.  
CC Genew; HGNC:6494; LAMC3.  
CC MW; 604349; C:extracellular matrix; TAS.  
CC GO; GO:0005578; C:extracellular matrix; TAS.  
CC GO; GO:0016020; C:membrane; TAS.  
CC GO; GO:0005198; F:structural molecule activity; TAS.  
CC InterPro; IPR006209; EGF like.  
CC InterPro; IPR008212; Lam N2.  
CC InterPro; IPR000034; Laminin\_B.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR008211; LamNT.  
CC Pfam; PF00052; laminin\_B; 1.  
CC Pfam; PF00053; laminin\_EGF; 9.  
CC Pfam; PF00055; laminin\_Nterm; 1.  
CC PRINTS; PR00011; EGF\_LAMININ.  
CC ProDom; PD002082; Lam N2; 1.  
CC SMART; SM00180; EGF\_Lam; 9.  
CC SMART; SM00136; LamNT; 1.  
CC PROSITE; PS00022; EGF\_1; 7.  
CC PROSITE; PS01186; EGF\_2; 2.  
CC PROSITE; PS01248; LAMININ TYPE EGF; 10.  
CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 1587  
FT DOMAIN 20 1587 LAMININ GAMMA-3 CHAIN  
FT DOMAIN 21 1587 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 271 326 LAMININ EGF-LIKE 1.  
FT DOMAIN 327 382 LAMININ EGF-LIKE 2.  
FT DOMAIN 383 429 LAMININ EGF-LIKE 3.  
FT DOMAIN 430 479 LAMININ EGF-LIKE 4.  
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT

FT DOMAIN 490 672 LAMININ DOMAIN IV.  
FT DOMAIN 673 706 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 707 754 LAMININ EGF-LIKE 6.  
FT DOMAIN 755 809 LAMININ EGF-LIKE 7.  
FT DOMAIN 810 865 LAMININ EGF-LIKE 8.  
FT DOMAIN 866 916 LAMININ EGF-LIKE 9.  
FT DOMAIN 917 964 LAMININ EGF-LIKE 10.  
FT DOMAIN 965 1013 LAMININ EGF-LIKE 11.  
FT DOMAIN 1014 1587 DOMAIN II AND I.  
FT DOMAIN 1071 1141 COILED COIL (POTENTIAL).  
FT DOMAIN 1200 1229 COILED COIL (POTENTIAL).  
FT DOMAIN 1424 1504 COILED COIL (POTENTIAL).  
FT DOMAIN 1535 1579 COILED COIL (POTENTIAL).  
FT SITE 1059 1061 CELL ATTACHMENT SITE (POTENTIAL).  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 631 631 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 837 837 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 980 980 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1185 1185 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 1587 AA; 172051 MW; 3CB6E09B5F203319 CRC64;  
Query Match 41.4%; Score 3596.5; DB 1; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 3.8e-128; Indels 77; Gaps 24;  
Matches 707; Conservative 258; Mismatches 571;  
20 LLAFLAAGVAGCVRAAMDECADEGGPQRCMPFVNAAFVTVVAVTNTCGTPPEYCVQVG 79  
12 LLAAPRAAGAG-----MGACYDGAGRPQRCLPVFENAAFGLQAQASHTCGSPEDFCFHV 66  
80 VTGVTKSCHLDAGQOHLQHGAFLTDYNNQADTTWQSTMLAGVQVPSNINLTFLHGK 139  
67 AAGAGAHQCORCAADAPQRRHNASYLTDFHSQESTWQSPMAFGVQVPTVNTLRLGK 126  
140 AFDITYVRLKFTSPESFAIYKRTREDGPMIPYQYSGSCENTYSKANRGFIPTGDEQ 199  
127 AYEIIYVRLKFTSPESFAIYKRSADGPWEYQFYASQCKTYGRPEGYLRPGEDE 186  
200 QALCTDEFSDISPLTGGNVAFSTLEGRSAYNFNSPVLOEWVTATDTRVTLNRLNTFGD 259  
187 VAFCTSEFSDISPLTGGNVAFSTLEGRSAYNFNSPVLOEWVTATDTRVTLNRLNTFGD 246  
260 EVFNDPKVLKSYIYAIISPFAVGRCCKNGHASECVKNEFDKLMCNCKNTYGVDCCKLP 319  
247 DIFKPKVLQSYIYAVSDFSVGRCCKNGHASECGPDYAGQLACRCQHTTGTDCERCLP 306  
320 FFDNRPMRATAESASECLPCDCNGRSOECYFDPPLYRSTGHGCHCTNCRDNTDGACER 379  
307 FFDNRPMRATAESASECLPCDCNGRSOECYFDPPLYRSTGHGCHCTNCRDNTDGACER 366  
380 CRENPFRLGNTACSPCHCSPVGSLSTQDSYGRCSCKPGVMGDKRCRCQPGFHSLEAG 439  
367 CQENFVHNDPRMPCQPCDCQASGLHLQCDTDTGTCAKPTVTGWKCDCLPGFHSLEAG 426  
440 CRPCSCDPSGSDTECNVETGRVCVDNVEGFNCERCKGFFNLESNPKGTCTPCFCFHS 499  
427 CRPCTCNAGSLDTCDPGRGRCPCKEVNEGNLDCRCFGTFLQPHNFAGSSCCFCYHS 486  
500 SVCTNAVGVSVVDISTFTQIDEDGWRVQEQDQSEASLEWSSDRQYIAVISDYPFRYFA 559  
487 KVCASDAQVQVHILSDFHQAGEGWARSVSGSEHSQWSPN-----GVLLSPDEEELTA 542  
560 PVKFLGNQVLSYQNLSPSFRVDRDTRLSADBLVLEGAGLRVSVPLIAQGNYSYSETTV 619  
543 PGKFLGQRFSGYQPLILTFRVPPGDSPLVQ-LRLEGTGLALS--LRHSSLSGPDABA 599  
620 KYIFRLH---EATDPWRPALSPFERFQKLLNLTSTIKIRGTYSEASG--YLLDDVTLSA 674  
600 SQGGRAGVPLQETSEDVAPLPFPFFHQRLLANLTSLRLAVSPGPGPAGVPFLTEVLTS 659

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 12.1415 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-18  
Perfect score: 8694  
Sequence: 1 MTGGRAALQPRGLWPL.....EDIKTLPTGCFNTPSIKXP 1605

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/iaa/5B COMB.pbp.\*  
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4: /cgn2\_6/ptodata/2/iaa/6B COMB.pbp.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pbp.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8694	100.0	1605	US-09-562-702A-30	Sequence 30, Appl
2	8694	100.0	1605	US-09-561-818A-26	Sequence 26, Appl
3	8527	98.1	1572	US-09-562-702A-32	Sequence 32, Appl
4	8527	98.1	1572	US-09-561-818A-28	Sequence 28, Appl
5	8148	93.7	1609	US-09-562-702A-22	Sequence 22, Appl
6	8148	93.7	1609	US-09-561-818A-22	Sequence 22, Appl
7	8148	93.7	1617	US-09-562-702A-26	Sequence 26, Appl
8	8043	92.5	1576	US-09-562-702A-24	Sequence 24, Appl
9	8043	92.5	1576	US-09-561-818A-24	Sequence 24, Appl
10	8043	92.5	1584	US-09-562-702A-28	Sequence 28, Appl
11	3596.5	41.4	1587	US-09-845-583A-10	Sequence 10, Appl
12	3596.5	41.4	1587	US-09-561-709B-3	Sequence 3, Appl
13	2591	29.8	1193	US-08-317-450B-13	Sequence 13, Appl
14	2591	29.8	1193	US-08-800-593-13	Sequence 13, Appl
15	2476.5	28.5	1111	US-08-317-450B-15	Sequence 15, Appl
16	2476.5	28.5	1111	US-08-800-593-15	Sequence 15, Appl
17	2306.5	26.5	1171	US-08-445-135-1	Sequence 1, Appl
18	1812.5	20.8	3106	US-09-562-702A-10	Sequence 10, Appl
19	1807.5	20.8	3084	US-09-562-702A-12	Sequence 12, Appl
20	1795.5	20.7	3110	US-09-562-702A-2	Sequence 2, Appl
21	1795.5	20.7	3110	US-09-562-702A-6	Sequence 6, Appl
22	1795.5	20.7	3110	US-09-561-709B-7	Sequence 7, Appl
23	1795	20.6	3111	US-08-460-309-4	Sequence 4, Appl
24	1795	20.6	3111	US-08-125-077-4	Sequence 4, Appl
25	1790	20.6	3088	US-09-562-702A-8	Sequence 8, Appl
26	1790	20.6	3089	US-09-562-702A-4	Sequence 4, Appl
27	1711	19.7	3075	US-08-460-309-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-562-702A-30  
; Sequence 30, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-562-702A-30

Query Match 100.0%; Score 8694; DB 4; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	VVATNTCGTPPEYCVQ	TGVTGSKCHL	CDAGQHLQGAFL	TDYNNQADTTWQSQT	120
Qy	121	MLAGVQYPSINLTHL	GKAFDITVYRL	KFHSRSPESFAI	YKRTREDGFWIPQYYSGSC	180
Db	121	MLAGVQYPSINLTHL	GKAFDITVYRL	KFHSRSPESFAI	YKRTREDGFWIPQYYSGSC	180
Qy	181	ENTYSKANRGFIR	TGGDEQAALCTDFSDI	SPLTGGNVAFSTLEGRPSA	YNFNSPVLQE	240
Db	181	ENTYSKANRGFIR	TGGDEQAALCTDFSDI	SPLTGGNVAFSTLEGRPSA	YNFNSPVLQE	240
Qy	241	WVTATDIRVTLNRL	NTFGDEVNDPKVLKSYVYAI	ISDFAVGGRCKNGHASCVCN	KEFDK	300
Db	241	WVTATDIRVTLNRL	NTFGDEVNDPKVLKSYVYAI	ISDFAVGGRCKNGHASCVCN	KEFDK	300



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QY 301 LMCNKHNTYGVDCCKLFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRSTG 360
Db 301 LMCNKHNTYGVDCCKLFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYRSTG 360
QY 361 HGGHCTNCRDNTDGAACRCRENFRNGTACSPCHSPVGSJSTOCDSPGSCCKPGV 420
Db 361 HGGHCTNCRDNTDGAACRCRENFRNGTACSPCHSPVGSJSTOCDSPGSCCKPGV 420
QY 421 MGDKCDRCQPGFHSLTEAGRCPCSDPSGSDTECNVETGRCVCKDNVEGNCRCCKPGFF 480
Db 421 MGDKCDRCQPGFHSLTEAGRCPCSDPSGSDTECNVETGRCVCKDNVEGNCRCCKPGFF 480
QY 481 NLESNPKGCTPCFCGHSSVCTNAGSVVDISTFQIDEDGWRVEQORDSEASLEWSS 540
Db 481 NLESNPKGCTPCFCGHSSVCTNAGSVVDISTFQIDEDGWRVEQORDSEASLEWSS 540
QY 541 DRQYIAVSDSYFPPYFAPVKFLGNQVLSFGONLSFSPFRVDRDRDRLSAEDLVLEGAGL 600
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QY 601 RVSVFLIAGNSYPSETTKYIFRLHEATDYPWRPALSPFFFOKLNNLTSIKIRGTYSSE 660
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Db 721 LCTCNHSTCDPETGVCDRCNDTAPHCCKSDGYGDSITLGTSSDCQPCPCGGSSCA 780
QY 781 IVPKTEVYVCHCPTGTAGKCELCDDGDFGDLGNSGVPVRLCRPCQCNNDIDNVAVNC 840
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QY 841 NRLTGECLACIYNTAGFYCDRCKEGFGNPLAPNADKCKACACNYGVQOQSSCNPTVG 900
Db 841 NRLTGECLACIYNTAGFYCDRCKEGFGNPLAPNADKCKACACNYGVQOQSSCNPTVG 900
QY 901 QOQCLPHVSGRCGTCDPGYNLSQSGCERCDCCHALSTNGQCDIRTGCECCQPGITGQ 960
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QY 961 HCERCETNHFPGPECKPCDCHHSGSLQCKDGRCEGREGFVGNRCDCQCEENYFNR 1020
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Db 1261 VEIYASVAQLTPVDSSEALNEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320
QY 1321 LEKGAEQQTADQLARADAALAEAAKGRSTLQEBANDILNNIKDPDRVNDNKATAA 1380
Db 1321 LEKGAEQQTADQLARADAALAEAAKGRSTLQEBANDILNNIKDPDRVNDNKATAA 1380
QY 1381 EZALRRIPAINRTIABANEKTRTQAOLGNAARADATEAKNKAHEABRIASAAQKNATSTK 1440
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QY 1501 KAKNSVSSLSQLNNLLDQGLDQVLDKLINEISGLNKAKDEMKASDLDRKVSDESE 1560
Db 1501 KAKNSVSSLSQLNNLLDQGLDQVLDKLINEISGLNKAKDEMKASDLDRKVSDESE 1560
QY 1561 ARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTFPIEKP 1605
Db 1561 ARKQEAAMIDYNRDIAEIIKDIHNLEDIKKTLPTGCFNTFPIEKP 1605
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## RESULT 2

US-09-561-818A-26  
Sequence 26, Application US/09561818A

Patent No. 6638907

GENERAL INFORMATION:

APPLICANT: Kortessmaa, Jarrko

APPLICANT: Tryggvason, Karl

TITLE OF INVENTION: Laminin 8 and Methods For Its Use

FILE REFERENCE: 99,274-D

CURRENT APPLICATION NUMBER: US/09/561,818A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 26

LENGTH: 1605

TYPE: PRT

ORGANISM: Mus musculus

US-09-561-818A-26

Query Match 100.0%; Score 8694; DB 4; Length 1605;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGGGAAALALQPRGLWFLAVLAAVAGCVRAAMDECADEGGRPORCMPEFVNAAFNVT 60

Db 1 MTGGGAAALALQPRGLWFLAVLAAVAGCVRAAMDECADEGGRPORCMPEFVNAAFNVT 60

QY 61 VVATNTCGTPPEYCVQGTGVTGKCHLCDAGQOHLQHGAAFLTDYNNQADTTWQSQ 120

Db 61 VVATNTCGTPPEYCVQGTGVTGKCHLCDAGQOHLQHGAAFLTDYNNQADTTWQSQ 120

QY 121 MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAYIKRTREDGPMIYYQYSGSC 180

Db 121 MLAGVQYPNSINLTLLHKGAFDITYVRLKFHTSRPESFAYIKRTREDGPMIYYQYSGSC 180

QY 181 ENTYSKANRGFIRTGDBEQALCTDFSDISPLTGGNVAFTLEGPRPSAINDNSPVLQ 240

Db 181 ENTYSKANRGFIRTGDBEQALCTDFSDISPLTGGNVAFTLEGPRPSAINDNSPVLQ 240

QY 241 WVTATDRLVTLNRLNTFGDFVNDPKVLSYYVAISDFAVGGRCKNGHASECVKNEFDK 300

Db 241 WVTATDRLVTLNRLNTFGDFVNDPKVLSYYVAISDFAVGGRCKNGHASECVKNEFDK 300

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Db 301 LMCNCKNTYGVDCCKLPPFNDRPWRRAATAESASECLPCDCNGRSQECYFDBELYSTG 360

QY 361 HGGHCTNCRDNTDGAACRCRENFRNGTACSPCHSPVGSJSTOCDSPGSCCKPGV 420

Db 361 HGGHCTNCRDNTDGAACRCRENFRNGTACSPCHSPVGSJSTOCDSPGSCCKPGV 420

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Db 421 MGDKCDRCQPGFHSLTEAGRCPCSDPSGSDTECNVETGRCVCKDNVEGNCRCCKPGFF 480

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Qy 601 RVSVPLAQNSYSPSETTKVIFRLEHATDPMRPAISPFEFQKLNLLNLSIKIRGTYS 660  
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Qy 661 RSAGYLDVLTQSLARPFGVPATVWESCTCPVGGGFCETCLPGYRRETPS:LPYSPCV 720  
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Qy 721 LCTCNHSETCDPTGVCDCRDNTAGPHCEKCSGYYGDSLTGTSSCQPCPCPGSSCA 780  
Db 721 LCTCNHSETCDPTGVCDCRDNTAGPHCEKCSGYYGDSLTGTSSCQPCPCPGSSCA 780  
Qy 781 IVPKTEVCHTCTGTAGKCE:CDGYPGDPPLGSGNPVRLCRPOCNDNIDPNVAGNC 840  
Db 781 IVPKTEVCHTCTGTAGKCE:CDGYPGDPPLGSGNPVRLCRPOCNDNIDPNVAGNC 840  
Qy 841 NRTGECIKCIYNTAGVFCDRCKEGFGNLPADPKKACACNYGTVOQSSCNPVTG 900  
Db 841 NRTGECIKCIYNTAGVFCDRCKEGFGNLPADPKKACACNYGTVOQSSCNPVTG 900  
Qy 901 QCQLPHVSGDCGTCPGYNLSGQGCRCDCCHALGSTNGQCDIRTGOCQCPGITG 960  
Db 901 QCQLPHVSGDCGTCPGYNLSGQGCRCDCCHALGSTNGQCDIRTGOCQCPGITG 960  
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Qy 1201 NETSABAYNLLRLTAGENQTALEI:BELNRYKYOAKNI:SQLEKQAAARVHEAKRAGDKA 1260  
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Qy 1261 VEIYASVAQLTPVDSEALENEANKI:KKEAADLRLIDQKLDYEDLREDMRGHEVKNL 1320  
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Qy 1501 KAKNSVSLISOLANLLDQGLQDQDVLNKLNETEGSLNKAQKBMKASDLDRKVSULESE 1560  
Db 1501 KAKNSVSLISOLANLLDQGLQDQDVLNKLNETEGSLNKAQKBMKASDLDRKVSULESE 1560  
Qy 1561 ARKQEAALMDYNRDI:AEI:KDHLEDI:KKT:PLTGCFTNPSIEKP 1605  
Db 1561 ARKQEAALMDYNRDI:AEI:KDHLEDI:KKT:PLTGCFTNPSIEKP 1605

RESULT 3  
US-09-562-702A-32  
; Sequence 32, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-562-702A-32

Query Match 98.1%; Score 8527; DB 4; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 34 ANDECADEGGRQRCMPPEFVNAFNVVATNTCGTPBEEYCVGTGVTKSKCHLCAG 93  
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Qy 94 QQLHQAFLDYNNQADTTWQSQTMLAGVQYPSNLTLLHLGKAFDITYVRLKFTS 153  
Db 61 QQLHQAFLDYNNQADTTWQSQTMLAGVQYPSNLTLLHLGKAFDITYVRLKFTS 120  
Qy 154 RPESFAYIKRTREDGFWIPYQYSSCENTYKANGIRGTGGDEQOALCTDEFSDISPL 213  
Db 121 RPESFAYIKRTREDGFWIPYQYSSCENTYKANGIRGTGGDEQOALCTDEFSDISPL 180  
Qy 214 TGNVAFSTLEGRPAYNFNDSPLVQEWTAIDIRVTNLRLNTFGDEVFNDPKVLKSY 273  
Db 181 TGNVAFSTLEGRPAYNFNDSPLVQEWTAIDIRVTNLRLNTFGDEVFNDPKVLKSY 240  
Qy 274 AISDFAVGGRCKONGHASECVKNEFDKLMCNCKNTYGVDCCKLPPFNDRPWRATAS 333  
Db 241 AISDFAVGGRCKONGHASECVKNEFDKLMCNCKNTYGVDCCKLPPFNDRPWRATAS 300  
Qy 334 ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDGAKCERENFRLGNTAC 393  
Db 301 ASECLPCDCNGRSQCYFDPPELYRSTGHGHTNCRDNTDGAKCERENFRLGNTAC 360  
Qy 394 SFCHSPVGSLSQCDSDYGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPSCDPSGSTE 453  
Db 361 SFCHSPVGSLSQCDSDYGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPSCDPSGSTE 420  
Qy 454 CNVETGRVCYKDNVGFNCERCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSVYDI 513  
Db 421 CNVETGRVCYKDNVGFNCERCKPGFFNLESNPKGCTPCFCFGHSSVCTNAVGSVYDI 480  
Qy 514 SSTFQIDEDGWRVEQRDGSSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYQ 573  
Db 481 SSTFQIDEDGWRVEQRDGSSEASLEWSSDRQYIAVSDSYFPRYFIAPVKFLGNQVLSYQ 540  
Qy 574 NLSFRRVDRRTRLSAEDLVLEAGLRSVPLIAQNSYSPSETTKVIFRLEHATDPM 633  
Db 541 NLSFRRVDRRTRLSAEDLVLEAGLRSVPLIAQNSYSPSETTKVIFRLEHATDPM 600  
Qy 634 RPALSPFEQKLNLLNLSIKIRGTYSERSAGYLDVLTQSLARPFGVPATVWESCTCPVG 693

Db 601 RPALSPFFQKLLNNLSIKIRGYSSAGYLDVTLQASRPGVPATWVSESTCPVG 660  
QY 694 YGQFCETCLPGYRRETPLSGPYGCVLCTCNHSETCDPCTGVCDRCRNTAGPHCEKCS 753  
Db 661 YGQFCETCLPGYRRETPLSGPYGCVLCTCNHSETCDPCTGVCDRCRNTAGPHCEKCS 720  
QY 754 DGYGDSLTGSSDCQPCPGSSCAIVPKTEVVTCTGTAGKRCCELDDGYFGDP 813  
Db 721 DGYGDSLTGSSDCQPCPGSSCAIVPKTEVVTCTGTAGKRCCELDDGYFGDP 780  
QY 814 LGSNGPVLCPCCQNDNIDPNAVGNCRNLGTGLCKIYNTAGFYCDRCKEGFGNPLAP 873  
Db 781 LGSNGPVLCPCCQNDNIDPNAVGNCRNLGTGLCKIYNTAGFYCDRCKEGFGNPLAP 840  
QY 874 NPADKACACNYGTVOQSSCNPTGQCCLPHVSRDGTCDPGYVNLQSGQCCERCD 933  
Db 841 NPADKACACNYGTVOQSSCNPTGQCCLPHVSRDGTCDPGYVNLQSGQCCERCD 900  
QY 934 CHALGSTNGQCDIITGQCEQPGITGQHCRCRNTNHFPGPCPKPCDCHHSGSLQCK 993  
Db 901 CHALGSTNGQCDIITGQCEQPGITGQHCRCRNTNHFPGPCPKPCDCHHSGSLQCK 960  
QY 994 DDCRCCEGFGVGNRCQCCENTFYNSWPGQCECPACVRLVKDAAEHVKLQELSLI 1053  
Db 961 DDCRCCEGFGVGNRCQCCENTFYNSWPGQCECPACVRLVKDAAEHVKLQELSLI 1020  
QY 1054 ANLGTGDDVTDQAFEDRLKEAREVTDLLREAEQVKVDQMLQRLQVNSLSQISR 1113  
Db 1021 ANLGTGDDVTDQAFEDRLKEAREVTDLLREAEQVKVDQMLQRLQVNSLSQISR 1080  
QY 1114 LQNRNTIETEGILAEARSRVSTEQIIEIASRELEKAKMAVSIITQPESTGPNNT 1173  
Db 1081 LQNRNTIETEGILAEARSRVSTEQIIEIASRELEKAKMAVSIITQPESTGPNNT 1140  
QY 1174 LLAERARLAEHQBADDIVRAKANTANETSABYVNLRTLAGNQTALIEELNRKYE 1233  
Db 1141 LLAERARLAEHQBADDIVRAKANTANETSABYVNLRTLAGNQTALIEELNRKYE 1200  
QY 1234 QAKNISDLEKQAAHVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293  
Db 1201 QAKNISDLEKQAAHVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
QY 1294 RLIDOKLKYEDLEBEDMRGHEHVKLLKGAQBOQTADOLLARADAAKALAEAAKGR 1353  
Db 1261 RLIDOKLKYEDLEBEDMRGHEHVKLLKGAQBOQTADOLLARADAAKALAEAAKGR 1320  
QY 1354 STLQEAANDILNLLKOPDRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAALGNAAA 1413  
Db 1321 STLQEAANDILNLLKOPDRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAALGNAAA 1380  
QY 1414 DATEAKNAHEAEKIASAAQKNTATSKADAERTFGEVTDLDNEVNGMLROLEAEANEK 1473  
Db 1381 DATEAKNAHEAEKIASAAQKNTATSKADAERTFGEVTDLDNEVNGMLROLEAEANEK 1440  
QY 1474 QDDADQDMMAGMASQAAEALNARKAKNSVSSLLSQNLNLLDQLQGLDLDVNLKLINE 1533  
Db 1441 QDDADQDMMAGMASQAAEALNARKAKNSVSSLLSQNLNLLDQLQGLDLDVNLKLINE 1500  
QY 1534 IEGSLNKADEMKAASDLDRKVSLESEARKQAAIMDYNRDAEIIKDHNLEIDIKTLP 1593  
Db 1501 IEGSLNKADEMKAASDLDRKVSLESEARKQAAIMDYNRDAEIIKDHNLEIDIKTLP 1560  
QY 1594 TGCNTPSIEKP 1605  
Db 1561 TGCNTPSIEKP 1572

## RESULT 4

US-09-561-818A-28  
; Sequence 28, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:

; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-561-818A-28

Query Match 98.1%; Score 8527; DB 4; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 AMDECADEGGRPQRCMPBFVNAAFNVTVATNTCGTPPEEYCVQTVGTGKLSCHLCDAG 93  
Db 1 AMDECADEGGRPQRCMPBFVNAAFNVTVATNTCGTPPEEYCVQTVGTGKLSCHLCDAG 60  
QY 94 QOHLQHGAAFLTDYNNQADTTWQSOQTLGAGVQVPSINLTLHLKAFDITYVRLKHTS 153  
Db 61 QOHLQHGAAFLTDYNNQADTTWQSOQTLGAGVQVPSINLTLHLKAFDITYVRLKHTS 120  
QY 154 RPESFALYKRTREDGFWPIQYIYSGSCENTYSKANRGFIETGDBQOALCTDFSDISPL 213  
Db 121 RPESFALYKRTREDGFWPIQYIYSGSCENTYSKANRGFIETGDBQOALCTDFSDISPL 180  
QY 214 TCGNVAFSTLEGRPSAYNFNSPVLQEWVATDTRVTLNRLNTFGDEVNDPKVLSYYY 273  
Db 181 TCGNVAFSTLEGRPSAYNFNSPVLQEWVATDTRVTLNRLNTFGDEVNDPKVLSYYY 240  
QY 274 A1SDFAVGRCKNGHASECYKNEFDFKLMCNKHTYGVDCBKCLPFFNDPWRRTAES 333  
Db 241 A1SDFAVGRCKNGHASECYKNEFDFKLMCNKHTYGVDCBKCLPFFNDPWRRTAES 300  
QY 334 ASECLPCDCNCRSQCYPDPPELYRSTGGHCHCTNCRDNTDGAKCERENFFRLGNTEAC 393  
Db 301 ASECLPCDCNCRSQCYPDPPELYRSTGGHCHCTNCRDNTDGAKCERENFFRLGNTEAC 360  
QY 394 SPCHSCPVSISTOCDSVGRCSCKPGVWGDKDRCPGFHSLTEAGCRPCSDPSGSTDE 453  
Db 361 SPCHSCPVSISTOCDSVGRCSCKPGVWGDKDRCPGFHSLTEAGCRPCSDPSGSTDE 420  
QY 454 CNVETGRCVCKNDVEGNCERCKEFGFNLESSNPKGCTPCFCFGHSSVCTNAVGVSYDI 513  
Db 421 CNVETGRCVCKNDVEGNCERCKEFGFNLESSNPKGCTPCFCFGHSSVCTNAVGVSYDI 480  
QY 514 STTFQIDEDGHRVQRDGSBASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 573  
Db 481 STTFQIDEDGHRVQRDGSBASLEWSSDRQYIAVISDSYFPRYFIAPVKFLGNQVLSYQ 540  
QY 574 NLSPSFYVDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 633  
Db 541 NLSPSFYVDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600  
QY 634 RPALSPFFQKLLNNLSIKIRGYSSAGYLDVTLQASRPGVPATWVSESTCPVG 693  
Db 601 RPALSPFFQKLLNNLSIKIRGYSSAGYLDVTLQASRPGVPATWVSESTCPVG 660  
QY 694 YGQFCETCLPGYRRETPLSGPYGCVLCTCNHSETCDPCTGVCDRCRNTAGPHCEKCS 753  
Db 661 YGQFCETCLPGYRRETPLSGPYGCVLCTCNHSETCDPCTGVCDRCRNTAGPHCEKCS 720  
QY 754 DGYGDSLTGSSDCQPCPGSSCAIVPKTEVVTCTGTAGKRCCELDDGYFGDP 813  
Db 721 DGYGDSLTGSSDCQPCPGSSCAIVPKTEVVTCTGTAGKRCCELDDGYFGDP 780  
QY 814 LGSNGPVLCPCCQNDNIDPNAVGNCRNLGTGLCKIYNTAGFYCDRCKEGFGNPLAP 873  
Db 781 LGSNGPVLCPCCQNDNIDPNAVGNCRNLGTGLCKIYNTAGFYCDRCKEGFGNPLAP 840

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QY 874 NPADKCKACACNYGTVOQSSCNPTVGOQCCLPHVSGRDCGTCDPGYNNLQSGGCECD 933
Db 841 NPADKCKACACNYGTVOQSSCNPTVGOQCCLPHVSGRDCGTCDPGYNNLQSGGCECD 900
QY 934 CHALGSTNGCQDRTGQCCQCGITGCHCERCETNHFGPGCKPCDCHHSGSLQCK 993
Db 901 CHALGSTNGCQDRTGQCCQCGITGCHCERCETNHFGPGCKPCDCHHSGSLQCK 960
QY 994 DGRCCRCGFGVGNRCDCQCEENFYNNRWPFGQCEPCACVRLVKDAAHRVKLOELSLI 1053
Db 961 DGRCCRCGFGVGNRCDCQCEENFYNNRWPFGQCEPCACVRLVKDAAHRVKLOELSLI 1020
QY 1054 ANLGTDGDMVTOAFEDRLKEAREVTDLLRAQEKVDQNLMDRLQVNSSLSHQSISR 1113
Db 1021 ANLGTDGDMVTOAFEDRLKEAREVTDLLRAQEKVDQNLMDRLQVNSSLSHQSISR 1080
QY 1114 LQNRNTIBETGILAEARSRVESTQELIEIASRELEKAKMAANVSITQPESTGEPNMT 1173
Db 1081 LQNRNTIBETGILAEARSRVESTQELIEIASRELEKAKMAANVSITQPESTGEPNMT 1140
QY 1174 LLAEEARRLAERHKQADDIIVAKTANETSAAEYNLLRLTAGENOTALIEISLNKYE 1233
Db 1141 LLAEEARRLAERHKQADDIIVAKTANETSAAEYNLLRLTAGENOTALIEISLNKYE 1200
QY 1234 QAKNISQDLEKQARVHEPAKAGDKAVEIYASVAQLTPVDSALNEBANKIKKEAADLD 1293
Db 1201 QAKNISQDLEKQARVHEPAKAGDKAVEIYASVAQLTPVDSALNEBANKIKKEAADLD 1260
QY 1294 RLIDQKLKDYEDRLDMRKEHEVNLLKKGABOOTADQLLARADAAKALAEBAKGR 1353
Db 1261 RLIDQKLKDYEDRLDMRKEHEVNLLKKGABOOTADQLLARADAAKALAEBAKGR 1320
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Db 1321 STLQZANDILNKKDFDRVNVNKTAAEBALRIPAINRTIAENKKTREAOALGNAAA 1380
QY 1414 DATEAKNKAHEAERIASAQAQKATSTKADABRTFGEVTDLQNEVNGMLRQLEEAENELK 1473
Db 1381 DATEAKNKAHEAERIASAQAQKATSTKADABRTFGEVTDLQNEVNGMLRQLEEAENELK 1440
QY 1474 QDADQDQMMAGMASQAQAELNARKAKNSVSLLSQLNLLDQLGQDTPVDLNKNE 1533
Db 1441 QDADQDQMMAGMASQAQAELNARKAKNSVSLLSQLNLLDQLGQDTPVDLNKNE 1500
QY 1534 IEGSLNKADEMKAASDLDRKVSLESEAKQBAATMDVNRDIAEIIKDHNLEDIKKTLP 1593
Db 1501 IEGSLNKADEMKAASDLDRKVSLESEAKQBAATMDVNRDIAEIIKDHNLEDIKKTLP 1560
QY 1594 TGCFTNTPSIEKP 1605
Db 1561 TGCFTNTPSIEKP 1572
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## RESULT 5

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US-09-562-702A-22
; Sequence 22, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-562-702A-22
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Query Match 93.7%; Score 8148; DB 4; Length 1609;

Best Local Similarity 92.8%; Fred. No. 0;

Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

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QY 1 MTGGGAAALALQPRGLRPLLAVAL--AAVAGCVBAAMDECADEGRQRCQMPFVNAAFN 58
Db 1 MRGSHRAAPALPRGLRPLLAVALAAAAAACAQAAAMDECTDEGRQRCQMPFVNAAFN 60
QY 59 VTVVATNTCGTPPEBYCVQGTGVTYKSKCHLADAGQOHLQHGAFLTDYNNQADTTWQS 118
Db 61 VTVVATNTCGTPPEBYCVQGTGVTYKSKCHLADAGQOHLQHGAFLTDYNNQADTTWQS 120
QY 119 QTMLAGVQVPNSINLTLLHKGAFDITVYRLKFTSRPESFAIYKRTREDGPMIPYQYYS 178
Db 121 QTMLAGVQVPNSINLTLLHKGAFDITVYRLKFTSRPESFAIYKRTREDGPMIPYQYYS 180
QY 179 SCENTYSKANRGFIITGDEQOALCTDEFSIDPLTGNVAFSTLEGRPSAYNFDSN 238
Db 181 SCENTYSKANRGFIITGDEQOALCTDEFSIDPLTGNVAFSTLEGRPSAYNFDSN 240
QY 239 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEF 298
Db 241 QEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECCLPCDCNGRSQRCYFDP 358
Db 301 DKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAESAECCLPCDCNGRSQRCYFDP 360
QY 359 TGHGCHTCNCRDNTDGAACERCENFRALGNTEACSPCHSPVGSLSQCDSTYGRCSCKP 418
Db 361 TGHGCHTCNCRDNTDGAACERCENFRALGNTEACSPCHSPVGSLSQCDSTYGRCSCKP 420
QY 419 GYMGDKCRCQPGFHSULTACRCPCSCDPSGSDTECNVETGRCVKCNVGFNCERCKPG 478
Db 421 GYMGDKCRCQPGFHSULTACRCPCSCDPSGSDTECNVETGRCVKCNVGFNCERCKPG 480
QY 479 FTFLESSNPKGCTPCFCFHSVSVCTNAVYSVYDISSTFQIDEDGWRVEQDSEASLEW 538
Db 481 FTFLESSNPKGCTPCFCFHSVSVCTNAVYSVYDISSTFQIDEDGWRVEQDSEASLEW 540
QY 539 SSROQYIAVISDSYPPRYPIAPVFLGNQVLSYQNLFSFRVDRDRTRLASADLVLEGA 598
Db 541 SSROQYIAVISDSYPPRYPIAPVFLGNQVLSYQNLFSFRVDRDRTRLASADLVLEGA 600
QY 599 GLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFFQKLLNNLTGIRGTY 658
Db 601 GLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFFQKLLNNLTGIRGTY 660
QY 659 SERSAGYLDVTLQASRPGPVPATWVESCTCPVYGGQFCETCLPGYRRETSGLPYSP 718
Db 661 SERSAGYLDVTLQASRPGPVPATWVESCTCPVYGGQFCETCLPGYRRETSGLPYSP 720
QY 719 CVLCTCNHSETCDPETGVCDCRNTAGPHCEKSCDGYVGDSTLTGSSDCQPCPCGSS 778
Db 721 CVLCTCNHSETCDPETGVCDCRNTAGPHCEKSCDGYVGDSTLTGSSDCQPCPCGSS 780
QY 779 CAIVPKTKVWVCTHCTGTAGRCCELDDGDFGDPPLGNSGPFVRLCRPCQCNNDIDNNAV 838
Db 781 CAIVPKTKVWVCTHCTGTAGRCCELDDGDFGDPPLGNSGPFVRLCRPCQCNNDIDNNAV 840
QY 839 NCNRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAPNPADCKKACACN-YGTVOQSSCNP 897
Db 841 NCNRLTGECLKIYNTAGFYCDRCCKEGFFGNPLAPNPADCKKACACN-YGTVOQSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDPGYNNLQSGGCECDCHALGSTNGCQDITGQCEQCGI 957
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Db 901 VTGQCECLPHVTGDCGACDPGFYNLQSGGQCCERCDCHALGSTNGQCDIRTGQCECPGI 960  
QY 958 TGOHCERCETHFGFEGGKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCCENYF 1017  
Db 961 TGOHCERCETHFGFEGGKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCCENYF 1020  
QY 1018 YNRSWPGQCECPACVRLVKDAAHVRVYKLAHESLIANLGTGDDMTDQAFEDRLKEAER 1077  
Db 1021 YNRSWPGQCECPACVRLVKDAAHVRVYKLAHESLIANLGTGDDMTDQAFEDRLKEAER 1080  
QY 1078 EVDLLREAQVQVDDQNDLDRORVNSLSHQSIRLQNTIRNTIETGILAEARSRVES 1137  
Db 1081 EVDLLREAQVQVDDQNDLDRORVNSLSHQSIRLQNTIRNTIETGILAEARSRVES 1140  
QY 1138 TEQIETIASRELEKAKM-AANVSTQPESTGEPPNNMTLLAEAEARRIAERHKEADIVRV 1196  
Db 1141 TERLEIETIASRELEKAKM-AANVSTQPESTGEPPNNMTLLAEAEARRIAERHKEADIVRV 1200  
QY 1197 AKTANETSAAEAYNLLRTLAGENOTALEIEELNARKYEQAKNISQDLEKQAAARVHEAKRA 1256  
Db 1201 AKTANDTSTEAYNLLRTLAGENOTALEIEELNARKYEQAKNISQDLEKQAAARVHEAKRA 1260  
QY 1257 GDKAVEIYASVAQTPVDSBALNEANKIKKEAADLRLIDQKLKDYEDLREDMRGKSE 1316  
Db 1261 GDKAVEIYASVAQTPVDSBALNEANKIKKEAADLRLIDQKLKDYEDLREDMRGKSE 1320  
QY 1317 VKNLLKRGKABOQTADOLLARADAALAEAAKGRSTLQEAANDILNLLKDFDRRVNDN 1376  
Db 1321 VKNLLKRGKTEQQTADOLLARADAALAEAAKGRSTLQEAANDILNLLKDFDRRVNDN 1380  
QY 1377 KTAEEALRRIPAINRTIATANEKTRBAQJALGNAADATEAKNKAHEABRIASAAQKNA 1436  
Db 1381 KTAEEALRRIPAINRTIATANEKTRBAQJALGNAADATEAKNKAHEABRIASAAQKNA 1440  
QY 1437 TSKADAERTFGEVTDLDNEVGMRLQLEBAENELKRRKODDADQDMWAGMASQAAQAE 1496  
Db 1441 TSKAERTFAEVTDLNENVMNLKQLEBAENELKRRKODDADQDMWAGMASQAAQAE 1500  
QY 1497 LNARKAKNSVSSLLSQNLNLLDQGLDVTDLNKLNEIGSLNKAENKASDLDRKYSV 1556  
Db 1501 LNARKAKNSVSSLLSQNLNLLDQGLDVTDLNKLNEIGSLNKAENKASDLDRKYSV 1560  
QY 1557 LESBARKQEAALVMDYNDRIABIIKDIHNLDEIKKTLPTGCFNTPSIEKP 1605  
Db 1561 LENAQKQEAALVMDYNDRIABIIKDIHNLDEIKKTLPTGCFNTPSIEKP 1609

## RESULT 6

US-09-561-818A-22  
; Sequence 22, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; TITLE OF INVENTION: Tryggvason, Karl  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-22

Query Match 93.7%; Score 8148; DB 4; Length 1609;  
Best Local Similarity 92.6%; Pred. No. 0;  
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;  
QY 1 MTGGGAALALQPRGLWELLAVL--AAVAGCVRAAMDECADEGGRRPQRCMPFVNAAFN 58  
Db 1 MRGSHRAAPALPRGLWELLAVLAAAAAGCAQAAAMDECTDEGGRRPQRCMPFVNAAFN 60

QY 59 VTVVATNTCTGTPPEBYCVOTGVTGVTKSHLCDAGQOHLQHGAAFLTDYNNQADTTWQS 118  
Db 61 VTVVATNTCTGTPPEBYCVOTGVTGVTKSHLCDAGQOHLQHGAAFLTDYNNQADTTWQS 120  
QY 119 QTMLAGVQVPSINLTLHLGKAFDITTYVRLKFTSRPSPFAIYKRTREDGWPVYQYISG 178  
Db 121 QTMLAGVQVPSINLTLHLGKAFDITTYVRLKFTSRPSPFAIYKRTREDGWPVYQYISG 180  
QY 179 SCENTYKANKRGFIRTPGDEQOALCTDEPSDISPLTGGNVAFTSTLEGPSAFAVNSPVL 238  
Db 181 SCENTYKANKRGFIRTPGDEQOALCTDEPSDISPLTGGNVAFTSTLEGPSAFAVNSPVL 240  
QY 239 QEWVTATDIRVTILNRLNTFGDEVFNDPKVLYKSYIAISDFAVGGRCCKNGHASECVKNEF 298  
Db 241 QEWVTATDIRVTILNRLNTFGDEVFNDPKVLYKSYIAISDFAVGGRCCKNGHASECVKNEF 300  
QY 299 DKLWCKNKNYGVDCCKLPFNDPRPWRATASASECLPCDCNRSQCEYFDBELYS 358  
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QY 359 TGRGHGCTNCRDNTDGAKECERENFRILGNTEACSPCHCSVPVGLSTQCDSYGRCSCKP 418  
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QY 419 GVMGDKDCRCQPFHSLTEAGRCPCDPSGSDTECNVETGRCYCKDNVEGFNCERCKPG 478  
Db 421 GVMGDKDCRCQPFHSLTEAGRCPCDPSGSDTECNVETGRCYCKDNVEGFNCERCKPG 480  
QY 479 FFLNLESSNPKGCTPCFCGHSSVCTNAVGYSYVDIISSTFQIDEDGWRVQEDSGSEASLEW 538  
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QY 539 SSDRQYIAVDSYPRYFIAPVKLGQVLSYGNLSFSFRVDRDRLTSLAEOLVLEGA 598  
Db 541 SSDRQYIAVDSYPRYFIAPVKLGQVLSYGNLSFSFRVDRDRLTSLAEOLVLEGA 600  
QY 599 GLRVSVPLIAQNSYPSSETTVKIIFRLHEATDYPWRPALSPFQKLLNLLTSIKIRGT 658  
Db 601 GLRVSVPLIAQNSYPSSETTVKIIFRLHEATDYPWRPALSPFQKLLNLLTSIKIRGT 660  
QY 659 SERSAGYLDVTLQASARPQGPVATWESCTCPVGYGQFCCTCLPGVRRTPSLGYSVP 718  
Db 661 SERSAGYLDVTLQASARPQGPVATWESCTCPVGYGQFCCTCLPGVRRTPSLGYSVP 720  
QY 719 CVLCTCNHSETCDPBTGVDCRDNNTAGHCKESDGYIGDSTLGTSSDCQPCPCPGSS 778  
Db 721 CVLCAHNGHSETCDPBTGVDCRDNNTAGHCKESDGYIGDSTLGTSSDCQPCPCPGSS 780  
QY 779 CAIVPKTEWCTHCTGTAGKRCCLDDGYFGDPLGNSGVPVRLCRPCQCNNDIDPNAVG 838  
Db 781 CAIVPKTEWCTHCTGTAGKRCCLDDGYFGDPLGNSGVPVRLCRPCQCNNDIDPNAVG 840  
QY 839 NKNRLTGECCKIYNTAGFYCDRCCKEFPFNGPLAPNADKCAKACN-YGTVOQSSCNP 897  
Db 841 NKNRLTGECCKIYNTAGFYCDRCCKEFPFNGPLAPNADKCAKACNYPYGTVMKQSSCNP 900  
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QY 1018 YNRSWPGQCECPACVRLVKDAAHVRVYKLAHESLIANLGTGDDMTDQAFEDRLKEAER 1077  
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QY 1078 EVDLLREAQVQVDDQNDLDRORVNSLSHQSIRLQNTIRNTIETGILAEARSRVES 1137  
Db 1081 EVDLLREAQVQVDDQNDLDRORVNSLSHQSIRLQNTIRNTIETGILAEARSRVES 1140







Db	1321	KKGRDITQAEANDIINLUKDPDRVNDNKTAAEBALRKIPAINQITITAEANEKTRAQALG	1380
Qy	1410	NAADATEAKNAHEAERIAAQAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEAN	1469
Db	1381	SAAADATEAKNAHEAERIAAQAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEAN	1440
Qy	1470	ELKQKQDADQDMMAGNASQAQAQAEINAKNAKNSVSLLSQNLNLLDOLGQDVTVDLN	1529
Db	1441	ELKQKQDADQDMMAGNASQAQAQAEINAKNAKNSVSLLSQNLNLLDOLGQDVTVDLN	1500
Qy	1530	KLNEIEGSLNKADEMKAESDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLBEDIK	1589
Db	1501	KLNEIEGTLNKADEMKVSDLRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLBEDIK	1560
Qy	1590	KTLPTGCFNTPSIEKP	1605
Db	1561	KTLPSGCFNTPSIEKP	1576
RESULT 9			
US-09-561-818A-24			
; Sequence 24, Application US/09561818A			
; Patent No. 6638907			
; GENERAL INFORMATION:			
; APPLICANT: Kortessmaa, Jarkko			
; APPLICANT: Tryggvason, Karl			
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use			
; FILE REFERENCE: 99/274-D			
; CURRENT APPLICATION NUMBER: US/09/561.818A			
; CURRENT FILING DATE: 2000-04-28			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 24			
; LENGTH: 1576			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-561-818A-24			
Query Match 92.5%; Score 8043; DB 4; Length 1576;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;			
Qy	32	RAAMDECADEGRPORCMPEFNAAFNVTVVATNTCGTPPEYCVQGTGVTGKSLCD	91
Db	1	QAAMDECTDEGRPORCMPEFNAAFNVTVVATNTCGTPPEYCVQGTGVTGKSLCD	60
Qy	92	AGQHLQGAFLDYNQADTTWQSOTMLAGVQYPSINLTLLHLSKAFDITVRLKPH	151
Db	61	AGQHLQGAFLDYNQADTTWQSOTMLAGVQYPSINLTLLHLSKAFDITVRLKPH	120
Qy	152	TSRPESFAIKRTREDGPMIPIQYVYSGSCENTYSKANRGFIRTCGDSQQAALCTDFPSDIS	211
Db	121	TSRPESFAIKRTREDGPMIPIQYVYSGSCENTYSKANRGFIRTCGDSQQAALCTDFPSDIS	180
Qy	212	PLTGNVAFSTLEGRPSAYNFDSVQLQEWYATDITVTLNRLNTFGDEVFNDPKVLKSY	271
Db	181	PLTGNVAFSTLEGRPSAYNFDSVQLQEWYATDITVTLNRLNTFGDEVFNDPKVLKSY	240
Qy	272	YYAISDFAVGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATA	331
Db	241	YYAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCBKCLPFFNDRPWRATA	300
Qy	332	ESASECLPCDNGRQECYFPELYRSTGHGHCTNCQDNTDGAHCRERENFRLGNTE	391
Db	301	ESASECLPCDNGRQECYFPELYRSTGHGHCTNCQDNTDGAHCRERENFRLGNTE	360
Qy	392	ACSPCHCSFVGLSTQCDYGRCSCKPGVMGDKCDRCQPGFHSITEAGCRPCSDPSGST	451
Db	361	ACSSCHCSFVGLSTQCDYGRCSCKPGVMGDKCDRCQPGFHSITEAGCRPCSDPSGSI	420
Qy	452	DECNVETGRVCVKDNEVFNCERCKPGFNLESSNPKCTPCRCFGHSSVCTNAVGSYV	511
Db	421	DECNVETGRVCVKDNEVFNCERCKPGFNLESSNPKCTPCRCFGHSSVCTNAVGSYV	480

Qy	512	DISSTFOIDEDWRVBOEDGSEASLEWSDROYTAVISDSYFPRYFIAPVFLGNQVLSY	571
Db	481	SISSTFOIDEDWRVBOEDGSEASLEWSSERODIAVISDSYFPRYFIAPKFLGQVLSY	540
Qy	572	GQNLSPSFVRDRLRLSAEDLVLEGAGLRVSPVLIAGNSYPSSETTVKYIFRLHEATDY	631
Db	541	GQNLSPSFVRDRLRLSAEDLVLEGAGLRVSPVLIAGNSYPSSETTVKYIFRLHEATDY	600
Qy	632	PWRPALSPPEFOKLNNLTSIKIRTYERSAGYLDVTLQASRPGVGPATWVESCCTP	691
Db	601	PWRPALTPPEFOKLNNLTSIKIRTYERSAGYLDVTLQASRPGVGPATWVESCCTP	660
Qy	692	VGVGGQFCETCLPGYARETESLPGSPCVLCTCNGHSETCDPETGVCDCRDNTAGPHCEK	751
Db	661	VGVGGQFCETCLPGYARETESLPGSPCVLCTCNGHSETCDPETGVCDCRDNTAGPHCEK	720
Qy	752	CSDGYVGDSTLTSSDCQPCPCGGSSCAIYVKTKEVVTCHTGTGTAGRCBLDDGYFG	811
Db	721	CSDGYVGDSTLTSSDCQPCPCGGSSCAVVEVKTKEVVTCHTGTGTAGRCBLDDGYFG	780
Qy	812	DPLGNGPVRLCRPCQCNNDIDPNAVGNCRNLGTCLKCIYNTAGFYCDRCKEGFGNPL	871
Db	781	DPLGNGPVRLCRPCQCNNDIDPNAVGNCRNLGTCLKCIYNTAGFYCDRCKEGFGNPL	840
Qy	872	APNPADKCKACACN-YGTVQQSSCNPTVTCQCLPHVSRDCGTCDPGYVNLQSGQCE	930
Db	841	APNPADKCKACACNPGYTMKQSSCNPTVTCQCLPHVTCQCGACDPCGFYVNLQSGQCE	900
Qy	931	RDCNALSTNGQCDIRTCQCECQPGITGOHCERCETHHFGPGSGCKPCDCHHSGSL	990
Db	901	RDCNALSTNGQCDIRTCQCECQPGITGOHCERCETHHFGPGSGCKPCDCHHSGSL	960
Qy	991	QCKDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCEPCACVRLVKDKAAEHRVLE	1050
Db	961	QCKDGRCECREGFGVGNRCDCQCEENYFYNRSWPGQCEPCACVRLVKDVADHRVLE	1020
Qy	1051	SLIANLTGDDMYTQAFEDRLKEAREVTDLLRQAQVQVQVQVQVQVQVQVQVQVQVQV	1110
Db	1021	SLIANLTGDDMYTQAFEDRLKEAREVTDLLRQAQVQVQVQVQVQVQVQVQVQVQVQV	1080
Qy	1111	ISRLQNRITIBETGLIARARSRYESTBOLTEIASRELEKAKM-AANVSITQPESTGEP	1169
Db	1081	ISRLQNRITIBETGLIARARSRYESTBOLTEIASRELEKAKM-AANVSITQPESTGEP	1140
Qy	1170	NNMTLAEARLARERHKEADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIELN	1229
Db	1141	NNMTLAEARLARERHKEADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIELN	1200
Qy	1230	RKYEQAQKNSIDLEKQAAVHEEAKAGDKAVEIYASVAQLTPVDSALENEANKIKKEA	1289
Db	1201	RKYEQAQKNSIDLEKQAAVHEEAKAGDKAVEIYASVAQLTPVDSALENEANKIKKEA	1260
Qy	1290	ADLRLIDQKLKDYEDLREDMFGKHEVKNLLEKKAQSOQTADQLLARAADAALAEBA	1349
Db	1261	ENLEQLIDQKLKDYEDLREDMFGKHEVKNLLEKKAQSOQTADQLLARAADAALAEBA	1320
Qy	1350	KKGRSTLOQANDILANNKDFDRVNDKTAEEALRRIPAINRTIAEANEKTRAQALG	1409
Db	1321	KKGRSTLOQANDILANNKDFDRVNDKTAEEALRRIPAINRTIAEANEKTRAQALG	1380
Qy	1410	NAAADATEAKNAHEAERIAAQAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEAN	1469
Db	1381	NAAADATEAKNAHEAERIAAQAQKATSTKADARTFGEVTDLDNEVNGMLRQLEAEAN	1440
Qy	1470	ELKQKQDADQDMMAGNASQAQAQAEINAKNAKNSVSLLSQNLNLLDOLGQDVTVDLN	1529
Db	1441	ELKQKQDADQDMMAGNASQAQAQAEINAKNAKNSVSLLSQNLNLLDOLGQDVTVDLN	1500
Qy	1530	KLNEIEGSLNKADEMKAESDLDRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLBEDIK	1589
Db	1501	KLNEIEGTLNKADEMKVSDLRKVSLESEARKQEAAMIDYNRDIAEIIKDIHNLBEDIK	1560



QY	1590	KTLPTGCGTNTSIEKP	1605
DB	1561	KTLPSGCGTNTSIEKP	1576
RESULT 10			
US-09-562-702A-28			
; Sequence 28, Application US/09562702A			
; Patent No. 6632790			
; GENERAL INFORMATION:			
; APPLICANT: Yurchenco, Peter			
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use			
; FILE REFERENCE: 99-274-B			
; CURRENT APPLICATION NUMBER: US/09/562,702A			
; CURRENT FILING DATE: 2000-04-28			
; PRIOR APPLICATION NUMBER: 60/155,945			
; PRIOR FILING DATE: 1999-09-24			
; PRIOR APPLICATION NUMBER: 60/143,289			
; PRIOR FILING DATE: 1999-07-12			
; PRIOR APPLICATION NUMBER: 60/139,198			
; PRIOR FILING DATE: 1999-06-15			
; PRIOR APPLICATION NUMBER: 60/131,720			
; PRIOR FILING DATE: 1999-04-30			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 28			
; TYPE: PRT			
; LENGTH: 1584			
; ORGANISM: Homo sapiens			
US-09-562-702A-28			

Query Match 92.5%; Score 8043; DB 4; Length 1584;			
Best Local Similarity 93.3%; Pred. No. 0;			
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;			
QY	32	RAAMDECADEGRRPCORCMPEFYNAAFNVTVVATNTCGTPPEYCVQTGVTGVTKSCHLCD	91
DB	1	QAAMDECTDEGRRPCORCMPEFYNAAFNVTVVATNTCGTPPEYCVQTGVTGVTKSCHLCD	60
QY	92	ACQHLQHGAFLTDNNQADTTWQSQTMLAGVQYPSINLTLLHKAFAIDITYVRLKFX	151
DB	61	ACQHLQHGAFLTDNNQADTTWQSQTMLAGVQYPSINLTLLHKAFAIDITYVRLKFX	120
QY	152	TSRPESFAYIKYTRDGPHIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDEFSIS	211
DB	121	TSRPESFAYIKYTRDGPHIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDEFSIS	180
QY	212	PLTGGNVATSTLEGRSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY	271
DB	181	PLTGGNVATSTLEGRSAYNFNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY	240
QY	272	YVAISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCXKLPFNDRPWRATA	331
DB	241	YVAISDFAVGGRCKNGHASECVKNEFDKLMCNCKHNTYGVDCXKLPFNDRPWRATA	300
QY	332	ESASECLPCDCNRSQECYFDPYELVYSTGHGHCTNCRDNTDGAKECERENFFRLGNTE	391
DB	301	ESASECLPCDCNRSQECYFDPYELVYSTGHGHCTNCRDNTDGAKECERENFFRLGNTE	360
QY	392	ACSPCHCSPVGSJSTQCDYGRCSCKPQGVMDKCDRCQPGFHSLTEAGCRPCSDPSGST	451
DB	361	ACSSCHCSPVGSJSTQCDYGRCSCKPQGVMDKCDRCQPGFHSLTEAGCRPCSDPSGI	420
QY	452	DECNVETGRVCCKDNVEGFCERCKPGFFNLSSNPKGCTPCFCGHSSVCTNAVGVSYV	511
DB	421	DECNVETGRVCCKDNVEGFCERCKPGFFNLSSNPKGCTPCFCGHSSVCTNAVGVSYV	480
QY	512	DISSTFQIDBDGWRVEQRDGSSEASLEWSDRQVIAVISDSYFPRYFIAPVKPLGNQVLSY	571
DB	481	SISSTFQIDBDGWRVEQRDGSSEASLEWSDRQVIAVISDSYFPRYFIAPVKPLGNQVLSY	540
QY	572	GQNLSPFRVDRDTRLASADLVLEGAGLRVSVPLIAQGNSEYSETTVKYIFRLHEADTY	631

RESULT 11  
US-09-845-583A-10

Sequence 10, Application US/0945583A  
Patent No. 6635616  
GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert  
APPLICANT: Brunken, William Joseph  
APPLICANT: Champliand, Marie-France  
APPLICANT: Hunter, Dale  
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
FILE REFERENCE: 10287-056001  
CURRENT APPLICATION NUMBER: US/09/845,583A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/200,863  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 1587  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-845-583A-10

Query Match 41.4%; Score 3596.5; DB 4; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 5.2e-207;  
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;

QY 20 LLAVLAAGCVRAAMDECEGRPORCMPEFVNAAFVTVVATVTCGTPPEYCVQVG 79  
DB 12 LLAPRAAG-----MGACDYGAGRPORCLPVFENAAFGLAQASHTCSPSPDFCPHV 66

QY 80 VTGVTKCHLCDAGQHQHGAFLTDYNNQADTTWQSQTLMAQVQYFNSINLTLHGLK 139  
DB 67 AAGAGACQRCDAADPORHNASVILDFHSQDSSTWQSPSMAFQVQYPTSVNITLRLGK 126

QY 140 AFDITYVRLKFTSRPSPFAIKRTREDGPMIPIYQYVSGCENTYKANKRGFTRTGDEQ 199  
DB 127 AYEITYVRLKFTSRPSPFAIKRSRADGPWEYQFYFASQCKYGRPEQYLRPGEDE 186

QY 200 QALCTDEFSISPLTGGNVAFTLEGPSAIFNDSNVLQEWTAIDTDIRVLRNLNFTGD 259  
DB 187 VAFCTSFSDISPLUGGNVAFSTLEGPSAYNFESGLQEWTSHELLISLRLNFTGD 246

QY 260 EVFNDPVLKSYIAYISDFAVGRCCKNGHASECVKNEFDKLMCNKHNTHYTVGDCBKCLP 319  
DB 247 DIFKDPKVLQSYIAYISDFSVGRCCKNGHASECGPDVAGLACRCQHNNTGTDCERCLP 306

QY 320 FNDPRWRRTAESASCLPCDCNGRSQECYFDPPELYSTGHGHCTNCRDNDTGAKCER 379  
DB 307 FFQDRPWARGTAAAHACLPCNCSGRSEECTFDRELPRSTGHGRCCHCRDHTAGHCE 366

QY 380 CRENFRLGNTAACPCHCPVGSLSLTCQDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAG 439  
DB 367 QENFYHWDPMPCQPCDCQSAGSLHLQCDTGTCAKPTVTGWKCDRCCLPGFHSLSGG 426

QY 440 CRPSCDPSGTDNCEVETGRUCVKNVEGNCERCKPGFNLESNPKCTPCFCFGHS 499  
DB 427 CRPCTCPAGSLDTCDFRSGRCPCNVEGNLDCRCPGTFNLPQHPNAGCSCFCYGHS 486

QY 500 SVCTNNAVGSYVDTSSTFOIDEDQWRQDRGSEASLEWSRDQYIAVSDSYPPRYFIA 559  
DB 487 KVCASTAQFQVHLLSDFHQAGCWARSVGGSEHSPQWSPN---GVLLSPDEBELTA 542

QY 560 PVKFLGNQVLSYGNLGSFRVDRRLTSLAEDLVLEGAGLRVSVPLIAGNSVPSETTV 619  
DB 543 PGKFLGDRFSGQPLILUTFRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPQDARA 599

QY 620 KYIFRLH---RATDYPWRPALSPFEOKLLNLTSLIKIRGYTSRSAG--YLDSDVTLQSA 674  
DB 600 SQGGAQVPLQETSEDVAPPLPPHFQRLANLTSLRLVSPGSPAGPVFLNEVRLTSA 659

QY 675 RPPGQVPAWVSECTCPVYGQGCFCETCLPOYRRETPSLGLPSPCYLCTCNHGHSETCDPE 734  
DB 660 RFLGSPASWVEICSCPTGYTGFCESCAPYKREMPQGGPYASVCPCTCNQHG-TCDPN 718

735 TGVCDNRDNTAGPHCEKXCSGYVGDSTLGTSSDCQPCPCPGSSCAIVPKTKVVCVTHCP 794  
DB 719 TGICVCSHHTEGPSCERCLFGFYGNFAGQADCCQPCPGQSACTTIPSSGEVVCVTHCP 778

QY 795 TGTAKEKCELDGDFGDFPLGNSGNPRLCRPCCQNDNDIPNAVGNRLTGECLKCIYNT 854  
DB 779 PQGRGRCEVCDGDFGDFPLGFGHPOPCQCCQSGNVDPNAVGNCDPLSGHCLRLHNT 838

QY 855 AGFYCDRCKEGFFGNPLAPNADKCKACACN-YGTVOQSSCNVPTGQCCLPHVSGRDC 913  
DB 839 TGDHCEHCQEGFYGSALAPRPADKCMPCSPQGSVSEQMPDVPVTCQCSCLPHVTRADC 898

QY 914 GTCDPGVYNLOSOGCERCDCCHALGSTNGQDITGTGCECOPGITGHCERCETNHFVG 973  
DB 899 SRCYPGFFDLPQGRGCRCKCHPLGSQEDQCHPTGQCTCEPVTGQACDQCLGFFGSS 958

QY 974 PEGCKPCDCHHEGSLSLQCKDDGRCECRGVGNRCOCENYFYNKSWPCQCPACYR 1033  
DB 959 IKGCRACRCSPLGAASAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTGHCQCPSCYA 1018

QY 1034 LVKDKAAEHRVKIQLLESILIANLGTGD-----DMVTQAFEDRLKEAREVTDLLRAQE 1088  
DB 1019 LVKESATLAKARLTLTEGWLQSGDCGSPWGLDILLGEAPRGDVIYQGH-----LLPGARE 1074

QY 1089 VKDVQNLMDRLQRVNSLSHSQISRLQNRNTIBETGILAEARARSVESTQLIEIASRE 1148  
DB 1075 A-----FLEQWMLGEGAVKAAAREQLRLNKGARCAQAGSOKTCTQLADLEAVLESSEE 1128

QY 1149 -LEKAKMAANVISITQPESTGEFNNWTLAEEARLAEHRHKEADDIVRVANTANETAE 1207  
DB 1129 ILHAAAILASLEIPO-EGPSQPTKWSHLAIEARALASHRTATKIATAWRALLASNTS 1187

QY 1208 YNLLRLTLAGENOTALETE-ELNRKYEQAKNISODLEKQAAVHEEAKRAGDKAVETAYAS 1266  
DB 1188 YALLNWL--EGRVALETQDLEDREYQVQAAQKALRTAVAEVLPEAE-----SVLAT 1238

QY 1267 VAQL-----TPVDSEA--LENEANKIKKEAADLRLDOKLKDYEDLRE 1308  
DB 1239 VQVCGADTAPVLLALASPGALPQKSAEDLGLKAKALEKTIVASQHMATEAARTLQTAQ 1298

QY 1309 -DMRKEHEVKNLLEKGAEQQTADOLLARADAAKALAEAAKKGSRSTLOEANDILANLK 1367  
DB 1299 ATLROTE---PLTWARSRLTATFASQLHOGRAALTOASSSVQAAVTVMGARTLLADLE 1355

QY 1368 DFDREVNDKTAABEALRRIPAINRTTAAENKRETAQALAGNAAADATEAKNAKHAER 1427  
DB 1356 GMKLQFPRPKQAAQKADSVSDRLADTRKTKQAERMLGNAAPLSSSSAKKGGREAV 1415

QY 1428 IASAAQKATSTKADAERTFGEVTDLDNEVNGMLRQL-EEAENELKRKODDADODMMAG 1486  
DB 1416 LAKDSAKLAKALLERKQAHRRASRLTSQTAQOASQCVLASEARRQEEAEERVGAG 1475

QY 1487 MASQAAQAEALNARKNSVSSLSQLNLLDQLDQLDT--VDLNLKLEIEGSLNKAKDE 1544  
DB 1476 LS-----EMEQQIRBSRISLEKDIETLSALLARGLSLDTHQAPALNETQWALERLRQ 1530

QY 1545 M-KASDLRKVSDLESSEARKQFAALMDYNDIAEIIKDIHNEIDIKTLPTGC 1596  
DB 1531 LGSPSLOKLSLLEQESQQEQLQIGFESDLAEIRADKQNLBAILHSLPENC 1583

## RESULT 12

US-09-561-7098-3  
Sequence 3, Application US/09561709B  
Patent No. 6682911  
GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert  
APPLICANT: Champliand, Marie-France  
APPLICANT: Olson, Pamela  
APPLICANT: Koch, Manuel  
APPLICANT: Brunken, William  
TITLE OF INVENTION: LAMININS AND USES THEREOF  
FILE REFERENCE: 10287-060001

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; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-3

Query Match      41.4%; Score 3596.5; DB 4; Length 1587;
Best Local Similarity 43.8%; Pred. No. 5.2e-207; Indels 77; Gaps 24;
Matches 707; Conservative 258; Mismatches 571;

QY 20 LLVLAAGVAVRAAMDECADEGGPQRCMPFVNAAFNVTATNTCGTPPEYCVQTG 79
DB 12 LLAPRAAGAG-----MGACYDGAGRFQCLPVFENAAFGRLAQASHTCGSPDFCPHVG 66
QY 80 VTGVTKSCHLDAGQOQHLOHGAFLTDYNNQADTTWQSOOTMLAGVOYPSNLTLLHKG 139
DB 67 AAGAGAHCCQRCDAADPQRHNASYLTDFHSODESTWQSPSMAFGVQVPTSVNITLRLGK 126
QY 140 AFDITVRLKFTSRPESFAIKRTRDQPMIPYOYSGSCENTYSKANRGFIRTGDEQ 199
DB 127 AEIITVRLKFTSRPESFAIKRTRDQPMIPYOYSGSCENTYSKANRGFIRTGDEQ 186
QY 200 QALCTDEFSDISPLTGGNVAFTSLGRPSAYNFNSPVLQEWVTATDTRVTLNRLNTPGD 259
DB 187 VAFCTSEFSDISPLTGGNVAFTSLGRPSAYNFNSPVLQEWVTATDTRVTLNRLNTPGD 246
QY 260 EVFNDPKVLKSYVYALSDFAVGRCKNGCHASECVKNEFDKLMCKNCKNTYGVDCCKLP 319
DB 247 DIFDKPKVLQSYVYALSDFAVGRCKNGCHASECVKNEFDKLMCKNCKNTYGVDCCKLP 306
QY 320 FNDPRWRRTAESAECFLPCDNGRSQFCYDPPELYRSTGHGCHTCNCRDNTDCAKER 379
DB 307 FFQDRPWARGTAAEAHECLPCNCSGRSECTDFELRSTGHGCHTCNCRDNTDCAKER 366
QY 380 CRENFRLNTEACSPCHSPVGLSTQCDVSGRCKPGVNGDKDCRCQPGFHSLSSEG 439
DB 367 CQENFYHDPMPQPCQDCQSGSLHLQCDTGTCAKFTVTGWKDCRLCPGFHSLSSEG 426
QY 440 CRPCSDPGSGTDECNVETGRVCNDVEGFNCERCKPGFFNLESSNPKGCTPCFCQHS 499
DB 427 CRECTCNPAGSLTDCPRSGRCPCKENVEGNLDCRCRPGTFLQPHNPAGCSCFCYGH 486
QY 500 SVCTNAVGSVYDISSTFQIDEDGWRVEORDGSEASLEWSRQYIAVSDSYFFRYFTA 559
DB 487 KVCASTAQFQVHHILSDFHQAGBGMWARSVGGSEHSPQSPN-----GVLLSPDEBEELTA 542
QY 560 PVKFLGNVLVYGNLSFSPVRDRTRLSAEDLVLEGAGLRVSVPLIAQGNYSYSETTV 619
DB 543 PGKFLGQDRSYGQPLILITFRVPGSPPLVQ-LRLEGTGLALS--LRHSSLGGQDARA 599
QY 620 KYIFRLH---EATDYPWRPALSFPFKLNNLTSIKRGTYSERAG--YLDVTVLQSA 674
DB 600 SQGGAQVPLQETSEDVAPLPFPHFORILANLTSRLRVSPGSPAGPVFLTEVRLTSA 659
QY 675 RPBGPVATVVESTCPVGGQFCETCLPGYRETPSLGYPSPVCLTCNQHSETCDE 734
DB 660 RPLSPASWVEICSCPTGTGTGFCSCAPGYKREMPQGGPYASCVPCTCNQH-TCDPN 718
QY 735 TGVCCDRNTAGPRCEKSCDGYGDSLTGTSQCPQCPGPGGSCAIVPKTEVVTCHCP 794
DB 719 TGICVCSHHTGPSCERCLPGFYGNPPAGQADDCQPCPGQSACTTIPESGEVWCTGP 778
QY 795 TGTAGKCELCDDGYFGDPLGSGNCPVRLCRPCQCNNDIDPNAGCNRLTGECLKCIYNT 854
DB 779 PGQGRRCRCEVCDGDFGDLPLGLFGHPQPCQCCQSGNVDPNAVGNCDPLSGHCLRLHNT 838
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QY 855 AGFYCDRCCKEGFNGNPLAPNPADKCKACACN-YGTVOQSSCNVPTGOCQCLPHVSGRDC 913
DB 839 TGDCHCHCEGFGYAGALAPRPADKCKWPSCHPQSGVSSQMPCDPTGQCSCLPHVTARD 898
QY 914 GTCDPGYNLQSGQCERCDCCHALGTINGQCDIRTGQCECQPGITGQCHERCETHHFG 973
DB 899 SRCYPGFFDLQPGRCRSCKCHPLGSDQCHPQCTGCTCRPGVGTGQACDRCLQFFGSS 958
QY 974 PEGCKPCDCHHSGSLQCKDGRCEBGFVGNRCDOCEENYFYNRSPGQCEGCPACVYR 1033
DB 959 IKGCRACRCSPLGAASAQCHYNGTCVCRPGFGYKCDRCHYNNFFLTADTGHCCQCESCVA 1018
QY 1034 LVKDKAAEHRVKIQLLESILIANLTGTD-----DMVTDQAFEDRLKBAEREVTDLREAEQ 1088
DB 1019 LVKEETAALKARLTLEGMQLQSDGSPWGPLDILLGEAPRGDVYQGHF-----LPGARE 1074
QY 1089 VKDQDNQLMDRLQVNVNSLSHSQISRLONIRNTIETGILAEARSRSVESTOLIEIASBE 1148
DB 1075 A-----FLEQWGLEGAVKAAAREQQLNKGAARCAQAGSKTCTQLADLEAVLESSEE 1128
QY 1149 -LEKAMAAANVSITQPESTGEPMNTLLAEARRLAERHKQDADDIVRVAKTANETSAA 1207
DB 1129 ILHAAAILLASLEIPQ-EGPSQPTKWSHLAEARALARSHRDATKIAATAMRALLASNTS 1187
QY 1208 YNLLRLTAGENOTALEIB-ELNRKYEQAKNISQDLEKQAAKVHEEAKRAGDKAVEIYAS 1266
DB 1188 YALLWNL--EGRVALETORDLEDYRQVQAAQKALRTAVAEVLPPEA-----SVLAT 1238
QY 1267 VAOL-----TPVDSEA--LENEANKIKKEAADLRLIDOKLKDVEDLRE 1308
DB 1239 VQVQADTAPYLLALLSPGALPKSRAEDLGLKAKALEKTVASQWQHMAATEAARTLQTAQ 1298
QY 1309 -DMRGKEHEVNULLEKGAEEQQTADQLLARAADAAXALAEAAKKGSTLQEBANDILNNLK 1367
DB 1299 ATLROTE---PLTMARSRLTATFASQLHQGARAALTQASSVQAATVTVNGARTLLADLE 1355
QY 1368 DEFRRVNDNTAAEALRIPAINRTIABANEKTRAEQALGALGNAADATEAKNKAHEAER 1427
DB 1356 GMKLQPPRPDQALQKADSVSDRLADTRKTKQAERMLGNAAPLSSSAKKKGREAEV 1415
QY 1428 IASAAQONATSTKADARTFGEVTDLDNVEVNGMLRL-EEAENELKRGQDDADQDMMWAG 1486
DB 1416 LAKDSAKLAKALLRERKQAHRRASRLTSQTQATLOQASQOVLASEARROELEAEAEVAG 1475
QY 1487 MASQAAQAEALNARKAKNSVSSLSOLNLLDOLGOLDT--VDLNKLNIEGSLNKADE 1544
DB 1476 LS-----EMQQIRESRISLEKDIETLSLLARLGSLDTHQAPALNETQWALERLQ 1530
QY 1545 M-KASDLDRKVSQDLESEARKQEAAMIDYNRDIAEIIKDINHLEDIKKTLP TGC 1596
DB 1531 LGSPGSLQKLSLLEQESQQELIQGFESDLAEIRADKQNLRAILHSLPENC 1583
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RESULT 13
US-08-317-450B-13
; Sequence 13, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,450B  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-317-450B-13

Query Match 29.8%; Score 2591; DB 1; Length 1193;  
Best Local Similarity 39.1%; Pred. No. 6.1e-147;  
Matches 510; Conservative 233; Mismatches 424; Indels 138; Gaps 13;

QY 317 CLPFPNDPWRATASASECLPCDCNGRSQECYFDPDELRYSTGGHCHTNCRDNTDGAK 376  
DB 9 CLCFLSLPAAATSRRE---VDCNGKSRQCIFDRELHEQTGNGFRCFLNCNDNTDGIH 64  
QY 377 CERENFRRLGNTACSPCHSPVGSLSQCDYSGRCCKPGVMGKDCRCQPHSLT 436  
DB 65 CEKCKNGFYRHRDRCLPCNCNKGSLARDCNSGRCKPGVTGARCDRLCPGFHMLT 124  
QY 437 EAGC-----RPGCDPFGSTDECNVETGRCKNVGFCNCRCKPGFPNLESNPK 488  
DB 125 DAGCTQDRLDLSKDCDPAIAGPC--DAGRCVKPAVTGERCDRCRSGYINLDGNPE 182  
QY 489 GCTPCFCFSGHSCVNTNAVGYVYDISSTFQIDEGWRVEQDGEASLEWSSDROYIAVI 548  
DB 183 GCTQFCYGHASCRSSAEYSHVHTITTFHODVDGKAVQVNGSPFALQMSQRQDVFSS 242  
QY 549 SDSYPRFYAPKVLGNQVLSYGNLTSFSPVDRDRRLSAEDLVLEAGLRVSVPLIA 608  
DB 243 AQLDPTVTFAPAKFLGNQVSYGSLSFYDVRGGRHPSAHDVILEGAGLRITAPLMP 302  
QY 609 QGNSYFSETTVKXIIFRLHEATDYPWRPALSPFQKLNLTSLKIRGTYSERSAGYLD 668  
DB 303 LGKTLPCGLTKTYTFLNEHPSNNWSPQSYFVYRRLRLNLTLRIATYGEYSTGYDN 362  
QY 669 VTLOSARPGVPATWVESCPCVYGGFCETCLPGYRRTPLSLGVPSPCVLCTCNHGS 728  
DB 363 VTLISARPVSGAPAPWVQCICPVYKGGFCQDCASGYKRSARLPGPGTCIPNCQG-G 421  
QY 729 EFTCDPETGVCDRDTAGPHCEKSDGYVGTSTLTGTSDDCQPCPCPGSSCAIYPKTKEV 788  
DB 422 GACDPTDTCYSGDENPDIEACDPCIGFVNDP--HDPKCPKPCCHNGFSCSVIPEEV 479  
QY 789 VTHCPTGTAGKRCBLDDGFGDPLGNGPVRCLRCPQCNDNDPNAVGNCLTGECL 848  
DB 480 VCNNGCPGVTGARCELCADGVDFGPHGVPVPCQCCNSNDPSASGNCRLTGRCL 539  
QY 849 KCIYNTAGYCDRCKEGFGNPLANPADKCKACACNYGTVQQSSCNFVTCQCCLPHV 908  
DB 540 KCIHNTAGYCDCKAGYFGDPLANPADKCAACN----- 576  
QY 909 SGRCDCGTDPGYNYLQSGGQCERCDCHALGSTNGQCDIRTGQCECQPGITQCHCERETN 968  
DB 577 ----- 576  
QY 969 HFGFGECKPCDCHHESLSLQCKDDGRCEGFGVGNRCDQCEENFYNRSWPGQCEC 1028

1029 PACYRLVKDKAAAEHRVKLELESILIANLGTGDVMVTDQAFEDRLKAEAREVVDLLREAOE 1088  
610 PACYNQVKIQMDQFMQQLQRMALISKAGGQGVVPDTELEGRMQQAQALQDILRDAQI 669  
1089 VKDVQNLMDRLQRVNSSLHSCISLQNIWRTIETGILAEARARSRVSTQOLIEASRE 1148  
670 SEGASRSLGLQAKVRSQENSYSQSLDLDLKMVTRVALGSGYQNRVDTHRLTKLQMLS 729  
1149 LEKAKMA-ANVSITQPESTGEPNNMTLLAEARRLAEHRHKEADDDIVRVAKTANETSAAE 1207  
730 LAESEASLQNTNIPASDHYVVGNGFKSLAQEAETRLAESHVESASNEQLTRETEDYSKQA 789  
1208 YNLLRLTL-----AGENQTALEIEELNRYKVEQAKNQSODLEKQAAARVHEBAKAGDKA 1260  
790 LSLVRKALHEGVGSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQHS 848  
1261 VEIYASVACLTPTVDSSEALE-NEANKIKKEAADLDLIDQKLKDYEDLREDMRGKEHVKN 1319  
849 LRLDSVSPLOGVSQVQVEEAKRIKQKADSLSSLVTRHMDPEFRTQKNLGNWKEEAQQ 908  
1320 LLEKGAEQCTADQLIARADAAKALAEAAKXGRSTLQFANDILNNLKDFFRRVNDNTA 1379  
909 LLQNGKSGREKSDQLLSRANLAKSRAQEAALSNGNATFYEVESILKNLREFDLQVDNRKAE 968  
1380 ABEALBRIPAINRTTAAANEKTRQAQLALGNAAADATKANKAHEAERTASAAQKNATST 1439  
969 ABEAKRLSYISQKVSADSKTQQAERALGSAADAAQAKNGAGALEISSIEIGSL 1028  
1440 KADAERTFGEVTDLQNVNGLRQLFEAEENELKRRQDDADQDMAGMASQAQAELNA 1499  
1029 NLEANTADGALAMEKGLASLAKSEMREVEGELERKELEBFTDNDVAVQMVITEAQKVDTRA 1088  
1500 RKANSVSSLQNLNLLDQLQDQTLVDLKNLEIEGSLNKADEKAKDEKASDLDRKYSDLES 1559  
1089 KNAGVTIQDTLNTLQGLLHMDQLSVDEEGVLVLEQKLSRAKTQIN-SQLRPMMSLEEE 1147  
1560 EARKQEAAMVDYNRDAEIIKHNLNEDIKTLPTGCFNTPSIEK 1604  
1148 RARQQRGHLHLETSIDGILADVKNLENIRDLNPPCYNTQALEQ 1192

RESULT 14  
US-08-800-593-13  
Sequence 13, Application US/08800593  
Patent No. 6143505  
GENERAL INFORMATION:  
APPLICANT: Tryggvason, Karl  
APPLICANT: Kallunki, Pekka  
APPLICANT: Pyke, Charles  
TITLE OF INVENTION: Laminin Chains: Diagnostic and  
TITLE OF INVENTION: Therapeutic Use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,593  
FILING DATE: 18-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/317,450  
FILING DATE: 04-OCT-1994

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-593-13

Query Match 29.8%; Score 2591; DB 3; Length 1193;
Best Local Similarity 39.1%; Pred. No. 6.1e-147;
Matches 510; Conservative 233; Mismatches 424; Indels 138; Gaps 13;

QY 317 CLPFDNDRPWRATAESASECLPCDCNGRSOEYFDPELYRSTGHGHCNCRDNTDGA 376
DB 9 CLCFSLLLPAPARSRRE----VDCNGKSRQCI FDRHLRQTNGFRCLNCNDNTDGIH 64
QY 377 CERCFENFRILNTEACSPCHSPVGSLSSTQDSYGRCSCKPGVMGDKDCQPGFHS 436
DB 65 CEKCKNGFYRHRERDRCLPCNCSKGLSARCDNSGRCSCKPGVTGARCDRLCPGFH 124
QY 437 EAGC-----RPSGCDPSGSTECEVETGRCVKCNVEGFCNCRKPGFNNLESNPX 488
DB 125 DAGCTQDQRLLDSKDCDPAIAGPC--DAGRCVKCPAVTGRCDCRSGYINLDGNGPE 182
QY 489 GCTPCFCGHSSVCTNAVYSYVDSISFTQIDEGWRVEQDSEASLEWSSDRQYIAYI 548
DB 183 GCTQCFYGHSSCHSSAEYSVHKITSFTFHQVDGKAVQNGSPAKLQWSQRHQDVFS 242
QY 549 SDSYFPRFIAPKVLGNQVLSYGNLSFSFRVDRDRTRLSAEDLVLEGRLVSPLIA 608
DB 243 AQRLDPVYFVAPAKFLNGQVSYGOSLFDYRDRGRHPSAHVDVILEGAGRLITAPLP 302
QY 609 QGNSVPSETTVKYIFRLHEATDYPRWPALSPFEFQKLNNLTSIKIRGTYSERSAGYLD 668
DB 303 LGKTLPCGLTKTYTFLRNLHSPNNWS PQLSYFEYERLLRNLTALRIRATYGEYSTG 362
QY 669 VTQSGARPGVPATWVESCPCVYGQGFCTCLPGYRRTPLSGPSPVCLTCNGHS 728
DB 363 VTLISAREVSGAPAPWVQCICPVYKQFCQDCASGYKRD SARLPGFGTCIPNCQG-G 421
QY 729 ETCDPDTGVCDRNDTAGPHCKSGDGYGDSLTGLTSSDCQPCPCPGSSCAIVPKTK 788
DB 422 GACDPTGDCVSGDENPDIEADCPIGYNDP--HDPKSCPCCHNGFSCSVIPETEEV 479
QY 789 VCHTCPTAGKRCBLCDGVFGDPLGNGPVRLCRPCQCNVDNDIDPNAVGNCLTGECL 848
DB 480 VCNNGCPVGTGARCELADGVFGDPFGSHGVPRPCQPCQCNNDVPSASGNCDELTRCL 539
QY 849 KCIYNTAGYCDRCKEGFGNPLAPNADKACACNYGTVCQSSCNPTVGQCQCLPHV 908
DB 540 KCIHNTAGYCDQCKAGYFGDPLAPNADKACRACN----- 576
QY 909 SGRCDCGTDPGYNYLQSGQGCRCRCDHALGSTNGQCDIRTGCECQPGITGQHCE 968
DB 577 ----- 576
QY 969 HFGFPGEGCKPCDCHHSGSLQCKDGRCECREGFGVGNRCQCEENFYNRSWPGQBC 1028
DB 577 -----PMGSEP-----VGRSDGTGCVCKPGFGPNCHE-----GAFSC 609
QY 1029 PACYRLVKDKAAHRVKLQELSLANLTGDMVTDQAFEDRLKEAREVTDLLRAQE 1088
DB 610 PACYNQVKIQMDFQWQLOQRMALLSKAGGGGVVPTDTELEGRMQAEQALQDILRAQ 669
QY 1089 VKVDQNLMDRLQRVNSLSHSQISRLQNTIETGTILAEARSRVESTQLIEASRE 1148
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DB 670 SEGASRLQLAKVRSQENSYSQSLDDDLKMTVERVRLGSGYQNRVDRTHLITQMQLS 729
QY 1149 LEKAKMA-ANVSIPTOPESTGEENNTLLAEERARRLAERHKBQADDIVRVAKTANETSAEA 1207
DB 730 LAESASLGNNTNPASDHVVGNGFKSLAQEAETRLAESHVESASNMEOQTRETEDYSKQA 789
QY 1208 YNLLRLTL-----AGENCATAETBELNRKYEQAKNISQDLEKQAARVHEEAKAGDKA 1260
DB 790 LSLVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSYQHS 848
QY 1261 VEIYASVAQLTPVDSEALE-NEANKIKKEADLDLIDQKLKDYEDLREDVRKKEHEVKN 1319
DB 849 LRLDLSVSPLOGVSDQSFQVEEAKRIKQKADSLSSLVTRHMDFFRTQKNLGNWKEBAQQ 908
QY 1320 LLEKKGAEQQTADQLLARADAAKALAEBAAKKGRSTLOEANDILNNLKFDRRVNDNTKA 1379
DB 909 LIQNGKSGREKSDQLLSRANLAKSRAQALSGNATFVEVESILKNLREFDLQVDRKAE 968
QY 1380 ABEALRRIPAINRTIAEANEKTRQAQLALGNAAADATAKNAKHAERIASAAQKNATST 1439
DB 969 ABEAMKRLSYISQKVSADSKTQQAERALGSAADAQRAKNGAGEALEISSIEQIGSL 1028
QY 1440 KADAERTFGEVTDLDNEVNGMLRQLEBAENELKQDDADQDMVAGMASQAAQAEALNA 1499
DB 1029 NLEANYTADGALAMEKGLASLKSEMEVEGELEKLEBFDITNDVAVQMVITEAQKVDTRA 1088
QY 1500 RKAQKSVSLLSQLNNLDPQLQDLTDVLDLKNLIEGSLINKAKDEMKASDLDKRVSDLES 1559
DB 1089 KNAGVTIQDTLNTDGLLHMDQLPSVDBEGLVLEQKLSRAKTQIN-SQLRPMMESEEE 1147
QY 1560 EARKQBAAMVDNRDIAETIKDIHNLDEIKKTLPTGCGFTPSIEK 1604
DB 1148 RARQQRGHLHLETSIDGILADVKNLIRDNLPFGCYNTQALEQ 1192

RESULT 15
US-08-317-4508-15
; Sequence 15, Application US/083174508
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,4508
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1111 amino acids
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:	TYPE:	amino acid
:	TOPOLOGY:	linear
:	MOLECULE TYPE:	protein
:	US-08-317-450B-15	
 Query Match            28.5%; Score 2476.5; DB 1; Length 1111; Best Local Similarity   39.4%; Pred. No. 4e-140;		
Matches	481; Conservative	215; Mismatches 389; Indels 137; Gaps 12;
QY	317	CLPFFNDPRWRRATASASACLCDGNGRSGEQCYFDPBELYSTGHGHCTNCRDNTDGAK 376
DB	9	CLCFSLLLPAAARTSRRE----VDCDNGKRGQCIFDLRLHRTQTGNRCUNCNDNTDGIH 64
QY	377	CERCENFFRLNGTEACSPCHCSVPVGSLSLTCDSYGRCSCCKPGVMGDKDRCPGFPHSLT 436
DB	65	CEKCKNGFYHRERDRCLPCNCSKGSLSARCDNSGRCSCKPGVTGARCDRLCGPFEMLT 124
QY	437	EAGC-----APCSDPSGSTDECNVETGRCVCXKDNVEGFCNERCKPFGFFNLSENPK 488
DB	125	DAGCTPDQRLLDSKDCDDCFAGIAPC--DAGRVCVKFAVTRGERCDRCRGGYNLDGNPE 182
QY	489	GCTPCFCFHSSVCTNAVGYSVDYISFTFOIDEDGMREVORDGESEASLEWSRQXIAYI 548
DB	183	GCTQCFCYGHSAACRSAAEYSVHKITSTFHQVDVGKAVQNGSPAKLQWSRHQDVFS 242
QY	549	SDSYFPPIPTAPVKFLGNQLSVLQSFRVDRDRTRLISAEDLVLEGAGLRVSUPLIA 608
DB	243	AQRLLDPYVFAPAKFLGNQQVSYQSLSFYRVDRGRHFSAHDVILEGAGLRITAPLM 302
QY	609	QGSNPSETTVKIYFLHEATDVPWRALSPFFOKLLNNLTSTIKIGTYSERASGYLDD 668
DB	303	LKTLPLGLTKTYTFLRNEHPSNWSQLSYFEVRLRLNLTALRIATYGEYSTGVIND 362
QY	669	VTLQSRPPGPVPATWVESCTPVYGGQFCETCLPGYRRETSLGYPSPCVILCTCNHGS 728
DB	363	VTLISARFVSGAPAWVEYQCICPVYGRQGFCQDCASGYKRDSARLGPPGTICPNCOG-G 421
QY	729	ETCDPETGVCDDRNTAGPCEKSDCYGDBGSLGTSSDCQPCPCPGGSSCAIVPKTKEV 788
DB	422	GACDPDTGDCVSGDENPDI ECADCPIGYNDP--HDFPSCKPCPCCHNGFSCSVIPETE 479
QY	789	VCTHCPTGTAGKRCELCDDGYFGDPLSGNFVRLCRPCQNCDNIIDPNAVGNCRNLTGCEL 848
DB	480	VCNCCPPGVTVGARCCLCADGYFGDPPFGEHGFPVRPCQCQCNNSVNDPSAGNCRLTGRL 539
QY	849	KCIYNTAGFVCDRCKEGFFGNPLAPNADKKACACNYGVVQOQSSCNPYTGQCCLPHV 908
DB	540	KCIHTNTAGICYDQCKAGYFGDPLAPNADKKACACN----- 576
QY	909	SGRDCGTGCDPYNQLSQGCRCERCDCHALAGSTNQCDIRTCQCECPGIGTQHCCERTN 968
DB	577	----- 576
QY	969	HFGPGPGCKPCDCHHSGLSLQCKDGRCECRGFGVGNRCDOCEEYFNYSWPQCQEC 1028
DB	577	-----PMGSEP-----VGCRRSDGTCVKFGFGPNCEH-----GAFSC 609
QY	1029	PACYRLVKDKAAAEHRVKLOELSLIANLGTGDDMVTDQAPEDRLKEAREVETDLLRAQE 1088
DB	610	PACINYVKIQMDQFMQOLQRMIALSKAQGGDGVVPDTELEGRMQQAEOALQDLIRDAQI 669
QY	1089	VKDQDNLMDRLQRVNSLSHQISRLLQNRINTIEETGILAEARSARVESTEQLIETIASRE 1148
DB	670	SEGASRLGLQAKVRSGENSYSQRLDCLKMTVERVRVALGSGYQNVVRDTHRLITQMQLS 729
QY	1149	LEKAKMA-AVNSITQPSTGSPNNMWTLLABEARILAERHHKOEADDIVRVAKTANETSAAE 1207
DB	730	LAESASLGNTNII PASHYIVCPNGFKSLAQEAETHLAESHVESASNMQFLTREDYISKQA 789
QY	1208	YNLLRLTI-----AGENOTALFEEELNRKYEQAKNISODLEKOAARVVHEAKRAGDKA 1260
DB	790	LSLVRKALHEGVGSGSGSPDGAV-VQGLEVKLETKSLAQOLTREATQATCAIEADRYSQHS 848

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 40.8326 Seconds

(without alignments)  
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Title: US-10-037-182-18

Perfect score: 8594

Sequence: 1 MTGGGAALALQPRGLWPL.....EDIKTLPTGCFNTPSIEKP 1605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	8627	99.2	1607	9	US-09-938-275-10
3	8527	98.1	1572	14	US-10-037-182-20
4	8148	93.7	1609	14	US-10-037-182-14
5	8148	93.7	1609	14	US-10-299-058-12
6	8144	93.7	1609	9	US-09-938-275-11
7	8144	93.7	1609	15	US-10-372-683-36
8	8043	92.5	1576	14	US-10-037-182-16
9	3596.5	41.4	1587	9	US-09-845-583-10
10	3596.5	41.4	1587	12	US-10-262-839-210
11	3593.5	41.3	1575	12	US-10-262-839-212
12	3393	36.7	1557	15	US-10-369-493-6816
13	2592	29.8	1193	12	US-10-392-113-14
14	2592	29.8	1193	14	US-10-171-311-115
15	2592	29.8	1193	14	US-10-053-662A-31

# ALIGNMENTS

## RESULT 1

US-10-037-182-18  
; Sequence 18, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-18

Query Match	100.0%	Score 8694;	DB 14;	Length 1605;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1605;	Conservative	0;		Gaps 0;
Qy	1	MTGGGAALALQPRGLWPLLA	VLA	AAVAGCVRAAMDECADEGGRCPCMCPEFVNAAFNVT 60
Db	1	MTGGGAALALQPRGLWPLLA	VLA	AAVAGCVRAAMDECADEGGRCPCMCPEFVNAAFNVT 60
Qy	61	VVAATNCGTPPEYCVQVTGVT	SKSCHL	CDAGQQHQAFLTYNNQADTTWQSQ 120
Db	61	VVAATNCGTPPEYCVQVTGVT	SKSCHL	CDAGQQHQAFLTYNNQADTTWQSQ 120
Qy	121	MLAGVQYPSINLTHLGKAFD	ITYRLK	FHTSPESFAIKRTREDGPWIPYQYSGSC 180

Sequence 390, App  
Sequence 1269, Ap  
Sequence 147, App  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 26, Appl  
Sequence 28, Appl  
Sequence 30, Appl  
Sequence 2, Appl  
Sequence 32, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 12, Appl  
Sequence 32, Appl  
Sequence 34, Appl  
Sequence 7, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 113, App  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 8, Appl  
Sequence 7, Appl  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 5220, Ap  
Sequence 5221, Ap

Db 121 MLAGVQVPSINLTLHLGKAFDITVYRLKFTSRPESFAIYKRTREDGPIWIPQYISGSC 180  
QY 181 ENTYSKANRGFIRTGDEQQALCTDEFSDI SPLTGGNVAFSTLEGRPSAYNFNDS PVLQE 240  
Db 181 ENTYSKANRGFIRTGDEQQALCTDEFSDI SPLTGGNVAFSTLEGRPSAYNFNDS PVLQE 240  
QY 241 WVTATDIRVTINRLNTFGDEVNPKVLKSYVYAI SDPAVGGRCCKNGHASECVKNEFDK 300  
Db 241 WVTATDIRVTINRLNTFGDEVNPKVLKSYVYAI SDPAVGGRCCKNGHASECVKNEFDK 300  
QY 301 LMCNCKHNTYGVDEKCLPFNDPRWRATAESASECLPCDCNCRSQCEYFDPPELYRSTG 360  
Db 301 LMCNCKHNTYGVDEKCLPFNDPRWRATAESASECLPCDCNCRSQCEYFDPPELYRSTG 360  
QY 361 HGGHCTNCRDNTDGAACBRCEBNTFRNGTACSPCHCS PVSLSLSTQCDYSGRCSCKPGV 420  
Db 361 HGGHCTNCRDNTDGAACBRCEBNTFRNGTACSPCHCS PVSLSLSTQCDYSGRCSCKPGV 420  
QY 421 MGDKCDRCQPGFHSLTEAGRCPCSDPSGSDENCVETGRVCCKDNVEGFCNCRCKPGFF 480  
Db 421 MGDKCDRCQPGFHSLTEAGRCPCSDPSGSDENCVETGRVCCKDNVEGFCNCRCKPGFF 480  
QY 481 NLESGNPKGCTPCFCFGHSSVCTNAVGSVYDI SSTFQIDBDGWRVQRQDGESEASLEWSS 540  
Db 481 NLESGNPKGCTPCFCFGHSSVCTNAVGSVYDI SSTFQIDBDGWRVQRQDGESEASLEWSS 540  
QY 541 DROXTAVISDSVFPYFTAPVKELGNQVLSYGQNLSPSFRVDRDRDTRL SAEIDLVEGAGL 600  
Db 541 DROXTAVISDSVFPYFTAPVKELGNQVLSYGQNLSPSFRVDRDRDTRL SAEIDLVEGAGL 600  
QY 601 RVSVPLIAQGSYPSETTVKYIFRLHEATDYPMPALSPFPEFQKLNNLTSIKIRGYSE 660  
Db 601 RVSVPLIAQGSYPSETTVKYIFRLHEATDYPMPALSPFPEFQKLNNLTSIKIRGYSE 660  
QY 661 RSAGYLDVDTLQSAHPGPGVATVWESCTCPVGGQPCERCLGYSRETPSLGYPSPCV 720  
Db 661 RSAGYLDVDTLQSAHPGPGVATVWESCTCPVGGQPCERCLGYSRETPSLGYPSPCV 720  
QY 721 LCTCNHGETCDPETGVDCDRDNTAGPHCEKCSGDIYGDSTLGTSSDCQPCPCPGGSSCA 780  
Db 721 LCTCNHGETCDPETGVDCDRDNTAGPHCEKCSGDIYGDSTLGTSSDCQPCPCPGGSSCA 780  
QY 781 IVPKTEVWVCHTCTGTAGKRCCLDDGYFGDPLGSGNPVRLCRPCQCNNDIDNVAVNC 840  
Db 781 IVPKTEVWVCHTCTGTAGKRCCLDDGYFGDPLGSGNPVRLCRPCQCNNDIDNVAVNC 840  
QY 841 NRLTCECLKCIINTAGFYCDRCKEGFGNPLAPNADKCKACACNYGTVOQSSCNFVTG 900  
Db 841 NRLTCECLKCIINTAGFYCDRCKEGFGNPLAPNADKCKACACNYGTVOQSSCNFVTG 900  
QY 901 QCQCLPHVSGRDCGTCDPGYVNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGITG 960  
Db 901 QCQCLPHVSGRDCGTCDPGYVNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECQPGITG 960  
QY 961 HCERCETHHFGPGSKPCDCHHSGSLQCKDDGRCEGFGVGNRCDOCEENYFNR 1020  
Db 961 HCERCETHHFGPGSKPCDCHHSGSLQCKDDGRCEGFGVGNRCDOCEENYFNR 1020  
QY 1021 SWFGQCECPACVRLVKDAAEHRVKLQBLESIANLGTGDDMTDQAFEDKLKAEREV 1080  
Db 1021 SWFGQCECPACVRLVKDAAEHRVKLQBLESIANLGTGDDMTDQAFEDKLKAEREV 1080  
QY 1081 DLLREAEQVKDQNDMLRQVNSLSHSQISRLQNIINTIETGILAEARARSVESTEQ 1140  
Db 1081 DLLREAEQVKDQNDMLRQVNSLSHSQISRLQNIINTIETGILAEARARSVESTEQ 1140  
QY 1141 LIEIASRELEKAKMAANVSITQESTGEPNNMTLLAEABARLAEHRHKEADDIRVAKTA 1200  
Db 1141 LIEIASRELEKAKMAANVSITQESTGEPNNMTLLAEABARLAEHRHKEADDIRVAKTA 1200  
QY 1201 NETSAPAYNLLRLTAGENQTALEIELNRYEQAKNISQDLEKQAAHVHEEAKRGDKA 1260  
Db 1201 NETSAPAYNLLRLTAGENQTALEIELNRYEQAKNISQDLEKQAAHVHEEAKRGDKA 1260

## RESULT 2

US-09-938-275-10

; Sequence 10, Application US/09938275

; Patent No. US20020111309A1

; GENERAL INFORMATION:

; APPLICANT: Gerardo Castillo

; APPLICANT: Alan Snow

; TITLE OF INVENTION: Therapeutic and Diagnostic Applications

; FILE REFERENCE: PRONTO.P03

; CURRENT APPLICATION NUMBER: US/09/938,275

; CURRENT FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 1607

; TYPE: PRT

; ORGANISM: Mus Musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Swissprot P02468

; DATABASE ENTRY DATE: 1989-07-01

; US-09-938-275-10

Query Match 99.2%; Score 8627; DB 9; Length 1607;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1598; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 1 MTGGGAAALALQPRGLWPLLAVALVAGCVRAAMDECADEGGRPQRCMPFVNAAFNVT 60

Db 1 MTGGGAAALALQPRGLWPLLAVALVAGCVRAAMDECADEGGRPQRCMPFVNAAFNVT 60

QY 61 VVATNCTGTPPEYCVQGTGVTGKSCLDAGQOHLQHGAAFLTDYNNQADTTWQSQ 120

Db 61 VVATNCTGTPPEYCVQGTGVTGKSCLDAGQOHLQHGAAFLTDYNNQADTTWQSQ 120

QY 121 MLAGVQVPSINLTLHLGKAFDITVYRLKFTSRPESFAIYKRTREDGPIWIPQYISGSC 180

Db 121 MLAGVQVPSINLTLHLGKAFDITVYRLKFTSRPESFAIYKRTREDGPIWIPQYISGSC 180

QY 181 ENTYSKANRGFIRTGDEQQALCTDEFSDI SPTGGNVAFSTLEGRPSAYNFNDS PVLQE 240

Db 181 ENTYSKANRGFIRTGDEQQALCTDEFSDI SPTGGNVAFSTLEGRPSAYNFNDS PVLQE 240

QY 241 WVTATDIRVTINRLNTFGDEVNPKVLKSYVYAI SDPAVGGRCCKNGHASECVKNEFDK 300

Db 241 WVTATDIRVTINRLNTFGDEVNPKVLKSYVYAI SDPAVGGRCCKNGHASECVKNEFDK 300



QY 301 LMCNCKHNTGYDCEKCLPFNDPWRPATAESASECLPCDCNGRSECEYFDPBELYSTG 360  
DB 301 LMCNCKHNTGYDCEKCLPFNDPWRPATAESASECLPCDCNGRSECEYFDPBELYSTG 360  
QY 361 HGGHCTNCRDNTDGAACRERENFFRLGNTACSPCHCSFVGSLSSTQDSYGRCSCKPGV 420  
DB 361 HGGHCTNCRDNTDGAACRERENFFRLGNTACSPCHCSFVGSLSSTQDSYGRCSCKPGV 420  
QY 421 MGDKCDRCQPGPHSLTEAGCRPCSDPSGSDTECNVETGRVCCKDNVGGNCRCKPGFF 480  
DB 421 MGDKCDRCQPGPHSLTEAGCRPCSDPSGSDTECNVETGRVCCKDNVGGNCRCKPGFF 480  
QY 481 NLESNPKGCTPCFCGHSSVCTNAGVSVYD1SSTFOIDEDGWRVQRDGESEASLEWSS 540  
DB 481 NLESNPKGCTPCFCGHSSVCTNAGVSVYD1SSTFOIDEDGWRVQRDGESEASLEWSS 540  
QY 541 DRQYLAIVSDSYFPRYFAPVKFLGNQVLSYQNLISFSDRDRDTRLSAEDVLGAGL 600  
DB 541 DRQYLAIVSDSYFPRYFAPVKFLGNQVLSYQNLISFSDRDRDTRLSAEDVLGAGL 600  
QY 601 RVSVPLIAQNSPSETTKYIFRLHEATDYPWPALSPFQKLLNNLTSIKIRTYSE 660  
DB 601 RVSVPLIAQNSPSETTKYIFRLHEATDYPWPALSPFQKLLNNLTSIKIRTYSE 660  
QY 661 RSAGYLDVDTLOSAPGPGVATWVESCTCPVGGGFCETCLPGYRRETPSLGPYSPCV 720  
DB 661 RSAGYLDVDTLOSAPGPGVATWVESCTCPVGGGFCETCLPGYRRETPSLGPYSPCV 720  
QY 721 LCTNGHSETCDPETHGVCDCRNTAGPHEKCSGYYGDSLTGTSQCPQPGSSCA 780  
DB 721 LCTNGHSETCDPETHGVCDCRNTAGPHEKCSGYYGDSLTGTSQCPQPGSSCA 780  
QY 781 IVPKTEVVVCHTGTAGKCELCDDGYFGDPLGSGPVRLCRPCQCNNDIPNAVNC 840  
DB 781 IVPKTEVVVCHTGTAGKCELCDDGYFGDPLGSGPVRLCRPCQCNNDIPNAVNC 840  
QY 841 NRLTGECLKIYNTAGFYCDRCKGFFONPLAPNADKACACN - YGTVOQSSCNPT 899  
DB 841 NRLTGECLKIYNTAGFYCDRCKGFFONPLAPNADKACACN - YGTVOQSSCNPT 900  
QY 900 GOCQCLPVSGRDCTDPGYNLSQGGCERCDCCHALGSTNGQCDRTGQCQPGITG 959  
DB 901 GOCQCLPVSGRDCTDPGYNLSQGGCERCDCCHALGSTNGQCDRTGQCQPGITG 960  
QY 960 QHCERTNHFPGPEGKPCDCHHEGSLSLQCKDDGRCEGFGVNRCDQCEENFYN 1019  
DB 961 QHCERTNHFPGPEGKPCDCHHEGSLSLQCKDDGRCEGFGVNRCDQCEENFYN 1020  
QY 1020 RSWPCCQCPACRYLVKDKAAEHVQLQELSLIANLGTGDMVTDQAFDRLEKAREV 1079  
DB 1021 RSWPCCQCPACRYLVKDKAAEHVQLQELSLIANLGTGDMVTDQAFDRLEKAREV 1080  
QY 1080 TDLLEAEQVKDQNLMDRLQVRNSSLHSQISRLQNRNTIETGILABRARSVESTE 1139  
DB 1081 TDLLEAEQVKDQNLMDRLQVRNSSLHSQISRLQNRNTIETGILABRARSVESTE 1140  
QY 1140 QLIETASRELEKAKM - AANVSI TOPESTGEPNNVTLAEARLAEHRKQEAADDIVRVAK 1198  
DB 1141 QLIETASRELEKAKM - AANVSI TOPESTGEPNNVTLAEARLAEHRKQEAADDIVRVAK 1200  
QY 1199 TANETSABAYNLLLTLAGENQTALEIBELNRKYEQAQNISQDLEKQAAHVHEAKRAGD 1258  
DB 1201 TANETSABAYNLLLTLAGENQTALEIBELNRKYEQAQNISQDLEKQAAHVHEAKRAGD 1260  
QY 1259 KAVEIYASVAQLTPVDSALNEANKIKKEAADDRLIDQKLDYEDLRDMGKEHEVK 1318  
DB 1261 KAVEIYASVAQLTPVDSALNEANKIKKEAADDRLIDQKLDYEDLRDMGKEHEVK 1320  
QY 1319 NLEKGAEQQTADOLLARADAALAEAAKGRSTLQEBANDILNNKDFDRVNDNKT 1378  
DB 1321 NLEKGAEQQTADOLLARADAALAEAAKGRSTLQEBANDILNNKDFDRVNDNKT 1380  
QY 1379 AAEEALRRIIPAINRTIAEANEKTRQAQLAGNAADATEAKNKAHEAERTASAVQKNATS 1438

DB 1381 AAEEALRRIIPAINRTIAEANEKTRQAQLAGNAADATEAKNKAHEAERTASAVQKNATS 1440  
QY 1439 TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRXQDDADQDMMAGMASQAQAEALN 1498  
DB 1441 TKADAERTFGEVTDLDNEVNGMLRQLEEAENELKRXQDDADQDMMAGMASQAQAEALN 1500  
QY 1499 ARKAKNSVSSLSLQNLNLLDOLGOLDIVDLNKLNEIEGSLNKAKDEMKAASDLDRKVSJLE 1558  
DB 1501 ARKAKNSVSSLSLQNLNLLDOLGOLDIVDLNKLNEIEGSLNKAKDEMKAASDLDRKVSJLE 1560  
QY 1559 SEARKQEAAMIDYNDRTIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605  
DB 1561 SEARKQEAAMIDYNDRTIAEIIKDIHNLEDIKKTLPTGCFNTPSIEKP 1607

## RESULT 3

US-10-037-182-20  
; Sequence 20, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-20

Query Match 98.1%; Score 8527; DB 14; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 AMDECADEGGPQRCMPEFVNAAFNVTVAATNTCGTPPEYCVQGTGVTGKLSCHLADAG 93  
DB 1 AMDECADEGGPQRCMPEFVNAAFNVTVAATNTCGTPPEYCVQGTGVTGKLSCHLADAG 60  
QY 94 QOHLQHGAAFLTDYNNQADTTWQSOTMLAGVOYPSINLTLLHKGAFDITYVRLAFHTS 153  
DB 61 QOHLQHGAAFLTDYNNQADTTWQSOTMLAGVOYPSINLTLLHKGAFDITYVRLAFHTS 120  
QY 154 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFFSDISPL 213  
DB 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFFSDISPL 180  
QY 214 TGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTTATDIRVTNLRLNTFGDEVNDPKVLKSYV 273  
DB 181 TGGNVAFSTLEGRPSAYNFDSNPSVLQEWVTTATDIRVTNLRLNTFGDEVNDPKVLKSYV 240  
QY 274 AISDFAVGRCCKNGHASECVQNEFQKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 333  
DB 241 AISDFAVGRCCKNGHASECVQNEFQKLMCNCKHNTYGVDCCKLPFFNDRPWRRTAES 300  
QY 334 ASECLPCDCNGRSECEYFDPBELYRSTGHGHCCTNCDNTDGAACRERENFFRLGNTAEAC 393  
DB 301 ASECLPCDCNGRSECEYFDPBELYRSTGHGHCCTNCDNTDGAACRERENFFRLGNTAEAC 360  
QY 394 SPCHCSFVGSLSSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGSTDE 453  
DB 361 SPCHCSFVGSLSSTQDSYGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPSGSTDE 420  
QY 454 CNVETGRVCCKDNVGGNCRCKPGFPNLESSNPKGCTPCFCFGHSSVCTNAGVSVYDI 513

Db 421 CNVETGCVCKNDVGEFNCERCKPGFNFENSSNPKGCTPCFCGHSSVCTNAVGSYDI 480  
Qy 514 SSTFQIDEDGWRVQROGSSEASLEWSSDROYIAVISDSYPRFYFIAPVKELGNVLSYGQ 573  
Db 481 SSTFQIDEDGWRVQROGSSEASLEWSSDROYIAVISDSYPRFYFIAPVKELGNVLSYGQ 540  
Qy 574 NLSFSFRVDRADTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 633  
Db 541 NLSFSFRVDRADTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
Qy 634 RPALSPFEKLLNNLSIKIRGYISRSAGYLDVTLQSRAPGPGVPAWVWSCPCPVG 693  
Db 601 RPALSPFEKLLNNLSIKIRGYISRSAGYLDVTLQSRAPGPGVPAWVWSCPCPVG 660  
Qy 694 YGGQFCETCLPGYRRETFSLGYPFCVLCCTCNHSETCDPETGYCDRDNATAGPHEKCS 753  
Db 661 YGGQFCETCLPGYRRETFSLGYPFCVLCCTCNHSETCDPETGYCDRDNATAGPHEKCS 720  
Qy 754 DGYGDSLTGSSDCQPCPCPGGSSCAIVPKTKWCTHCTGTAGRCCLDDGYFGDP 813  
Db 721 DGYGDSLTGSSDCQPCPCPGGSSCAIVPKTKWCTHCTGTAGRCCLDDGYFGDP 780  
Qy 814 LGSNGPVRLCPCQCNNDNDNAYGNCNRLTGECLKCIYNTAGFYCDRCKEGFGNPLAP 873  
Db 781 LGSNGPVRLCPCQCNNDNDNAYGNCNRLTGECLKCIYNTAGFYCDRCKEGFGNPLAP 840  
Qy 874 NPADKCKACANYGVQOQSCNPNVTGQCQCLPHVSGRDCGTCDPGYNLSQGGCERCD 933  
Db 841 NPADKCKACANYGVQOQSCNPNVTGQCQCLPHVSGRDCGTCDPGYNLSQGGCERCD 900  
Qy 934 CHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGPCGKPCDCHHEGSLSLQCK 993  
Db 901 CHALGSTNGQCDIRTGQCECQPGITGQHCERCETNHFGFEGPCGKPCDCHHEGSLSLQCK 960  
Qy 994 DDGRCCEGFGVGNRCDQCBENYFNRSWPCQCEPCACRYLVKDKAAHVRVKGLESLI 1053  
Db 961 DDGRCCEGFGVGNRCDQCBENYFNRSWPCQCEPCACRYLVKDKAAHVRVKGLESLI 1020  
Qy 1054 ANLGTGDDNVTDQAFEDRLKAEAREVTDLLREAOBKVDQNDLRLQVNSSLSHSOISR 1113  
Db 1021 ANLGTGDDNVTDQAFEDRLKAEAREVTDLLREAOBKVDQNDLRLQVNSSLSHSOISR 1080  
Qy 1114 LQNIIRNTIETGILAEARSRVSETEQIEIASRELEKAKAAVNSITQPESTGEPNMT 1173  
Db 1081 LQNIIRNTIETGILAEARSRVSETEQIEIASRELEKAKAAVNSITQPESTGEPNMT 1140  
Qy 1174 LLAEARLAEHKEADDIRVAKTANETSAEAVNLLRLTAGENOTALFIEELNRKYE 1233  
Db 1141 LLAEARLAEHKEADDIRVAKTANETSAEAVNLLRLTAGENOTALFIEELNRKYE 1200  
Qy 1234 QAKNISQDLEKQAAVHBEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293  
Db 1201 QAKNISQDLEKQAAVHBEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260  
Qy 1294 RLIDOKLDYEDLRDMRGEHEVKNLLEKGAEOQTADQLARADAKALAEAAKGR 1353  
Db 1261 RLIDOKLDYEDLRDMRGEHEVKNLLEKGAEOQTADQLARADAKALAEAAKGR 1320  
Qy 1354 STLQANDLNNLKQDFDRVNDKTAABEALRRIPAINRTIAEANEKTRQAALGNAAA 1413  
Db 1321 STLQANDLNNLKQDFDRVNDKTAABEALRRIPAINRTIAEANEKTRQAALGNAAA 1380  
Qy 1414 DATEAKNKAHEARLAEASAKKATSTKADAEFTFGEVTDLDNEVNGMLRQLEBAENELKR 1473  
Db 1381 DATEAKNKAHEARLAEASAKKATSTKADAEFTFGEVTDLDNEVNGMLRQLEBAENELKR 1440  
Qy 1474 KQDDADQDDMMAGMSQAQAQAEALNARKAKNSVSLLSQNLNLDQLQDQDVLINKLINE 1533  
Db 1441 KQDDADQDDMMAGMSQAQAQAEALNARKAKNSVSLLSQNLNLDQLQDQDVLINKLINE 1500  
Qy 1534 IEGSLNKAKDEMKAESDLDRKVSLESEARKQBAAMDNVNDIAEIIKDIHNLEDIKKTLP 1593

Db 1501 IEGSLNKAKDEMKAESDLDRKVSLESEARKQBAAMDNVNDIAEIIKDIHNLEDIKKTLP 1560  
Qy 1594 TGCFTNPSIEXP 1605  
Db 1561 TGCFTNPSIEXP 1572  
RESULT 4  
US-10-037-182-14  
; Sequence 14, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-14  
Query Match 93.7%; Score 8148; DB 14; Length 1609;  
Best Local Similarity 92.8%; Pred. No. 0;  
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;  
Qy 1 MTGGRAALALOPRGELMPLLAVAL--AAVAGCVRAAMDECADEGGRCPORCMPEFVNAAFN 58  
Db 1 MRGSHRAAPALPRGLMPVLAVALAAAGCAQAADECTDEGGRCPORCMPEFVNAAFN 60  
Qy 59 VTVAINTCGTPPEYCVQTVGTGVTGKCHLCAQOHLQGAALFTDYNQADTTWQS 118  
Db 61 VTVAINTCGTPPEYCVQTVGTGVTGKCHLCAQOHLQGAALFTDYNQADTTWQS 120  
Qy 119 QTMLAGVQVPSNINLTLLHGKAFDITVRLKHTSRPESFAYIKRTREDGMPWIPYQYISG 178  
Db 121 QTMLAGVQVPSNINLTLLHGKAFDITVRLKHTSRPESFAYIKRTREDGMPWIPYQYISG 180  
Qy 179 SCENTYSKANRGFIRTGDEQALCTDFSDISPLTGGNVAPSTLEGRPSAIFNDSVPL 238  
Db 181 SCENTYSKANRGFIRTGDEQALCTDFSDISPLTGGNVAPSTLEGRPSAIFNDSVPL 240  
Qy 239 QEWTTATDIRVTLNRLNLTGDEVNDPKVLKSYVVAISDFAVGGRCCKNGHASECVKNEF 298  
Db 241 QEWTTATDIRVTLNRLNLTGDEVNDPKVLKSYVVAISDFAVGGRCCKNGHASECVKNEF 300  
Qy 299 DKLMCKENKTYGVDCCKCLPFNDPRMRRATAESASCLPCDCNRSQECYFDPDELAYS 358  
Db 301 DKLMCKENKTYGVDCCKCLPFNDPRMRRATAESASCLPCDCNRSQECYFDPDELAYS 360  
Qy 359 TGHGCHTNCNRTNDQAKCERENFFRLNGNTEACSPCHSPVGSISTOCDSYGRCSCKP 418  
Db 361 TGHGCHTNCNRTNDQAKCERENFFRLNGNTEACSPCHSPVGSISTOCDSYGRCSCKP 420  
Qy 419 GVMGDKCDRCQPGFHSLLTEAGRCPCDPSGSDTECNVETGRCVCKDNVEGNCERCKPG 478  
Db 421 GVMGDKCDRCQPGFHSLLTEAGRCPCDPSGSDTECNVETGRCVCKDNVEGNCERCKPG 480  
Qy 479 FFMLESNPKGCTPCFCFHSSVCTNAVGSYVDVSSSTFQIDEDGWRVQROGSSEASLEW 538  
Db 481 FFMLESNPKGCTPCFCFHSSVCTNAVGSYVDVSSSTFQIDEDGWRVQROGSSEASLEW 540  
Qy 539 SSDRQYIAVISDSYPRFYFIAPVKELGNVLSYQNLSPFRVDRDTRLSAEDLVLEGA 598

541 SSERQDIAVSDSYFPRYFIAPAKFLGKQVLSYQNLSPFRVDRDRTRLAEDLVLEGA 600  
QY GLRVSVPJLAQNSVPBETTKYIFRLHEATDYPRPALSPFEPQKLLNLTSLKIRGT 658  
Db GLRVSVPJLAQNSVPBETTKYIFRLHEATDYPRPALSPFEPQKLLNLTSLKIRGT 660  
QY SERSAGYLDVTLQASRPGVPATWBSCTCPVYGQFCETCLPGYRRETPSLGPSP 718  
Db SERSAGYLDVTLQASRPGVPATWBSCTCPVYGQFCETCLPGYRRETPSLGPSP 720  
QY CVLCTNGHSTCDPBTGVCDCRONTAGPHCEKSDGYGDSSTLGTSSDCQPCPGSS 778  
Db CVLCAQNSHSTCDPBTGVCDCRONTAGPHCEKSDGYGDSSTLGTSSDCQPCPGSS 780  
QY CAIVPKTEVCTHCTGTAGKRCCLDDGDFGDPGLSGNSGPRVLCRQCNDINDPNAV 838  
Db CAIVPKTEVCTHCTGTAGKRCCLDDGDFGDPGLSGNSGPRVLCRQCNDINDPNAV 840  
QY NCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADCKKACACN-YGTVOQSSCNP 897  
Db NCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADCKKACACN-PYGTMTKQSSCNP 900  
QY VTGQCQCLPHVSGRDCGTCDFGYNLSQSGCCERCDCHALGSTNGQCDIRTGQCEQPGI 957  
Db VTGQCQCLPHVSGRDCGTCDFGYNLSQSGCCERCDCHALGSTNGQCDIRTGQCEQPGI 960  
QY TGOHCERCETNHFQFEGEGCKPCDCHHEGSLSLQCKDDGRCCEBGFVGNRCQCBENYF 1017  
Db TGOHCERCETNHFQFEGEGCKPCDCHHEGSLSLQCKDDGRCCEBGFVGNRCQCBENYF 1020  
QY YNRSPWGOECPACVRLVKDAAEHRVKLQLESILANLGTGDDVTDQAFEDRLKEABR 1077  
Db YNRSPWGOECPACVRLVKDAAEHRVKLQLESILANLGTGDDVTDQAFEDRLKEABR 1080  
QY EVTDLLREAEQVQDQNLMDRLQRVNSSLHSQISRLQNTINTIETGILAEARSVES 1137  
Db EVTDLLREAEQVQDQNLMDRLQRVNSSLHSQISRLQNTINTIETGILAEARSVES 1140  
QY TEQILIASRELEKAKM-AANVSTOPESTGEFNNMTLLAEABRLAEHRKQEDDIVR 1196  
Db TEQILIASRELEKAKM-AANVSTOPESTGEFNNMTLLAEABRLAEHRKQEDDIVR 1200  
QY AKTANETSAEAYNLLRTLAGENQTALEIEELNRYEQAKNISQLEKQAAARVHEEA 1256  
Db AKTANETSAEAYNLLRTLAGENQTALEIEELNRYEQAKNISQLEKQAAARVHEEA 1260  
QY GDKAVEIYASVAQITPVDSEALENEANKIKKEAADLRLIDOKLKOYEDLREDMRGKEHE 1316  
Db GDKAVEIYASVAQITPVDSEALENEANKIKKEAADLRLIDOKLKOYEDLREDMRGKEHE 1320  
QY VKNLLEKGAQOQTADQLLARADAAKALAEAAKKGRTSLQEAANDILNLLKQDPRRVNDN 1376  
Db VKNLLEKGAQOQTADQLLARADAAKALAEAAKKGRTSLQEAANDILNLLKQDPRRVNDN 1380  
QY KTAABEALRRIPALNRTIAENETRAQALGNAADATEAKNAHEABRISAAQKNA 1436  
Db KTAABEALRRIPALNRTIAENETRAQALGNAADATEAKNAHEABRISAAQKNA 1440  
QY TSTKADAEKTEGVTDLNENVMGLRQLEAEENELKQKDDADQMMAGMASQAQAEAE 1496  
Db TSTKADAEKTEGVTDLNENVMGLRQLEAEENELKQKDDADQMMAGMASQAQAEAE 1500  
QY LNAKAKNSVSLLSQNLNLLDQIGOLDVTDNLKNEIEGSLNKAEMKASDLDRKVS 1556  
Db LNAKAKNSVSLLSQNLNLLDQIGOLDVTDNLKNEIEGSLNKAEMKASDLDRKVS 1560  
QY LESSEARQEAAMNDYNDIARIIIDHNLEIDIKTTLPTGCFNTPSIEKP 1605  
Db LESSEARQEAAMNDYNDIARIIIDHNLEIDIKTTLPTGCFNTPSIEKP 1609

RESULT 5

US-10-299-058-12

Sequence 12, Application US/10299058  
Publication No. US20030103975A1  
GENERAL INFORMATION:  
APPLICANT: JONES, JONATHAN C.R.  
APPLICANT: GONZALES, MEREDITH  
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION  
FILE REFERENCE: 1720-1-002 CIP  
CURRENT APPLICATION NUMBER: US/10/299,058  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 09/706,235  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: 60/163,199  
PRIOR FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 1609  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-299-058-12

Query Match 93.7%; Score 8148; DB 14; Length 1609;

Best Local Similarity 92.8%; Pred. No. 0;

Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

QY 1 MTGGGAALALOPRGELPPLAIVL--AAVAGCVRAAMDECADEGGRPORCMPEFVNAAFN 58  
Db 1 MRGSHRAAPALPRGLMPVLAVLAAAGCAQAAMDECTDEGGRPORCMPEFVNAAFN 60  
QY 59 VTVVATNTCGTPEPEYCVQGTGVTGKSHLCAQOQLHGAAPLTDYNNQADTTWQS 118  
Db 61 VTVVATNTCGTPEPEYCVQGTGVTGKSHLCAQOQLHGAAPLTDYNNQADTTWQS 120  
QY 119 QTMLAGVQPSNINLTLLHGKAFDITYYRLKHTSRPESFAYIKRTREDGWPVQYYS 178  
Db 121 QTMLAGVQPSNINLTLLHGKAFDITYYRLKHTSRPESFAYIKRTREDGWPVQYYS 180  
QY 179 SCENTYSKANRFIRITGGDEQALCTDEFSDISPLTGGNVAFTSTDEGRPSAYNFONS 238  
Db 181 SCENTYSKANRFIRITGGDEQALCTDEFSDISPLTGGNVAFTSTDEGRPSAYNFONS 240  
QY 239 QEWVTATDIRVTLNRLNTFTGDEVFNDPKVLSYVIAISDFAVGGRCKNGHASECVKQEF 298  
Db 241 QEWVTATDIRVTLNRLNTFTGDEVFNDPKVLSYVIAISDFAVGGRCKNGHASECVKQEF 300  
QY 299 DKLMCKNCKNTYGVDCCKLPFFNDRPWRATASASCLPCDCNCRSQECYFDELYRS 358  
Db 301 DKLMCKNCKNTYGVDCCKLPFFNDRPWRATASASCLPCDCNCRSQECYFDELYRS 360  
QY 359 TGHGGHCTNCRDNTDGAKECERENFRILGNTAECSPCHCSFVGLSTQCDYSGRCSCKP 418  
Db 361 TGHGGHCTNCRDNTDGAKECERENFRILGNTAECSPCHCSFVGLSTQCDYSGRCSCKP 420  
QY 419 GVMGDKCRQCPGFHSLTEAGRCPCDPSGSDTSCNVTGRCVCKNDVGFNCBRCKPG 478  
Db 421 GVMGDKCRQCPGFHSLTEAGRCPCDPSGSDTSCNVTGRCVCKNDVGFNCBRCKPG 480  
QY 479 FPNLESSNPKGCTPCFCFHHSSVCTNAVGSYVDIISSTFQIDEDGWRVEQDGSSEASLEW 538  
Db 481 FPNLESSNPKGCTPCFCFHHSSVCTNAVGSYVDIISSTFQIDEDGWRVEQDGSSEASLEW 540  
QY 539 SDRQYIAVISDSYPRFYIAPVKELGNQVLSYGNLSPFRVDRDRTLSNEDLVLGA 598  
Db 541 SDRQYIAVISDSYPRFYIAPVKELGNQVLSYGNLSPFRVDRDRTLSNEDLVLGA 600  
QY 599 GLRVSVPJLAQNSVPSETTKYIFRLHEATDYPRPALSPFEPQKLLNLTSLKIRGT 658  
Db 601 GLRVSVPJLAQNSVPSETTKYIFRLHEATDYPRPALSPFEPQKLLNLTSLKIRGT 660  
QY 659 SERSAGYLDVTLQASRPGVPATWBSCTCPVYGQFCETCLPGYRRETPSLGPSP 718  
Db 661 SERSAGYLDVTLQASRPGVPATWBSCTCPVYGQFCETCLPGYRRETPSLGPSP 720

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QY 719 CVLCTCNHSTCPETGVCDCRNTAGPHCEKSDGYHGSTGTGTSDDCQPCPCPGSS 778
Db 721 CVLCAACNHSSTCPETGVCNCRNTAGPHCEKSDGYHGSTGTGTSDDCQPCPCPGSS 780
QY 779 CAIVPKTEVCTHCTAGKRCCLDDGDFGDPGLSGNVPRLCRPCQCNNDNDPNAV 838
Db 781 CAIVPKTEVCTHCTAGKRCCLDDGDFGDPGLSGNVPRLCRCLCQSDNDNDPNAV 840
QY 839 NCNRLTGCLKCIYNTAGFYCDRCCKEFGFNPAPNADKCKACACN-YGTVOQSSCNP 897
Db 841 NCNRLTGCLKCIYNTAGFYCDRCCKEFGFNPAPNADKCKACNPNPYGTMKQSSCNP 900
QY 898 VTGQOCCLPHYSGRDCTGDCGYNLQSGOCERCDCCHALGSTNGQCDIRTGQCECOPGI 957
Db 901 VTGQCECLPHVTGQDCGACDPFGYNLQSGOCERCDCCHALGSTNGQCDIRTGQCECOPGI 960
QY 958 TGQHCERCETNHFPGPCKPCDCHHEGSLSLQCKDDGRCEGFGVGNRCDCQENYF 1017
Db 961 TGQHCERCENHFGPCKPCDCHHEGSLSLQCKDDGRCEGFGVGNRCDCQENYF 1020
QY 1018 YNRSWPGQCECPACVRLVKDAAEHRVKLOBESLIANLGTGDDMVTDQAFEDLKEAR 1077
Db 1021 YNRSWPGQCECPACVRLVKDAAEHRVKLOBESLIANLGTGDDMVTDQAFEDLKEAR 1080
QY 1078 EYTDLLRAQEVKDYDQMLRQVNSLSHSQISRLQNIENITIEETGILAEARSRVES 1137
Db 1081 EYTDLLRAQEVKDYDQMLRQVNSLSHSQISRLQNIENITIEETGILAEARSRVES 1140
QY 1138 TQOLIEIASRELEKAM-AANVSITQPESTGEPNNMTLLAEARLAEHRKHQBADDIVRV 1196
Db 1141 TQOLIEIASRELEKAM-AANVSITQPESTGEPNNMTLLAEARLAEHRKHQBADDIVRV 1200
QY 1197 AKTANETSAEAYNLLRLTAGNQTALEELNRYEQAKNISODLEKQAAARVHEEAKRA 1256
Db 1201 AKTANETSAEAYNLLRLTAGNQTALEELNRYEQAKNISODLEKQAAARVHEEAKRA 1260
QY 1257 GDKAVEIYASVAQLTFVPSEALENANKIKKEADLRLDQKUYEDLREDVRGKEHE 1316
Db 1261 GDKAVEIYASVAQLTFVPSEALENANKIKKEADLRLDQKUYEDLREDVRGKEHE 1320
QY 1317 VKNLEKGAEOOTADQALLARADAKALAEAAKKGSTLOEANDILNNLKDFFRRVNDN 1376
Db 1321 VKNLEKGAEOOTADQALLARADAKALAEAAKKGSTLOEANDILNNLKDFFRRVNDN 1380
QY 1377 KTAABEALRRIPAINRTIAEANEKTRAEQALGNAADATEAKNAHEAEIAASAAQNA 1436
Db 1381 KTAABEALRRIPAINRTIAEANEKTRAEQALGNAADATEAKNAHEAEIAASAAQNA 1440
QY 1437 TSKKADAERTFGEVTDLNEVNGMLRQLEAEANELKRDODDQDDMMAGNASQAQAEAE 1496
Db 1441 TSKKADAERTFGEVTDLNEVNGMLRQLEAEANELKRDODDQDDMMAGNASQAQAEAE 1500
QY 1497 LNARAKQSVSLLSQNLNLLDQGLDQTLVNLKLNIEGSLINKAKDEMKAASDLDRKYS 1556
Db 1501 LNARAKQSVSLLSQNLNLLDQGLDQTLVNLKLNIEGSLINKAKDEMKAASDLDRKYS 1560
QY 1557 LSEARKQSAALMDYNRDIAEIIKOIHNLEDIKTLPTGCFNTPSIEKP 1605
Db 1561 LSEARKQSAALMDYNRDIAEIIKOIHNLEDIKTLPTGCFNTPSIEKP 1609
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## RESULT 6

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US-09-938-275-11
; Sequence 11, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P11047
; DATABASE ENTRY DATE: 1991-11-01
; US-09-938-275-11
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Query Match 93.7%; Score 8144; DB 9; Length 1609;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;
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QY 1 MTGGGAALALOPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPORCMPEFVNAAN 58
Db 1 MRGSHRAAPALPRGLWPLLAVALAAAGCAQAMDECTDEGGRPORCMPEFVNAAN 60
QY 59 VTVATNTCGTPEEYCVQTVGTGVTGKSHLQDAQOQLHQAALFDYNNQADTTWQS 118
Db 61 VTVATNTCGTPEEYCVQTVGTGVTGKSHLQDAQOQLHQAALFDYNNQADTTWQS 120
QY 119 QTMLAGVQVPSNINLTHLGKAFDITYVRLKHTSRPSPFAIYKRTRENGPMIPQYVSG 178
Db 121 QTMLAGVQVPSNINLTHLGKAFDITYVRLKHTSRPSPFAIYKRTRENGPMIPQYVSG 180
QY 179 SCENTYSKANRFRIRTGDEQOALCTDEPDSIDISPLTGGNVAFSTLEGPSAYNFDNSPVL 238
Db 181 SCENTYSKANRFRIRTGDEQOALCTDEPDSIDISPLTGGNVAFSTLEGPSAYNFDNSPVL 240
QY 239 QEWVTATDIRTLNRLNTFGDVFNDPKVLKYYIAISDPFVAGGRCKNGHASECKNEF 298
Db 241 QEWVTATDIRTLNRLNTFGDVFNDPKVLKYYIAISDPFVAGGRCKNGHASECKNEF 300
QY 299 DKLMCKNCKNTYGVDCCKLPFNDRPWRATASASECLPCDCNRSOECYFDPDELAYS 358
Db 301 DKLVCKNCKNTYGVDCCKLPFNDRPWRATASASECLPCDCNRSOECYFDPDELAYS 360
QY 359 TGHGHCITNCRDNTDGAKCERENFRNLGNTAECSPCHCSVGSLSLSTQCDYGRCSCKP 418
Db 361 TGHGHCITNCRDNTDGAKCERENFRNLGNTAECSPCHCSVGSLSLSTQCDYGRCSCKP 420
QY 419 GYMGDKDCRCQPFHSLTEAGRCPCSDGSDTDEQVETGRVCVCKDNVEGNCERCCKPG 478
Db 421 GYMGDKDCRCQPFHSLTEAGRCPCSDGSDTDEQVETGRVCVCKDNVEGNCERCCKPG 480
QY 479 FFXLESNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGMRVQRDGSSEASLEW 538
Db 481 FFXLESNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGMRVQRDGSSEASLEW 540
QY 539 SSDRQVIAVISDSYFPRPIAPVKFLGNQVLSYGVQNLSPSPRVDRDRLSADLVLEGA 598
Db 541 SSDRQVIAVISDSYFPRPIAPVKFLGNQVLSYGVQNLSPSPRVDRDRLSADLVLEGA 600
QY 599 GLRVSVPFLTAQNSYSPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTATSIKIRGY 658
Db 601 GLRVSVPFLTAQNSYSPSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTATSIKIRGY 660
QY 659 SERSAGYLDVTLQOSARPQGPVPATWVESCTPVYGGQGFCTCLPGYRRETPSLGYPSP 718
Db 661 SERSAGYLDVTLQOSARPQGPVPATWVESCTPVYGGQGFCTCLPGYRRETPSLGYPSP 720
QY 719 CVLCTCNHSETCDPTGVCDCRNTAGPHCEKSDGYHGSTGTGTSDDCQPCPCPGSS 778
Db 721 CVLCAACNHSSTCPETGVCNCRNTAGPHCEKSDGYHGSTGTGTSDDCQPCPCPGSS 780
QY 779 CAIVPKTEVCTHCTAGKRCCLDDGDFGDPGLSGNVPRLCRPCQCNNDNDPNAV 838
Db 781 CAIVPKTEVCTHCTAGKRCCLDDGDFGDPGLSGNVPRLCRCLCQSDNDNDPNAV 840
QY 839 NCNRLTGCLKCIYNTAGFYCDRCCKEFGFNPAPNADKCKACACN-YGTVOQSSCNP 897
Db 841 NCNRLTGCLKCIYNTAGFYCDRCCKEFGFNPAPNADKCKACNPNPYGTMKQSSCNP 900
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Db 841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNPLNPNADKCKACNCNPGYTMKQSSCNP 900
Qy 898 VTGQCQCLPHVSGRDCGTPGYNNLQSGGCRBCDCHALGSTNGQCDIRTGQCEQPGI 957
Db 901 VTGQCECLPHVTGQDGCACDPFYNLQSGGCRBCDCHALGSTNGQCDIRTGQCEQPGI 960
Qy 958 TQHCERCEVNHGPGEGCKPCDCHHGSLSLQCKDDGCECEGPGVGNRCDCQCENYF 1017
Db 961 TQHCERCEVNHGPGEGCKPCDCHHGSLSLQCKDDGCECEGPGVGNRCDCQCENYF 1020
Qy 1018 YNRSWPGQCPCACRYLRVKDKAAEHRVKLQELSLIANLTGDDMTDQAFEDRLKEAR 1077
Db 1021 YNRSWPGQCPCACRYLRVKDKADHRVKLQELSLIANLTGDDMTDQAFEDRLKEAR 1080
Qy 1078 EVTDLLEAEQVVDONLMDRLQRVNSSLSHOSI SLQNLIRNTIETGTLAEARSRVES 1137
Db 1081 EVMDLLEAEQVVDONLMDRLQRVNNLTSSQI SLQNLIRNTIETGTLAEARSRVES 1140
Qy 1138 TEOLIELASLELEKAKM-AANVSITOPSTGEFNNMTLLAEARLRKQADDIRV 1196
Db 1141 TERLIELASLELEKAKVAAANVSITOPSTGDPNNMTLLAEARLRKQADDIRV 1200
Qy 1197 AKTANETSABAYNLLRLTAGENOTALIEBELNRKYEQAQNI SODLEKQAAHVHEAKRA 1256
Db 1201 AKTANDTSTAYNLLRLTAGENOTALIEBELNRKYEQAQNI SODLEKQAAHVHEAKRA 1260
Qy 1257 GDKAVEIYASVAOLTPVDSEALENEANKIKKEAADLRLDQKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVEIYASVAQSPUDSETLENEANNIKVEAENLEQLDQKDYEDLREDMRGKEHE 1320
Qy 1317 VQNLLEKGAEQQTADQLLARAADAALAEBAKKGSTLOEANDILNLLKOPDRRVNDN 1376
Db 1321 VQNLLEKGTQEQTADQLLARAADAALAEBAKKGSTLOEANDILNLLKOPDRRVNDN 1380
Qy 1377 KTAABEALRRIPALNRTIAEANEKTRQAOLAGAAADA TEAKNKAHEARIRASAAQKNA 1436
Db 1381 KTAABEALRRIPALNRTIAEANEKTRQAOLAGAAADA TEAKNKAHEARIRASAVQKNA 1440
Qy 1437 TSKADAERTFGEVTDLDNEVNGMLRQLEBAENELKPKQDADODMMWMAQAAQAE 1496
Db 1441 TSKAAEARTFAEVTDLNENVMMLKQLEAEKELKQDADQDMMWMAQAAQAE 1500
Qy 1497 LNARKAKNSVSLLSQLANLLDOLGQDVTDLANKLNEIGSLNKADEMKASDLDRKVS 1556
Db 1501 INARKAKNSVTSLSIINDLEQLGQDVTDLANKLNEIGSLNKADEMKASDLDRKVS 1560
Qy 1557 LESEARKQEAAMIDYNRDIAEIIKDIHNLEDIKTLPTGCFNTPSIEKP 1605
Db 1561 LENEAKQEAAMIDYNRDIEIMKDIRNLEDIKTLPTGCFNTPSIEKP 1609

RESULT 7
US-10-372-683-36
; Sequence 36, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERBETSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 36
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-36
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Query Match 93.7%; Score 8144; DB 15; Length 1609;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;

Qy 1 MTGGGAAALALQPRGRLLWPLLAIVL--AAVAGCVRAAMDECADEGRFQRCMPFVNAAFN 58
Db 1 MEGSHRAAPALPRGRLLWPLLAIVLAAAAAACAQAAMDECTDEGRFQRCMPFVNAAFN 60
Qy 59 VTVVATNTCGTPPEYCVQGTGVTGKSLCHLADGQOHLQGAAPLTDYNNQADTTWQS 118
Db 61 VTVVATNTCGTPPEYCVQGTGVTGKSLCHLADGQOHLQGAAPLTDYNNQADTTWQS 120
Qy 119 QTLMLAGVQPSINLTLHLKAFDITVYRLKFTSRPESFAIYKRTREDGFWIPYQYISG 178
Db 121 QTLMLAGVQPSINLTLHLKAFDITVYRLKFTSRPESFAIYKRTREDGFWIPYQYISG 180
Qy 179 SCENTYSKANRGFIRTGDEBOOALCTDFPSDISLTGTVNAFSTLEGRPSAIFNDFNSVL 238
Db 181 SCENTYSKANRGFIRTGDEBOOALCTDFPSDISLTGTVNAFSTLEGRPSAIFNDFNSVL 240
Qy 239 QEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYIYASDFAVGGRCKNGHASECKNEF 298
Db 241 QEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYIYASDFAVGGRCKNGHASECKNEF 300
Qy 299 DKLMCNCKHNTYGVDCXCLPFNFDRPWRRTAESAESCLPCDCNGRSQECYFDPPELYRS 358
Db 301 DKLMCNCKHNTYGVDCXCLPFNFDRPWRRTAESAESCLPCDCNGRSQECYFDPPELYRS 360
Qy 359 TGHGHCNTCNDNTGAKCERENFRLGNTEACSPCHCSPVGLSLTQCCSYGRCSCKP 418
Db 361 TGHGHCNTCNDNTGAKCERENFRLGNTEACSPCHCSPVGLSLTQCCSYGRCSCKP 420
Qy 419 GWGDKDRCPGPHSLTEAGRCPCSDPGSTDECNVETGRCVCKNVEGFNCERCKPG 478
Db 421 GWGDKDRCPGPHSLTEAGRCPCSDPGSTDECNVETGRCVCKNVEGFNCERCKPG 480
Qy 479 FNLLESSNPKGTCFCFCHSVCTNAGVSYVDISSTFOIDEDGWRVQDGESEASLEW 538
Db 481 FNLLESSNPKGTCFCFCHSVCTNAGVSYVDISSTFOIDEDGWRVQDGESEASLEW 540
Qy 539 SSDRQYIAVSDSYPPRYFIAPVFLGNQVLSYQNLSFSFRVDRDRTRLSAEDLVLEGA 598
Db 541 SSERQDIAVSDSYPPRYFIAPVFLGNQVLSYQNLSFSFRVDRDRTRLSAEDLVLEGA 600
Qy 599 GLRVSVPILIAQNSYPSSETTKYIFRLHEATDYPWRPALSPFEQKLNLTSTIKIRGTY 658
Db 601 GLRVSVPILIAQNSYPSSETTKYIFRLHEATDYPWRPALSPFEQKLNLTSTIKIRGTY 660
Qy 659 SERSAGYLDVTLQARPGVPATWVESCTCPVGYGQFCETCLPGYRRETPLSIGPYSP 718
Db 661 SERSAGYLDVTLQARPGVPATWVESCTCPVGYGQFCETCLPGYRRETPLSIGPYSP 720
Qy 719 CVLCTCNHSETCDPETGVCDONRTAGPHCEKSDGYIGYSTLTGTSDDCQPCPCPGSS 778
Db 721 CVLCACNHSETCDPETGVCDONRTAGPHCEKSDGYIGYSTLTGTSDDCQPCPCPGSS 780
Qy 779 CAIVPKTEVWCTHCTGTAGRCBELCDDGYFGDPLGNGVPVRLCRPCQCNNDIDPNAV 838
Db 781 CAIVPKTEVWCTHCTGTAGRCBELCDDGYFGDPLGNGVPVRLCRCLCCSNDIDPNAV 840
Qy 839 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNPLNPNADKCKACACN-YGTVOQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGNPLNPNADKCKACACNPGYTMKQSSCNP 900
Qy 898 VTGQCQCLPHVSGRDCGTPGYNNLQSGGCRBCDCHALGSTNGQCDIRTGQCEQPGI 957
Db 901 VTGQCQCLPHVSGRDCGTPGYNNLQSGGCRBCDCHALGSTNGQCDIRTGQCEQPGI 960
Qy 958 TQHCERCEVNHGPGEGCKPCDCHHGSLSLQCKDDGCECEGPGVGNRCDCQCENYF 1017
Db 961 TQHCERCEVNHGPGEGCKPCDCHHGSLSLQCKDDGCECEGPGVGNRCDCQCENYF 1020
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QY 1018 YNRSPGCGECPACVRLVKDKAAEHRVKQLBESLIANLGTGDDMTVDQAFEDRLKEAR 1077  
 Db 1021 YNRSPGCGECPACVRLVKDKAAEHRVKQLBESLIANLGTGDDMTVDQAFEDRLKEAR 1080  
 QY 1078 EVTDLLREAQVQKVDQNLMDRLQVRNSSLHSQISRLQNRINTTIEETGIIAERARSVES 1137  
 Db 1081 EVDMLREAQVQKVDQNLMDRLQVRNSSLHSQISRLQNRINTTIEETGNLAQARAHVEN 1140  
 QY 1138 TEQLEIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEEAPLAEHRKHQEAADDIVRV 1196  
 Db 1141 TERLEIASRELEKAKAAANVSITQPESTGEPNNMTLLAEEAPLAEHRKHQEAADDIVRV 1200  
 QY 1197 AKTANETSABEAYNLLRLTAGENQTALEIEELNRKYEQAKNISQLEKQAAARVHEEAKRA 1256  
 Db 1201 AKTANDTSTEAYNLLRLTAGENQTALEIEELNRKYEQAKNISQLEKQAAARVHEEAKRA 1260  
 QY 1257 GDAVEIIVASVAQLTPVDSEALENEANKIKKAAADLRLDQKLKDYEDLREDMRGKEHE 1316  
 Db 1261 GDAVEIIVASVAQLSPDSELENEANNIKKAAADLRLDQKLKDYEDLREDMRGKEHE 1320  
 QY 1317 VKNLLEKGAECQQTADQLARADAALAEBAKKGSTLQEAANDILNNLKDFDRRVNDN 1376  
 Db 1321 VKNLLEKGTTCQQTADQLARADAKALAEBAKKGRTLQEAANDILNNLKDFDRRVNDN 1380  
 QY 1377 KTAABEALRRIPAINRTTAEANEKTRAEQALGALNAADATAPAKNAHEABRIASAAQKNA 1436  
 Db 1381 KTAABEALRKIPAINQTTTAEANEKTRAEQALGALNAADATAPAKNAHEABRIASAVQKNA 1440  
 QY 1437 TSTKADAERTGEVTDLNEVNGMLRQLEAEANELKQDDADODMMWAGMASAAQEA 1496  
 Db 1441 TSTKADAERTFAEVTDLNEVNNMLKQLEAEANELKQDDADODMMWAGMASAAQEA 1500  
 QY 1497 LNARAKNSVSSLSQLNNLLDQLDQDTPVNLKNEIEGSLNKADEMKAASDLDRKVS 1556  
 Db 1501 INARAKNSVTSLSIINDLLEQLQDQDTPVNLKNEIEGTLNKADEMKAASDLDRKVS 1560  
 QY 1557 LESEARKQEAAMNDYNDIAEIIKDIHNLDEIKKTLPTGCENTPSIEKP 1605  
 Db 1561 LENEAKQEAAMNDYNDIEEIMKDINLEDIRKTLPSGCENTPSIEKP 1609

## RESULT 8

US-10-037-182-18  
 ; Sequence 16, Application US/10037182  
 ; Publication No. US20030044899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tryggvason, Karl  
 ; APPLICANT: Doi, Masayuki  
 ; APPLICANT: Thyboll, Jill  
 ; TITLE OF INVENTION: Recombinant Laminin 10  
 ; FILE REFERENCE: 99-274-F  
 ; CURRENT APPLICATION NUMBER: US/10/037,182  
 ; CURRENT FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: 60/257,449  
 ; PRIOR FILING DATE: 2000-12-21  
 ; PRIOR APPLICATION NUMBER: 60/279,282  
 ; PRIOR FILING DATE: 2001-03-28  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 1576  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-037-182-18

Query Match 92.5%; Score 8043; DB 14; Length 1576;  
 Best Local Similarity 93.3%; Pred. No. 0;  
 Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;  
 QY 32 RAAMDECADEGGRPCORCMPEFYNAAFNVTVVATNTCGTPPBEYCVQGTGVTGKSLCD 91  
 Db 1 QAAMDECTDEGGRPCORCMPEFYNAAFNVTVVATNTCGTPPBEYCVQGTGVTGKSLCD 60

QY 92 AGQQLHQHGAAPLTDDNNQADTTWQSOTMLAGVQYPSNINLTLLHGLKAFDITYVRLKPH 151  
 Db 61 AGQPHLHQHGAAPLTDDNNQADTTWQSOTMLAGVQYPSNINLTLLHGLKAFDITYVRLKPH 120  
 QY 152 TSRPESFAIYKRTREDDGWIPIYQYSGSCENTYSKANRGFIRTGDEQALCTDFFSDIS 211  
 Db 121 TSRPESFAIYKRTREDDGWIPIYQYSGSCENTYSKANRGFIRTGDEQALCTDFFSDIS 180  
 QY 212 PUTGGNVAFTLEGPPSAYNFONSPLQEWWTATDIRVTNLRLNTFGDEVFNDPVLKSY 271  
 Db 181 PUTGGNVAFTLEGPPSAYNFONSPLQEWWTATDIRVTNLRLNTFGDEVFNDPVLKSY 240  
 QY 272 YYAISDFAVGGCKNKGHASECQKNEFEKLMCNCHNTYGVDCCKLFFFNDRPARRATA 331  
 Db 241 YYAISDFAVGGCKNKGHASECQKNEFEKLMCNCHNTYGVDCCKLFFFNDRPARRATA 300  
 QY 332 ESASECLPCDCNCRSGOEYFDELPYRSTGHGCHNCNCRDNTDGAECERENFFRLGNTE 391  
 Db 301 ESASECLPCDCNCRSGOEYFDELPYRSTGHGCHNCNCRDNTDGAECERENFFRLGNTE 360  
 QY 392 ACSPPCHSPVGLSTQCDYSYGRCSCKPGVMGDKDRCCQPGFHSLTEAGCRPCSDPSSGT 451  
 Db 361 ACSSCHCSPPVGLSTQCDYSYGRCSCKPGVMGDKDRCCQPGFHSLTEAGCRPCSDPSSGT 420  
 QY 452 DECNVETGECVKDNVEGFNCERCKGPFNLESSNPKGCTPCFCFGHSSVCTNAVGYSYV 511  
 Db 421 DECNVETGECVKDNVEGFNCERCKGPFNLESSNPKGCTPCFCFGHSSVCTNAVGYSYV 480  
 QY 512 DISSYFQIDEDQWRVEQRDSEASLEWSSDRQYIAVISDYPFPIYFAPVKFLNQVLSY 571  
 Db 481 SISSYFQIDEDQWRVEQRDSEASLEWSSDRQYIAVISDYPFPIYFAPVKFLNQVLSY 540  
 QY 572 GQNLSPFVDRDRDRLSAEDLVLEGAGLRVSPLIAQNSYSPSETTVKYIFRLHEATDY 631  
 Db 541 GQNLSPFVDRDRDRLSAEDLVLEGAGLRVSPLIAQNSYSPSETTVKYIFRLHEATDY 600  
 QY 632 PWRPALSPPEFQKLANLNTSIKIRGTYSERSAGYLDVDTLASARPQGPVATPWESCTCP 691  
 Db 601 PWRPALTPPEFQKLANLNTSIKIRGTYSERSAGYLDVDTLASARPQGPVATPWESCTCP 660  
 QY 692 VYGGQFCSTCLPGYRRETPSLGYPSPVLCNCHSSETCDPBTGVCDCRONTAGPHECK 751  
 Db 661 VYGGQFCSTCLPGYRRETPSLGYPSPVLCNCHSSETCDPBTGVCDCRONTAGPHECK 720  
 QY 752 CSDGYGDDTLGTSSDCQPCPCGGSSCAIVPKTKKEVWCTHCTGTGTAGKRCCLCDDGYFG 811  
 Db 721 CSDGYGDDTLGTSSDCQPCPCGGSSCAIVPKTKKEVWCTHCTGTGTAGKRCCLCDDGYFG 780  
 QY 812 DPLGNSGPVRLCRPCQCNNDNIDFNAGVNCNRLTGECLKCIYNTAGFYCDRCKEGFGNPL 871  
 Db 781 DPLGRNGPVRLCRPCQCNNDNIDFNAGVNCNRLTGECLKCIYNTAGFYCDRCKEGFGNPL 840  
 QY 872 APNPADKCKACACN-YGTVQOQSSCNPTVTCQCLPHVSGRDCGTCDPGYNNLQSQGCE 930  
 Db 841 APNPADKCKACACN-YGTVQOQSSCNPTVTCQCLPHVSGRDCGTCDPGYNNLQSQGCE 900  
 QY 931 RCDCHALGSTNGQCDIRTCQCECPGIGTQHCERTNHFHFGPGECKPCDCHHEGSLSL 990  
 Db 901 RCDCHALGSTNGQCDIRTCQCECPGIGTQHCERTNHFHFGPGECKPCDCHHEGSLSL 960  
 QY 991 QCKDGRCECREGFGVNRCDQCEENFYNRSWPGQCEACVRLVKDKAAEHRVKLQELE 1050  
 Db 961 QCKDGRCECREGFGVNRCDQCEENFYNRSWPGQCEACVRLVKDKAAEHRVKLQELE 1020  
 QY 1051 SLIANLGTGDDMTVDQAFEDRLKEAREVTDLLREAQVQKVDQNLMDRLQVRNSSLHSQ 1110  
 Db 1021 SLIANLGTGDDMTVDQAFEDRLKEAREVTDLLREAQVQKVDQNLMDRLQVRNSSLHSQ 1080  
 QY 1111 ISLQINRINTTIEETGIIAERARSVESTQLTEIASRELEKAKM-AANVSITQPESTGSP 1169  
 Db 1081 ISLQINRINTTIEETGIIAERARSVESTQLTEIASRELEKAKM-AANVSITQPESTGSP 1140  
 QY 1170 NNWTLAEEARRLAERHKQEAADDIVRAKTANETSABEAYNLLRLTAGENQTALEIEELN 1229

Db 1141 NNTLTAABARKLAERHKQEAADIVRAKTAANDTSTEAYNLLRLTLAGENQATFIEELN 1200  
QY 1230 RXYEQAKNTSODLEKQAAARVHEEAKGADKAVEIIVASVAQLTPVDSEALLENANKIKKEA 1289  
Db 1201 RXYEQAKNTSODLEKQAAARVHEEAKGADKAVEIIVASVAQLSPLOSETLENANKIKKEA 1260  
QY 1290 ADLRLIDOKLKYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAALAEAA 1349  
Db 1261 ENLEQLIDOKLKYEDLREDMRGKEHEVKNLLEKGAEOQTADQLLARADAALAEAA 1320  
QY 1350 KKRSTLOANDLNNLKDFDRVNDKNTAAEALERRIPAINRTTAENKERTREAOALG 1409  
Db 1321 KGRDRLQANDLNNLKDFDRVNDKNTAAEALERRIPAINRTTEANERTREAOALG 1380  
QY 1410 NAAADATEAKNAHEAERIASAAQKNATSTKADAERTFGEVTDLONEVNGMLRQLEBAEN 1469  
Db 1381 SAAADATEAKNAHEAERIASAVKNATSTKAEARTPAEVTDLONEVNNMLKQLEAEK 1440  
QY 1470 ELKRRKODDADMMWAGMASQAQAQAEALNARKAKNSVSLLSQANLLDOLGOLDVDLN 1529  
Db 1441 ELKRRKODDADMMWAGMASQAQAQAEALNARKAKNSVSLLSIINDLEQLGOLDVDLN 1500  
QY 1530 KLINEIGSLNKADEMKAISDLDRKVSJDLSEARKQBAAMNDYNRDIABIIKDIHNLEDIK 1589  
Db 1501 KLINEIGSLNKADEMKAISDLDRKVSJDLSEARKQBAAMNDYNRDIABIIKDIHNLEDIK 1560  
QY 1590 KTLPTGCFNTPSIEKP 1605  
Db 1561 KTLPTGCFNTPSIEKP 1576

RESULT 9  
US-09-845-583-10  
; Sequence 10, Application US/09845583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champliad, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCES: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-10

Query Match 41.4%; Score 3596.5; DB 9; Length 1587;  
Best Local Similarity 43.8%; Pred. No. 2.2e-201;  
Matches 707; Conservative 258; Mismatches 571; Indels 77; Gaps 24;

QY 20 LLAVLAAGVAVRAADECADGGRPQRCMPPEFVNAAFNVVATNTCGTPEEYCVQTG 79  
Db 12 LLAPRAAGAG-----MGACVYDAGRPQRCMPPEFVNAAFNVVATNTCGTPEEYCVQTG 66  
QY 80 VTGVTKSCHLADGQOHLQGAFLTDYNNQADTTWQSCQTMAGVQVYNSNLTILHLK 139  
Db 67 AAGAGAHQRCDAADPQRHNSYLTDFHSQDESTWQSPSMAFVQVYPTSVNITLRLCK 126  
QY 140 AFDITVRLKFTSRPESFAIYKRTEDGWPVYQYSGSCENTYSKANRGFIRTGDBQ 199  
Db 127 AYEITVRLKFTSRPESFAIYKRSRAGDWPVYQYSGSCENTYSKANRGFIRTGDBQ 186  
QY 200 QALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDSFVLQEWVTAFTDITVTLNRLNTFGD 259

Db 187 VAFCTSFSDISPLSGNVAFSTLEGRPSAYNFDSFVLQEWVTAFTDITVTLNRLNTFGD 246  
QY 260 EVFNDRPKVLSYVYAIISDFAVGRCCKNGHASECVKNEFQKLMCNCKHNTYGVDCCKLP 319  
Db 247 DIFKDPKVLQSYVYVDFSVGRCCKNGHASECGPDVAGOLACRCOHNTGTDCERCLP 306  
QY 320 FFNDRPWRATAESASCLPCDCNRSQOEYFPELRYSTGHGHCCTCNCNDTGDGAKCR 379  
Db 307 FFQDRPWARGTAAEAHCLPCNCNRSQOEYFPELRYSTGHGHCCTCNCNDTGDGAKCR 366  
QY 380 CRENFRLNGTEACSPCHSPVGSLSSTQCDYGRSCCKPGVMGDKCDRCOPGFHSLTEAG 439  
Db 367 COENFYHWDPRMPCQPCDCQASGSLHLQCDDTGTGACKPTVTGWKDCRLPGFHSLEGG 426  
QY 440 CRPSCDPSGSTDECNVETGRCKVCKNGVEGFNCERCKPGFPNLESSNPKCTCFCEGHS 499  
Db 427 CRPCTCNFAGSLDTCDFRSGRCCKENVEGNLDCRCRPGTFNLQPHNPAGCSCFCYGHS 486  
QY 500 SVCTNNAVYSVYDTSSTFQIDEDGVRVEQDGSSEASLEWSSDRQYIAVSDSYPPRYFA 559  
Db 487 KYCASTAQFVHHLLSDPHQGAEGWARSVGGSEHSPQWSPN---GVLLSPEDEBELTA 542  
QY 560 PVKFLGNQVLSYQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSVPSSTTV 619  
Db 543 PGKFLGDRFSYGOPLITFRVDPGDSPLVQ-LRLEGTGLALS--LRHSSLSGPDARA 599  
QY 620 KYIFRLH--EATDYPRPALSPPEFQKLLNLTISIKIRGTYSERSAG--YLDVDTLQSA 674  
Db 600 SQGRAQVPLQETSEDVAPPLPPHFORLLANLTLSLRVSPGSPGAPFVLEVRITSA 659  
QY 675 RPFGVPATWVESCTCPVYGGOFCETCLPGYRRETPSLQPSFVLCTCNGHSETCDPE 734  
Db 660 RPGLSPASWVEICSCPTGYTQFCESAPGYKREMPQGGPYASCVPCTCNQHG--TCDPN 718  
QY 735 TGVCDCHRDNTAGPHCEKCSGYGDSLTGTSDDCPCPCGGSSCALVPKTKVVCCHCP 794  
Db 719 TGICVCSHTEGSPCERCLFGFVGNFAGQADQCCPCPGQACTTIPSSGEVVCCHCP 778  
QY 795 TGTAGKCELCDDGYFGDPLGSGNGPVLCRCPCQCNNDINPNAVGNCLTGECLKCIYNT 854  
Db 779 PGQGRRCVCDGFFGCDPLGLFGHPQPCQCQSGNVDPNAVGNCDPLSGHCLRLHNT 838  
QY 855 AGFYCDRCCKGFFGNPLAPNAPKAKACACN-YGTVOQSSCNPVTCOCCLPHVSGRDC 913  
Db 839 TGDCEHCQEGFYGALAPRPAKCMPCSCHPQGSVSEQMPCDPVTGQCCLPHVTARDC 898  
QY 914 GTCDPGYNLQSGGCGERCDCCHALGSTNGQCDLRTGQCEQPGITGCHCRCTNHPFG 973  
Db 899 SRCYPGFDFLQPGRCRCKCHPLGSDQDCHPKTGCTCPCGTGQACDRCQLGPFSS 958  
QY 974 PEGCKPCDCHHEGSLSLQCKDDGRCECRGFGVGNRCQCEENFYNRSPGQCECPACYR 1033  
Db 959 IKGCRACRCSPLGAASAQAQCHYNGTCVCRPGFEGYKCDRCHYNFPLTADGTHCQCCPSYA 1018  
QY 1034 LVKDKAAEHRVKQLQELSLIANLTGD-----DMVTDOAFEDRLKBAEREVTDLLREAOE 1088  
Db 1019 LVKEETAKLRLTLTBNWQGGSDCSFWGLPDLILGEAPRGVYQGH-----LLPGARE 1074  
QY 1089 VKQVDQNLDRQVNSLSHSQISRLQNIERTTETGILAEARARSRVESTEQLEIASRE 1148  
Db 1075 A-----FLQMMGLEGAVKAAEQRLQNKGARCAQAQSQKCTQLADLEAVLESSEE 1128  
QY 1149 -LEKAKVAAVNSITPESCTGEPNNMTLLAEARLAEHRKQEAADDIVRVAKTANETSAEA 1207  
Db 1129 ILHAAATLASLEIPQ-EGPSQPTKWSHLAEARLAEHRKQEAADDIVRVAKTANETSAEA 1187  
QY 1208 YNMLRLTAGENOTALIE-ELNRKYEQAKNISQDLEKQAAHVHEBAKAGRAKAVEIYAS 1266  
Db 1188 YALLWNL--EGRVALETQDLEDRVQEQVAAQKALRTAFAEVLPEAE-----SVLAT 1238  
QY 1267 VAQL-----TPVDSEA--LENBANKIKKEAADLRLIDOKLKYEDLRE 1308  
Db 1239 VQVQGDATPAPYALLASFGALPQKRAEDLGLKAKALEKTVASWQHMAATEARTLQTAQ 1298







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.7709 Seconds  
(without alignments)

10452.141 Million cell updates/sec

Title: US-10-037-182-18

Perfect score: 8694  
Sequence: 1 MTGGRAALALQPRGLMPL.....EDIKTLTPGCFNTPTSIKPK 1605

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8627	99.2	1607	1	MMHUB2
2	8144	93.7	1609	1	MMHUB2
3	3469	39.9	1639	1	MMHUB2
4	3193	36.7	1557	2	T28211
5	2591	29.8	1133	2	A44018
6	2400.5	27.6	1192	2	S69000
7	1812.5	20.8	3106	1	S53868
8	1784	20.5	3084	1	MMHUB2
9	1742	20.0	3075	2	S14258
10	1682	19.3	1786	1	MMHUB1
11	1661.5	19.1	1786	1	MMHUB1
12	1655.5	19.0	1790	1	MMHUB1
13	1632	18.8	2823	2	T23064
14	1632	18.8	2823	2	F87908
15	1632	18.8	3102	2	T43291
16	1625.5	18.7	1808	2	T15099
17	1592	18.3	1801	1	MMHUB1
18	1568	18.0	1798	2	S53869
19	1475.5	17.0	1797	2	A55677
20	1455	16.7	3712	2	S18253
21	1384	15.9	3672	2	T23433
22	1384	15.9	3672	2	T37316
23	1347.5	15.5	3635	2	T10053
24	1162	13.4	806	2	A54665
25	1045	12.0	581	2	B54665
26	986.5	11.3	612	2	JH0799
27	939.5	10.8	1170	2	A53612
28	905	10.4	1168	2	I56985
29	903.5	10.4	4391	2	A38096

30	877.5	10.1	3707	2	S18252
31	637.5	7.3	1160	2	F88369
32	637.5	7.3	2295	2	C88369
33	637.5	7.3	3375	2	T19821
34	619	7.1	1751	1	MMHUBH
35	590	6.8	1620	1	T27283
36	586	6.7	1816	1	S68860
37	555.5	6.4	1574	2	T13954
38	551	6.3	1111	2	T26972
39	514	5.9	1713	2	A55347
40	490	5.6	400	2	T46383
41	477	5.5	2471	2	A49128
42	471	5.4	303	2	B45067
43	466.5	5.4	2703	1	A24420
44	466	5.4	2318	2	S45306
45	459.5	5.3	2352	2	T30201

## ALIGNMENTS

### RESULT 1

MMHUB2  
laminin gamma-1 chain precursor mouse  
N:Alternate names: laminin chain B2  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999  
C:Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552  
R:Sasaki, M.; Yamada, Y.  
G-Protein: CreM. 262, 17111-17117, 1987  
A:Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.  
A:Reference number: A28469; MUID:88059118; PMID:3680290  
A:Accession: A28469  
A:Molecule type: mRNA  
A:Residues: 1-1607 <SAS>  
A:Cross-references: EMBL:J03484; NID:gl98694; PIDN:AAA39405.1; PID:g293688  
R:Durkin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.  
Biochemistry 27, 5198-5204, 1988  
A:Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.  
A:Reference number: A27729; MUID:89000737; PMID:3167041  
A:Accession: A27729  
A:Molecule type: mRNA  
A:Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'  
A:Cross-references: EMBL:J03930; NID:gl98702; PIDN:AAA39408.1; PID:g293691  
A:Note: The authors translated the codon TAT for residue 544 as Asp and GCG for residue  
R:Ogawa, K.; Burbelo, P.D.; Sasaki, M.; Yamada, Y.  
J. Biol. Chem. 263, 8384-8389, 1988  
A:Title: The laminin B2 chain promoter contains unique repeat sequences and is active in  
A:Reference number: A28082; MUID:88228071; PMID:2836421  
A:Accession: A28082  
A:Molecule type: DNA  
A:Residues: 1-215, 'A', 217-239 <CGA>  
A:Cross-references: EMBL:J03749; NID:gl98704; PIDN:AAA39409.1; PID:g554184  
R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02680  
A:Molecule type: protein  
A:Residues: 227-238 <PUJ>  
R:Hartl, L.; Oberbauer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A:Title: The N terminus of laminin A chain is homologous to the B chains.  
A:Reference number: S00624; MUID:88225080; PMID:3267223  
A:Accession: S05327  
A:Molecule type: protein  
A:Residues: 227-238; 387-393, 'F', 395-405; 881-912; 1022-1034 <HAR>  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-  
A:Reference number: S01790; MUID:89030693; PMID:3181157  
A:Accession: S02037  
A:Molecule type: protein

heparan sulfate pr  
protein unc-52 (im  
protein unc-52 (im  
hypothetical prote  
laminin alpha-2 ch  
hypothetical prote  
hypothetical prote  
laminin alpha-4 ch  
MEGF6 protein - ra  
hypothetical prote  
adhesive ligand ep  
hypothetical prote  
cell-fate determin  
laminin B1 chain -  
notch protein - fr  
notch 3 protein -  
Notch homolog prot

A;Residues: 1362-1377,'X',1379-1392,'X',1394-1406 <DEU>  
R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.  
EMBO J. 3, 2355-2362, 1984  
A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a  
A;Reference number: A02870; MUID:85051302; PMID:6209134  
A;Accession: A02870  
A;Molecule type: mRNA  
A;Residues: 1391-1474,'K',1476-1575,'N',1577-1607 <BAR>  
A;Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:G817975  
R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
EMBO J. 4, 309-316, 1985  
A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
A;Reference number: S13543; MUID:85257455; PMID:3848400  
A;Accession: S13544  
A;Molecule type: protein  
A;Residues: 1506-1523,'X',1525 <PAU>  
R;Olsson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
Lab. Invest. 60, 772-782, 1989  
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A;Reference number: A34961; MUID:89280632; PMID:2733383  
A;Accession: S14552  
A;Molecule type: protein  
A;Residues: 881-912;1022-1034;1364-1377;1379-1392;1394-1409;1506-1525;1593-1606 <OLS>  
C;Genetics:  
A;Gene: Lamb-2  
A;Map position: 1  
A;Introns: 138/1; 239/3  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:  
A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-1607/Product: laminin gamma-1 chain #status predicted <MAT>  
F;34-283/Domain: VI <DOM6>  
F;284-502/Domain: V <DOM5>  
F;284-337/Domain: laminin-type EGF-like homology #status atypical <LE01>  
F;340-393/Domain: laminin-type EGF-like homology <LE02>  
F;396-440/Domain: laminin-type EGF-like homology <LE03>  
F;443-490/Domain: laminin-type EGF-like homology <LE04>  
F;493-502/Domain: laminin-type EGF-like homology <LE05>  
F;503-687/Domain: IV <DOM4>  
F;688-1033/Domain: III <DOM3>  
F;688-719/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F;722-768/Domain: laminin-type EGF-like homology <LE07>  
F;771-823/Domain: laminin-type EGF-like homology <LE08>  
F;826-879/Domain: laminin-type EGF-like homology <LE09>  
F;882-930/Domain: laminin-type EGF-like homology <LE10>  
F;933-978/Domain: laminin-type EGF-like homology <LE11>  
F;981-1026/Domain: laminin-type EGF-like homology <LE12>  
F;1033-1607/Domain: II/I <DOM2>  
F;1033-1607/Region: heptad repeats  
F;38-48/Disulfide bonds: #status predicted  
F;58,132,574,648,1020,1105,1159,1173,1203,1221,1239,1437/Binding site: carbohydrate (Asn  
F;1029,1032/Disulfide bonds: interchain #status predicted  
F;1378,1393/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;1598/Disulfide bonds: interchain (to chain B1) #status experimental

Query Match 99.2%; Score 8627; DB 1; Length 1607;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1598; Conservative 2; Mismatches 5; Indels 2; Gaps 2;

QY 1 MTGGGAAALALQPRGLMPLLAVALAAGCVRAAMDECAEGGRPQRCMPEFVNAAFNVT 60  
DB 1 MTGGGAAALALQPRGLMPLLAVALAAGCVRAAMDECAEGGRPQRCMPEFVNAAFNVT 60  
QY 61 VVATNTCGTPPEYCVQGTGVTGTSKCHLADAGQGHQGHGAFLTDYNNQADTTWQSQT 120  
DB 61 VVATNTCGTPPEYCVQGTGVTGTSKCHLADAGQGHQGHGAFLTDYNNQADTTWQSQT 120  
QY 121 MLAGVQYPSINLTLHLGKAFDITVRLKFTSPSPESFAYIKRTREDGPMPYQYSGSC 180  
DB 121 MLAGVQYPSINLTLHLGKAFDITVRLKFTSPSPESFAYIKRTREDGPMPYQYSGSC 180

QY 181 ENTYSKANRGFIRTCGDSQQAALCTDTEFSDISPLTGGNVAFTSLGRPSAYNFNDSPVLQE 240  
DB 181 ENTYSKANRGFIRTCGDSQQAALCTDTEFSDISPLTGGNVAFTSLGRPSAYNFNDSPVLQE 240  
QY 241 WVTATDIRVTNLRLNTFGDEVFNDFPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300  
DB 241 WVTATDIRVTNLRLNTFGDEVFNDFPKVLKSYYYAISDFAVGRCCKNGHASECVKNEFDK 300  
QY 301 LMCNCKHNTYGVDCSEKCLPFENDPWRATASASECLPCDCNGRSQECYFDPPLYSTG 360  
DB 301 LMCNCKHNTYGVDCSEKCLPFENDPWRATASASECLPCDCNGRSQECYFDPPLYSTG 360  
QY 361 HGHCTNCRDNTDGAKECRERENFFRLGNTAECSPVGSLSLSTQDSYGRCSCKPGV 420  
DB 361 HGHCTNCRDNTDGAKECRERENFFRLGNTAECSPVGSLSLSTQDSYGRCSCKPGV 420  
QY 421 MDGKDCRCQPGFHSUTEAGCPSCDPSGSDGNCVETGRVCCKNVGRCNCRCKGFF 480  
DB 421 MDGKDCRCQPGFHSUTEAGCPSCDPSGSDGNCVETGRVCCKNVGRCNCRCKGFF 480  
QY 481 NLESNPKGCTPCFCFHHSSVCTNAVGYSVYDISTSFTQIDEDGWRVQRDGSSEASLEWSS 540  
DB 481 NLESNPKGCTPCFCFHHSSVCTNAVGYSVYDISTSFTQIDEDGWRVQRDGSSEASLEWSS 540  
QY 541 DROYIAVISDSYFERYFTAPVKFIGNOVLSYQNLSEFSDVDRDTRLSAEDLVLEGAGL 600  
DB 541 DROYIAVISDSYFERYFTAPVKFIGNOVLSYQNLSEFSDVDRDTRLSAEDLVLEGAGL 600  
QY 601 RVSVELIAQGSYSSETTVKIFRLEATDYPWRPALSPFEFQKLLNLTSLIKRTYSE 660  
DB 601 RVSVELIAQGSYSSETTVKIFRLEATDYPWRPALSPFEFQKLLNLTSLIKRTYSE 660  
QY 661 RSAGVLDVTLQSRAPGPGVATWVESCTCEVGVGGOFCTCLPGVRRTPSLGVPSPCV 720  
DB 661 RSAGVLDVTLQSRAPGPGVATWVESCTCEVGVGGOFCTCLPGVRRTPSLGVPSPCV 720  
QY 721 LCTNGHSETCPETGVCDRCNDTAGPHCKSDGYYGDSLTGTSDDQCPGCGSSCA 780  
DB 721 LCTNGHSETCPETGVCDRCNDTAGPHCKSDGYYGDSLTGTSDDQCPGCGSSCA 780  
QY 781 IVPKTEVVCTHCTGTAGKCELCDDGFGDPLGNSGVRLCPCOCDNDIDPNAVNC 840  
DB 781 IVPKTEVVCTHCTGTAGKCELCDDGFGDPLGNSGVRLCPCOCDNDIDPNAVNC 840  
QY 841 NLTGCECLKIYNTAGFYCDCKEGFNGPLAPNADKCKACACN-YGTVOQSSCNVPT 899  
DB 841 NLTGCECLKIYNTAGFYCDCKEGFNGPLAPNADKCKACACN-YGTVOQSSCNVPT 899  
QY 900 GQCQLPHVSGRDCGTCDPGYNNLQSGGRCDCCHALGSTNGCCDRTGQCCQPGITG 959  
DB 900 GQCQLPHVSGRDCGTCDPGYNNLQSGGRCDCCHALGSTNGCCDRTGQCCQPGITG 959  
QY 960 QHCERCETHFPGFEGCKPCDCHHEGSLQCKDGRCEGFGVGNRCDCQCEENFYVN 1019  
DB 960 QHCERCETHFPGFEGCKPCDCHHEGSLQCKDGRCEGFGVGNRCDCQCEENFYVN 1019  
QY 1020 RSWPGCQCPACYRLVKDAEHRVKLOELESILIANLGTGDDMTQDAEPDLKEAREV 1079  
DB 1020 RSWPGCQCPACYRLVKDAEHRVKLOELESILIANLGTGDDMTQDAEPDLKEAREV 1079  
QY 1080 TDLLEAEQVVDQNDLRLQVRNSSLHSQISRLQNIRNTIETGILAEARARSVESTE 1139  
DB 1080 TDLLEAEQVVDQNDLRLQVRNSSLHSQISRLQNIRNTIETGILAEARARSVESTE 1139  
QY 1140 QLIETASRELEKAKW-AANVSITQPESTGEPNNMTLLAEARLAEHRKQEAADDIVRVAK 1198  
DB 1140 QLIETASRELEKAKW-AANVSITQPESTGEPNNMTLLAEARLAEHRKQEAADDIVRVAK 1198  
QY 1199 TANETSAEYNNLLRTLAGENQTALETEELNRYEQAKNISQLEKQAAARVHEAARAGD 1258  
DB 1201 TANETSAEYNNLLRTLAGENQTALETEELNRYEQAKNISQLEKQAAARVHEAARAGD 1260

QY 1259 KAVEIYASVAQLTPVDSALNEANKIKKEAADLRLDIDOKLYEDLREDMRGKEHEVK 1318  
 Db |||||  
 QY 1319 NLEKGAEOQTADQLARADAALAEAAKGRSTLOEANDILNKLKDFDRVNDNKT 1378  
 Db |||||  
 QY 1321 NLEKGAEOQTADQLARADAALAEAAKGRSTLOEANDILNKLKDFDRVNDNKT 1380  
 Db |||||  
 QY 1379 AAEALRIRIPAINRTIAEANEKTRAEQALGNAADAATEAKNKAHEAERIASAAQKNATS 1438  
 Db |||||  
 QY 1381 AAEALRIRIPAINRTIAEANEKTRAEQALGNAADAATEAKNKAHEAERIASAVQKNATS 1440  
 Db |||||  
 QY 1439 TKADAERTFGEVTDLDNEVNGMLRQLEAEANELKRXQDDADQDMMWAGMASQAQAEALN 1498  
 Db |||||  
 QY 1441 TKADAERTFGEVTDLDNEVNGMLRQLEAEANELKRXQDDADQDMMWAGMASQAQAEALN 1500  
 Db |||||  
 QY 1499 ARKAKNSVSSLSQNLNLDQGGQDVTDLANKLNIEGSLNKADEMKASDLDRKVSLE 1558  
 Db |||||  
 QY 1501 ARKAKNSVSSLSQNLNLDQGGQDVTDLANKLNIEGSLNKADEMKASDLDRKVSLE 1560  
 Db |||||  
 QY 1559 SEARKOEAAIMDYNRDIAEIIKNDIHNELEDIKKTLPTGCFNTPSIEKP 1605  
 Db |||||  
 QY 1561 SEARKOEAAIMDYNRDIAEIIKNDIHNELEDIKKTLPTGCFNTPSIEKP 1607  
 Db |||||

RESULT 2  
 MMHUB2  
 Laminin gamma-1 chain precursor - human  
 N:Alternate names: laminin chain B2  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999  
 C:Accession: S13548; A28158; S13549; B34961; S14664; S23567  
 R:Kallunki, T.; Ikonen, J.; Chow, L.L.; Kallunki, P.; Tryggvason, K.  
 J. Biol. Chem. 266, 221-228, 1991  
 A:Title: Structure of the human laminin B2 chain gene reveals extensive divergence from  
 A:Reference number: S13548; MUID:91093128; PMID:1985895  
 A:Accession: S13548  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1609 <KAL>  
 A:Cross-references: GB:M55217; NID:g186937  
 A:Note: The nucleotide sequence was submitted to GenBank, February 1991  
 R:Pikkarainen, I.; Kallunki, T.; Tryggvason, K.  
 J. Biol. Chem. 263, 6751-6758, 1988  
 A:Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the  
 A:Reference number: A28158; MUID:88198245; PMID:3360804  
 A:Accession: A28158  
 A:Molecule type: mRNA  
 A:Residues: 1-211, 'I', 213-1609 <PIK>  
 A:Cross-references: EMBL:M27654; NID:g186916; PIDN:AAA59488.1; PID:g307107  
 R:Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He  
 Cytogenet. Cell Genet. 48, 137-141, 1988  
 A:Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene  
 A:Reference number: S13549; MUID:89169663; PMID:3234037  
 A:Accession: S13549  
 A:Molecule type: mRNA  
 A:Residues: 1393-1609 <FKU>  
 A:Cross-references: EMBL:M27654; NID:g186923; PIDN:AAA59489.1; PID:g186924  
 R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
 Lab. Invest. 60, 772-782, 1989  
 A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
 A:Reference number: A34961; MUID:89280632; PMID:2733383  
 A:Accession: B34961  
 A:Molecule type: mRNA  
 A:Residues: 868-1551, 'N', 1553-1609 <OLS>  
 R:Santos, C.L.S.; Sabbaga, J.; Brentani, R.  
 DNA Seq. 1, 275-277, 1991  
 A:Title: Differences in human laminin B2 sequences.  
 A:Reference number: S14664; MUID:92216129; PMID:1806043  
 A:Accession: S14664  
 A:Molecule type: mRNA  
 A:Residues: 1282-1609 <SAN>  
 A:Cross-references: EMBL:X13939; NID:g34237; PIDN:CAA32122.1; PID:g34238

R:Vuolteenaho, R.; Kallunki, T.; Chow, L.L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.  
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P  
 A:Title: Genes for the human laminin B1 and B2 chains.  
 A:Reference number: S23566

A:Accession: S23567  
 A:Molecule type: DNA  
 A:Residues: 801-1481, 'R', 1483-1609 <VUO>  
 A:Note: mRNA was also sequenced  
 C:Genetics:  
 A:Gene: GDB:LAMC1; LAMB2  
 A:Cross-references: GDB:120136; OMIM:150290  
 A:Map position: 1q31-q31  
 A:Introns: 140/1, 241/3, 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;  
 /3; 1525/1  
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C:Function:  
 A:Description: interact with cells and with other basement membrane proteins to promote  
 C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:34-1609/Product: laminin gamma-1 chain #status predicted <MAT>  
 F:34-285/Domain: VI <DOM5>  
 F:286-504/Domain: V <DOM5>  
 F:286-339/Domain: laminin-type EGF-like homology <LE01>  
 F:342-395/Domain: laminin-type EGF-like homology <LE02>  
 F:398-442/Domain: laminin-type EGF-like homology <LE03>  
 F:445-492/Domain: laminin-type EGF-like homology <LE04>  
 F:495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:505-689/Domain: IV <DOM4>  
 F:690-1034/Domain: III <DOM3>  
 F:690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>  
 F:724-770/Domain: laminin-type EGF-like homology <LE07>  
 F:773-825/Domain: laminin-type EGF-like homology <LE08>  
 F:828-881/Domain: laminin-type EGF-like homology <LE09>  
 F:884-932/Domain: laminin-type EGF-like homology <LE10>  
 F:935-980/Domain: laminin-type EGF-like homology <LE11>  
 F:983-1028/Domain: laminin-type EGF-like homology <LE12>  
 F:1035-1609/Domain: II/I <DOM1>  
 F:1035-1609/Region: heptad repeats  
 F:40-50/Disulfide bonds: #status predicted  
 F:60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbohy  
 F:1031,1034,1600/Disulfide bonds: interchange #status predicted

Query Match 93.7%; Score 8144; DB 1; Length 1609;  
 Best Local Similarity 92.7%; Pred. No. 3;e-302;  
 Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;

QY 1 MTGGGAALALOPRGLWPLAVL--AAVAGCVRAAMDECADEGGPQRCMPPEFVNAAFN 58  
 Db 1 MRGSHRAAPALPRGRLLWPLVLAALAAAGCAQAAYDECTDEGGPQRCMPPEFVNAAFN 60  
 QY 59 VTVVATNTCGTPPEEYCVQGTGVTKSKCHLCDAGQHQHGAFLTDYNNQADTTWQOS 118  
 Db 61 VTVVATNTCGTPPEEYCVQGTGVTKSKCHLCDAGQHQHGAFLTDYNNQADTTWQOS 120  
 QY 119 QTMLAGVQYFNSINLTHLGAFDIYVRLKFTSPESFAIYKRTREGDPWIPYQYSG 178  
 Db 121 QTMLAGVQYFESSINLTHLGAFDIYVRLKFTSPESFAIYKRTREGDPWIPYQYSG 180  
 QY 179 SCENTYSKANRGFIRTGDDQQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFNDSPLV 238  
 Db 181 SCENTYSKANRGFIRTGDDQQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFNDSPLV 240  
 QY 239 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYVYIAISDFAVGGRCKNGHASECKNKF 298  
 Db 241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYVYIAISDFAVGGRCKNGHASECKNKF 300  
 QY 299 DKLMCNCKHNTYGVDCCKCLPFNFDRWRRAATAESASECLPCDCNGRSQBCYDPPELYRS 358  
 Db 301 DKLMCNCKHNTYGVDCCKCLPFNFDRWRRAATAESASECLPCDCNGRSQBCYDPPELYRS 360  
 QY 359 TGHGGHCTNCRDNTDGAKCRRCPNFRLLGNVTACSPCHGSPVGSJSTQCDSVGRCSCKP 418

361 TGHGGHCTNCDQNTDGAHCERCENFRFLGNNEACSSCHSPVGSLSSTQCDSYGRCSCKP 420  
419 GVMGDKCDRCQOPGSHSLTEAGCRPCSDPSSGSDDECNVETGRCVKCNVVEGFCNCRCKP 478  
421 GVMGDKCDRCQOPGSHSLTEAGCRPCSDPSSGSDDECNVETGRCVKCNVVEGFCNCRCKP 480  
479 FPNLESNPKGCTPCFCFSGSSVCTNAGVSVVDISTFOIDEDGHRVORDGSEASLEW 538  
481 FPNLESNPKGCTPCFCFSGSSVCTNAGVSVVDISTFOIDEDGHRVORDGSEASLEW 540  
539 SSDROYIAVSDSYFFPYFAPVFXFLGNQVLSYGVNLSFSGFRVDRDRTRLSAEDLVLEGA 598  
541 SSERQDIAVSDSYFFPYFAPVFXFLGNQVLSYGVNLSFSGFRVDRDRTRLSAEDLVLEGA 600  
599 GLRVSVPLIAQNSYPSSETTKYIFRLHEATDVPWRPALSPFFQKLLNNLTISKIRGTY 658  
601 GLRVSVPLIAQNSYPSSETTKYIFRLHEATDVPWRPALSPFFQKLLNNLTISKIRGTY 660  
659 SERAGVLDVLTLOSAPGCPVATWVESCPCPVYGGQFCETCLPGYRRETSLGYPSP 718  
661 SERAGVLDVLTLOSAPGCPVATWVESCPCPVYGGQFCETCLPGYRRETSLGYPSP 720  
719 CVLCTCNHSETCPETGVCDCRDNATAGPHEKCSGYYGDSSTLGTSSDCQPCPCGGSS 778  
721 CVLCAHGHSETCPETGVCDCRDNATAGPHEKCSGYYGDSSTLGTSSDCQPCPCGGSS 780  
779 CAIVPKTEVYCTHCPGTAGKRCLELDDGVFGDPLGNSGVPRLCRPCQCNIDNIDNAV 838  
781 CAIVPKTEVYCTHCPGTAGKRCLELDDGVFGDPLGNSGVPRLCRPCQCNIDNIDNAV 840  
839 NCNRLTGELCKIYNTAGFYCDRCCKGFFGNFLAPNADPKKACACN-YGTVOQQSSCNP 897  
841 NCNRLTGELCKIYNTAGFYCDRCCKGFFGNFLAPNADPKKACACNPFYGMKQSSCNP 900  
898 VTGQCCPLPHVSGRDCGTCDPYNLSGQCCERCDHALSTNGQCDITGQCECQPGI 957  
901 VTGQCCPLPHVSGRDCGTCDPYNLSGQCCERCDHALSTNGQCDITGQCECQPGI 960  
958 TGOHCERCETHFGFPGGCKPCDCHHEGSLSLCKDDGRCRFGVGNRCQCEBNYF 1017  
961 TGOHCERCETHFGFPGGCKPCDCHHEGSLSLCKDDGRCRFGVGNRCQCEBNYF 1020  
1018 YNRSWPGQCECPACVRLVKDAAEHRVKLOBESLIANLGTGDDMTDQAFEDLKEAER 1077  
1021 YNRSWPGQCECPACVRLVKDAAEHRVKLOBESLIANLGTGDDMTDQAFEDLKEAER 1080  
1078 EVDLLREAEQVKVDQNLMDRLQVNSLSHQSRLQNTIRNTIETGILAEARSVES 1137  
1081 EVDLLREAEQVKVDQNLMDRLQVNSLSHQSRLQNTIRNTIETGILAEARSVES 1140  
1138 TEQLIETIASRELEKAKM-AANVSITQPESTGCEPNNMTLLAEARLAEHRKHQEAADDIVR 1196  
1141 TEQLIETIASRELEKAKVAAANVSITQPESTGCEPNNMTLLAEARLAEHRKHQEAADDIVR 1200  
1197 AKTANETSAEAYNLLRLTAGENQTALEIEBELNKYEQAQKNSIDLEKQAAHVHEAKRA 1256  
1201 AKTANDTSTAYNLLRLTAGENQTALEIEBELNKYEQAQKNSIDLEKQAAHVHEAKRA 1260  
1257 GDKAVEIYASVAQLTPVDSEALEANKIKKEAADLRLIDQKLKDYEDLREDNRGKEHE 1316  
1261 GDKAVEIYASVAQLTPVDSEALEANKIKKEAADLRLIDQKLKDYEDLREDNRGKEHE 1320  
1317 VKNLLEKKAEEQQTADQALLARADAALAEBAKKGSTLQEAANDILNNLKQDPRRVNDN 1376  
1321 VKNLLEKKGTEQQTADQALLARADAALAEBAKKGSTLQEAANDILNNLKQDPRRVNDN 1380  
1377 KTAPEALRRPAPINRTTAEANEKTRAEQALGNAADATAEAKNAHEAERIASAAQKNA 1436  
1381 KTAPEALRRPAPINQTTTAEANEKTRAEQALGSAADATAEAKNAHEAERIASAVQKNA 1440  
1437 TSTKADAERTFGEVTDLNEVNGMLRJOLEEAENELEKRRQDDADQMMWAGASQAQAEAE 1496  
1441 TSTKAEABRTFAEVTDLNEVNNMLKQLEAEKELKRRQDDADQMMWAGASQAQAEAE 1500

QY 1497 LNARKAKSVSSLSQLNNLLDQLGOLDTVDLKNLKNIEGSLNKAKDEMKASDLDRKVS 1556  
Db INARAKKSVSSLSQLNNLLDQLGOLDTVDLKNLKNIEGSLNKAKDEMKASDLDRKVS 1560  
QY 1557 LESEARKQEAALMDYNRDIAEIIKDHNLEDIKKTLPCTGCFNTPSIEKP 1605  
Db LENEAKQEAALMDYNRDIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609

## RESULT 3

## MMFFB2

laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)

N.Alternate names: laminin chain B2

C.Species: Drosophila melanogaster

C.Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000

C.Accession: A31483; A33737; S01733; A40502

R:Chi, H.C.; Hui, C.F.

J. Biol. Chem. 264, 1543-1550, 1989

A.Title: Primary structure of the Drosophila laminin B2 chain and comparison with human,  
A.Reference number: A31483; MUID:89109164; PMID:2912972

A.Accession: A31483

A.Molecule type: mRNA

A.Residues: 1-1639 <CHI>

A.Cross-references: EMBL:M25063; NID:g157803; PIDN:AAA28664.1; PID:g157804

R.Montell, D.J.; Goodman, C.S.

J. Cell Biol. 109, 2441-2453, 1989

A.Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits  
A.Reference number: A33737; MUID:90037237; PMID:2808533

A.Accession: A33737

A.Molecule type: mRNA

A.Residues: 1-39, 'T', 'L', '893-1106', 'T', '1108-1459', 'HV', '1462-1581', 'G', '1583-1639' <MON  
A.Note: 831-Tyr was also found

R:Chi, H.C.; Hui, C.F.

Nucleic Acids Res. 16, 7205-7206, 1988

A.Title: CDNA and amino acid sequences of Drosophila laminin B2 chain.

A.Reference number: S01733; MUID:88303364; PMID:3405777

A.Accession: S01733

A.Molecule type: mRNA

A.Residues: 344-1639 <CH2>

A.Cross-references: EMBL:X07806; NID:g8179; PIDN:CAA30665.1; PID:g1335618

A.Note: The authors translated the codon GGC for residue 409 as Phe  
R:Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.

DNA Cell Biol. 10, 451-466, 1991

A>Title: Structure of the Drosophila gene for the laminin B2 chain.

A.Reference number: A40502; MUID:91299161; PMID:1840513

A.Accession: A40502

A.Molecule type: DNA

A.Residues: 1-891, 'L', '893-1639' <CH3>

A.Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806

C.Genetics:

A.Gene: lamB2

A.Cross-references: FlyBase:FBgn0002528

A.Map position: 3L 67C

A.Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1

C.Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C.Function: Interact with cells and with other basement membrane proteins to promote

A.Description: laminin beta-1 chain; laminin-type EGF-like homology

C.Superfamily: laminin-type EGF-like homology

C.Keywords: Basement membrane; calcium binding; cell binding; coiled coil; extracellular

F;1-33/Domain: signal sequence #status predicted <Sig>

F;34-1639/Product: laminin gamma-1 chain #status predicted <Mat>

F;34-297/Domain: VI <DOM5>

F;298-528/Domain: V <DOM5>

F;299-356/Domain: laminin-type EGF-like homology <LE01>

F;359-411/Domain: laminin-type EGF-like homology <LE02>

F;414-458/Domain: laminin-type EGF-like homology <LE03>

F;461-511/Domain: laminin-type EGF-like homology <LE04>

F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>

F;529-705/Domain: IV <DOM4>

F;706-1057/Domain: III <DOM3>

F;710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>

F;744-750/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.12547 Seconds  
(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-18

Perfect score: 8694

Sequence: 1 NTGGGGAALALQPRGLMPL.....EDIKTLPGCENTPSIEKP 1605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8627	99.2	1607	1	LMG1_MOUSE
2	8144	93.7	1609	1	LMG1_HUMAN
3	3596.5	41.4	1587	1	LMG3_HUMAN
4	3500	40.3	1581	1	LMG3_MOUSE
5	3476	40.0	1639	1	LMG1_DROME
6	3176	36.5	1535	1	LMG1_MOUSE
7	2592	29.8	1193	1	LMG2_HUMAN
8	2475	28.5	1191	1	LMG2_MOUSE
9	1822.5	20.8	3106	1	LMG2_MOUSE
10	1795.5	20.7	3110	1	LMG2_MOUSE
11	1784	20.5	3084	1	LMG1_MOUSE
12	1742	20.0	3075	1	LMG1_HUMAN
13	1682	19.3	1786	1	LMG1_MOUSE
14	1661.5	19.1	1786	1	LMG1_MOUSE
15	1656.5	19.1	1790	1	LMG1_DROME
16	1592	18.3	1801	1	LMG2_MOUSE
17	1562	18.0	1798	1	LMG2_HUMAN
18	1552	17.9	1799	1	LMG2_MOUSE
19	1455	16.7	3712	1	LMG1_MOUSE
20	1396	16.1	3718	1	LMG1_MOUSE
21	1384	15.9	3672	1	LMG2_MOUSE
22	1356.5	15.6	3695	1	LMG1_MOUSE
23	1167	13.4	604	1	NET1_MOUSE
24	1163.5	13.4	604	1	NET1_MOUSE
25	1162.5	13.4	3333	1	LMG3_MOUSE
26	1162	13.4	606	1	NET1_MOUSE
27	1045	12.0	581	1	NET2_MOUSE
28	986.5	11.3	612	1	LMG1_MOUSE
29	949.5	10.9	1172	1	LMG3_HUMAN
30	904	10.4	1168	1	LMG3_MOUSE
31	903.5	10.4	4391	1	PCBM_MOUSE
32	883	10.2	727	1	NETA_MOUSE
33	877.5	10.1	3707	1	PCBM_MOUSE

34 853 9.8 793 1 NETB\_DROME  
35 637.5 7.3 3375 1 UN52\_CAEEL  
36 623.5 7.2 539 1 NTG1\_MOUSE  
37 585 6.7 1816 1 LMA4\_HUMAN  
38 574.5 6.6 1816 1 LMA4\_MOUSE  
39 566.5 6.5 530 1 NTG2\_HUMAN  
40 532 6.1 589 1 NTG2\_MOUSE  
41 514 5.9 1713 1 LMA3\_HUMAN  
42 479 5.5 2470 1 NTG2\_MOUSE  
43 477 5.5 2471 1 NTG2\_MOUSE  
44 471 5.4 303 1 LMB1\_CHICK  
45 469.5 5.4 2703 1 NOTC\_DROME

#### ALIGNMENTS

RESULT 1  
LMG1\_MOUSE  
ID LMG1\_MOUSE STANDARD; PRT; 1607 AA.  
AC P02468;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin gamma-1 chain precursor (laminin B2 chain).  
GN LAMC1 OR LAMC-1 OR LAMB-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88059118; PubMed=3680290;  
RA Sasaki M., Yamada Y.;  
RT "The laminin B2 chain has a multidomain structure homologous to the  
RT B1 chain."  
RL J. Biol. Chem. 262:17111-17117(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89000737; PubMed=3167041;  
RA Durkin M.E., Bates B.B., Liu S.-H., Phillips S.L., Chung A.E.;  
RT "Primary structure of the mouse laminin B2 chain and comparison with  
RT laminin B1."  
RL Biochemistry 27:5198-5204(1988).  
RN [3]  
RP SEQUENCE OF 1-239 FROM N.A.  
RX MEDLINE=88228071; PubMed=2836421;  
RA Ogawa K., Burtelo P.D., Sasaki M., Yamada Y.;  
RT "The laminin B2 chain promoter contains unique repeat sequences and  
RT is active in transient transfection."  
RL J. Biol. Chem. 263:9384-9389(1988).  
RN [4]  
RP SEQUENCE OF 1391-1607 FROM N.A.  
RX MEDLINE=85051302; PubMed=6209134;  
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
RT coiled-coil alpha-helix."  
RL EMBO J. 3:2355-2362(1984).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.  
RX MEDLINE=96196434; PubMed=8648630;  
RA Stetefeld J., Mayer U., Timpl R., Huber R.;  
RT "Crystal structure of three consecutive laminin-type epidermal growth  
RT factor-like (IE) modules of laminin gammal chain harboring the  
RT nidogen binding site."  
RL J. Mol. Biol. 257:644-657(1996).  
RN [6]  
RP STRUCTURE BY NMR OF 824-881.  
RX MEDLINE=96196435; PubMed=8648631;  
RA Baumgartner R., Zisch M., Mayer U., Poeschl E., Huber R.,  
RA Timpl R., Holak T.A.;  
RT "Structure of the nidogen binding LE module of the laminin gammal  
RT chain in solution."

Q24568 drosophila  
Q06561 caenorhabdi  
Q8r490 mus muscuku  
Q16383 homo sapien  
P97927 mus muscuku  
Q96cw9 homo sapien  
Q8r4f1 mus muscuku  
Q16787 homo sapien  
Q35516 mus muscuku  
Q9qwk3 rattus norv  
Q01635 gallus gall  
P07207 drosophila

FT	DOMAIN	1029	1607	COILED COIL (POTENTIAL).	DOMAIN II AND I.
FT	DOMAIN	1034	1594	BY SIMILARITY.	
FT	DISULFID	340	349	BY SIMILARITY.	
FT	DISULFID	342	365	BY SIMILARITY.	
FT	DISULFID	368	377	BY SIMILARITY.	
FT	DISULFID	380	393	BY SIMILARITY.	
FT	DISULFID	396	408	BY SIMILARITY.	
FT	DISULFID	398	414	BY SIMILARITY.	
FT	DISULFID	416	425	BY SIMILARITY.	
FT	DISULFID	428	440	BY SIMILARITY.	
FT	DISULFID	443	454	BY SIMILARITY.	
FT	DISULFID	445	461	BY SIMILARITY.	
FT	DISULFID	463	472	BY SIMILARITY.	
FT	DISULFID	475	490	BY SIMILARITY.	
FT	DISULFID	722	731	BY SIMILARITY.	
FT	DISULFID	724	738	BY SIMILARITY.	
FT	DISULFID	740	749	BY SIMILARITY.	
FT	DISULFID	752	768	BY SIMILARITY.	
FT	DISULFID	771	779	BY SIMILARITY.	
FT	DISULFID	773	790		
FT	DISULFID	793	802		
FT	DISULFID	805	823		
FT	DISULFID	826	840		
FT	DISULFID	828	847		
FT	DISULFID	850	859		
FT	DISULFID	862	879		
FT	DISULFID	882	896		
FT	DISULFID	884	903		
FT	DISULFID	905	914		
FT	DISULFID	917	930		
FT	DISULFID	933	945	BY SIMILARITY.	
FT	DISULFID	935	952	BY SIMILARITY.	
FT	DISULFID	954	963	BY SIMILARITY.	
FT	DISULFID	966	978	BY SIMILARITY.	
FT	DISULFID	981	993	BY SIMILARITY.	
FT	DISULFID	983	999	BY SIMILARITY.	
FT	DISULFID	1001	1010	BY SIMILARITY.	
FT	DISULFID	1013	1026	BY SIMILARITY.	
FT	DISULFID	1029	1039	INTERCHAIN (PROBABLE).	
FT	DISULFID	1032	1032	INTERCHAIN (PROBABLE).	
FT	DISULFID	1598	1598	INTERCHAIN (WITH BETA-1 CHAIN).	
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	648	648	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1020	1020	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1105	1105	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1159	1159	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1173	1173	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1203	1203	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1221	1221	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1239	1239	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	1437	1437	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CONFLICT	216	216	G -> A (IN REF. 3).	
FT	CONFLICT	260	260	E -> D (IN REF. 2).	
FT	CONFLICT	337	337	S -> C (IN REF. 2).	
FT	CONFLICT	447	447	LR -> PS (IN REF. 2).	
FT	CONFLICT	544	544	D -> Y (IN REF. 2).	
FT	CONFLICT	662	662	T -> S (IN REF. 2).	
FT	CONFLICT	886	886	MISSING (IN REF. 2).	
FT	CONFLICT	1158	1158	MISSING (IN REF. 2).	
FT	CONFLICT	1434	1434	V -> A (IN REF. 2).	
FT	CONFLICT	1475	1475	R -> K (IN REF. 4).	
FT	CONFLICT	1576	1576	D -> N (IN REF. 4).	
FT	TURN	775	776		
FT	STRAND	779	781		
FT	STRAND	788	790		
FT	TURN	795	796		
FT	STRAND	797	798		
FT	TURN	800	801		
FT	STRAND	804	805		

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 42.7526 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-16  
Perfect score: 8544  
Sequence: 1 QAADECTDEGGRCQRCME.....EDIRKTLPSGCCNTPSIEKP 1576

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8544	100.0	1576	3 AAB19802	Aab19802 Human lam
2	8544	100.0	1576	3 AAB48453	Aab48453 Human lam
3	8544	100.0	1576	5 ABB81595	Abb81595 Human lam
4	8544	100.0	1584	3 AAB19804	Aab19804 Human lam
5	8544	100.0	1609	3 AAB19801	Aab19801 Human lam
6	8544	100.0	1609	3 AAB48452	Aab48452 Human lam
7	8544	100.0	1609	5 ABB81594	Abb81594 Human lam
8	8544	100.0	1609	7 ADC01887	Adc01887 Human lam
9	8544	100.0	1617	3 AAB19803	Aab19803 Human lam
10	8540	100.0	1609	2 AAW50898	Aaw50898 Human lam
11	8043	94.1	1605	3 AAB19805	Aab19805 Mouse lam
12	8043	94.1	1605	3 AAB48454	Aab48454 Mouse lam
13	8043	94.1	1605	5 ABB81596	Abb81596 Mouse lam
14	8042	94.1	1607	2 AAW50897	Aaw50897 Mouse lam
15	8038	94.1	1572	3 AAB19806	Aab19806 Mouse lam
16	8038	94.1	1572	3 AAB48455	Aab48455 Mouse lam
17	8038	94.1	1572	5 ABB81597	Abb81597 Mouse lam
18	3602	42.2	1587	3 AAB40917	Aab40917 Human ORF
19	3600	42.1	1587	5 AAM50361	Aam50361 Mouse lam
20	3600	42.1	1587	6 ABR58467	Abr58467 Human NOV
21	3598	42.1	1575	6 ABR58468	Abr58468 Human NOV
22	3463.5	40.5	1524	2 AAY35458	Aay35458 Human lam
23	3440	40.3	1639	4 ABB59807	Abb59807 Drosophil
24	2637	30.9	1193	2 AAR91427	Aar91427 Kalinin/1
25	2637	30.9	1193	3 AAB48468	Aab48468 Human lam

26	2637	30.9	1193	5 AAE14712	Aae14712 Human lam
27	2637	30.9	1193	5 AAO14992	Aao14992 Laminin g
28	2637	30.9	1193	6 ABR48214	Abr48214 Human bla
29	2637	30.9	1193	6 ABUS6513	AbuS6513 Lung canc
30	2637	30.9	1193	6 ABUS6696	AbuS6696 Lung canc
31	2637	30.9	1193	6 ABR92103	Abr92103 Human cer
32	2637	30.9	1193	6 ADA74120	Ada74120 Human lam
33	2630	30.8	1172	3 AAB48469	Aab48469 Human lam
34	2629	30.8	1193	3 AAB48470	Aab48470 Human lam
35	2622	30.7	1172	3 AAB48471	Aab48471 Human lam
36	2612.5	30.6	1190	6 ADA74091	Ada74091 Equine la
37	2516.5	29.5	1111	2 AAR91428	Aar91428 Kalinin/1
38	2516.5	29.5	1111	5 AAE14713	Aae14713 Human lam
39	2516.5	29.5	1111	5 AAO14993	Aao14993 Laminin g
40	2454.5	28.7	1171	3 AAB48473	Aab48473 Mouse lam
41	2454.5	28.7	1192	3 AAB48472	Aab48472 Mouse lam
42	2454.5	28.7	1192	5 AAE14711	Aae14711 Mouse lam
43	2454.5	28.7	1192	6 ADA74121	Ada74121 Murine la
44	2355.5	27.6	1171	2 AAW26583	Aaw26583 Rat hemid
45	1783.5	20.9	3084	4 AAE11215	Aae11215 Mouse lam

ALIGNMENTS

RESULT 1  
AAB19802  
ID AAB19802 standard; protein; 1576 AA.  
XX

AC AAB19802;

DT 05-MAR-2001 (first entry)

DE Human laminin 2 mature gamma-1 chain.

KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
degenerative muscle disorder; muscular dystrophy; cell therapy.

OS Homo sapiens.

PN WO200066730-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US011378.

PR 30-APR-1999; 99US-0131720P.

PR 15-JUN-1999; 99US-0139198P.

PR 12-JUL-1999; 99US-0143289P.

PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

DR WPI: 2000-687537/67.

DR N-PSDB; AAA88902.

PS Claim 5; Page 251-256; 305pp; English.

CC The present sequence is that of human laminin 2 gamma-1 chain mature protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding

CC	them (see AAA8891-906), methods for making recombinant laminin 2, cells
CC	that express recombinant laminin 2, and methods for using purified
CC	laminin 2 for research and therapeutic purposes including peripheral
CC	nerve regeneration, treatment of degenerative muscle disorders,
CC	angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC	cell therapy, improving the take of grafts, improving the
CC	biocompatibility of medical devices and preparing improved culture
CC	devices and media
XX	
SQ	Sequence 1576 AA;
	Query Match 100.0%; Score 8544; DB 3; Length 1576;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 QAADECTDEGGPQRCMPPEFVNAENVTVAATCGTPPEEYCVGTGVTKSHCLCD 60
Db	1 QAADECTDEGGPQRCMPPEFVNAENVTVAATCGTPPEEYCVGTGVTKSHCLCD 60
Qy	61 AGPHLGHGAFLTDYNNQADTTWQSQTMAGVQVPSSINLTGLHGAFTDITYVLKHF 120
Db	61 AGPHLGHGAFLTDYNNQADTTWQSQTMAGVQVPSSINLTGLHGAFTDITYVLKHF 120
Qy	121 TSPPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIITGGDEQALCTDEPDSIS 180
Db	121 TSPPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIITGGDEQALCTDEPDSIS 180
Qy	181 PLTCGNVAFSTLEGRPAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSY 240
Db	181 PLTCGNVAFSTLEGRPAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSY 240
Qy	241 YYA-SDPAVGRCCKNGHASECMKNBPDKLVCMCKNTYGVDCCKLPFPNDRPWRATA 300
Db	241 YYA-SDPAVGRCCKNGHASECMKNBPDKLVCMCKNTYGVDCCKLPFPNDRPWRATA 300
Qy	301 ESASECLPCDNGSQSCYCFDPELYRSTGHGHCNTCQDNTDGAHCERCKRENFRLGNNE 360
Db	301 ESASECLPCDNGSQSCYCFDPELYRSTGHGHCNTCQDNTDGAHCERCKRENFRLGNNE 360
Qy	361 ACSSCHSPVGSISTQCDSTYGRSCCKPGVMGDKDRCPQGFHSLTAGCRPCSDPSGSI 420
Db	361 ACSSCHSPVGSISTQCDSTYGRSCCKPGVMGDKDRCPQGFHSLTAGCRPCSDPSGSI 420
Qy	421 DECNVETGRCKNDVGENCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Db	421 DECNVETGRCKNDVGENCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNAVGYSVY 480
Qy	481 SISSTFOIDEDGMRAEQDSEASLEWSERQDIATISDSYFPFYFTAPAKFLGKQVLSY 540
Db	481 SISSTFOIDEDGMRAEQDSEASLEWSERQDIATISDSYFPFYFTAPAKFLGKQVLSY 540
Qy	541 QNLSFGRVDRRTRLSAEDLVLEGAGLVSVPLIAQGNYSYSETTVKVYFRLHEATDY 600
Db	541 QNLSFGRVDRRTRLSAEDLVLEGAGLVSVPLIAQGNYSYSETTVKVYFRLHEATDY 600
Qy	601 PWRPALTPFEQKLNLTSTIKRGTYSEASAGYLDVTLASARPFGVPATVWESCTCP 660
Db	601 PWRPALTPFEQKLNLTSTIKRGTYSEASAGYLDVTLASARPFGVPATVWESCTCP 660
Qy	661 VGYGQFCFEMCLSGYRRETNLGPSPCVLCAKNHSETCDPETHVCNCRDNTAGHCEK 720
Db	661 VGYGQFCFEMCLSGYRRETNLGPSPCVLCAKNHSETCDPETHVCNCRDNTAGHCEK 720
Qy	721 CSDGYGDSGTAGTSSDQCPGSGSSCAVVPKTKKEVVCTNCPTGTTGKCELCDDGYFG 780
Db	721 CSDGYGDSGTAGTSSDQCPGSGSSCAVVPKTKKEVVCTNCPTGTTGKCELCDDGYFG 780
Qy	781 DPLGNGPVRCLRCQCSNDTDPNAVGNCRNLATGCECLKCIYNTAGFYCDRCXGFFGNPL 840
Db	781 DPLGNGPVRCLRCQCSNDTDPNAVGNCRNLATGCECLKCIYNTAGFYCDRCXGFFGNPL 840
Qy	841 APNPADCKACNCPYGTMKQSSCNPTVGCECLPHVTGQCGACDPGFVNLQSGGCE 900

Db	841 APNPADCKACNCPYGTMKQSSCNPTVGCECLPHVTGQCGACDPGFVNLQSGGCE 900
Qy	901 RCDCHALGSTNGQCDIITGQCECOPGITGHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
Db	901 RCDCHALGSTNGQCDIITGQCECOPGITGHCERCEVNHFGFEGCKPCDCHPEGSLSL 960
Qy	961 QCKDDGRCEGREGFVGNRCQCEENYPYNSWPQCEPCACYRLVKDADHRVKLOELE 1020
Db	961 QCKDDGRCEGREGFVGNRCQCEENYPYNSWPQCEPCACYRLVKDADHRVKLOELE 1020
Qy	1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAOVDVQDQNDLQRLQVNTTSSQ 1080
Db	1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAOVDVQDQNDLQRLQVNTTSSQ 1080
Qy	1081 ISRLQNTIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQESTGDP 1140
Db	1081 ISRLQNTIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQESTGDP 1140
Qy	1141 NNWTLAABEARKLAERHKQADDIRVAKTANDTSTEAYNLLRTLAGENQTAFEIELN 1200
Db	1141 NNWTLAABEARKLAERHKQADDIRVAKTANDTSTEAYNLLRTLAGENQTAFEIELN 1200
Qy	1201 RKEQAKNISQLEKQAAHVHEEAKRAGDKAVEIYASVAQLSPIDSETLENEANNIKMEA 1260
Db	1201 RKEQAKNISQLEKQAAHVHEEAKRAGDKAVEIYASVAQLSPIDSETLENEANNIKMEA 1260
Qy	1261 ENLEQIDQKLKQYEDLREDVRGKELEVKNLLEKGTQQTADQLLARADAALASEAA 1320
Db	1261 ENLEQIDQKLKQYEDLREDVRGKELEVKNLLEKGTQQTADQLLARADAALASEAA 1320
Qy	1321 KKGRTTQLEANDIINNLIKDFRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG 1380
Db	1321 KKGRTTQLEANDIINNLIKDFRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG 1380
Qy	1381 SAAADATEAKNAHEAERIASAVQKATSTKAEAEARTFAEVTDLNNEVNNMLKQLEAEK 1440
Db	1381 SAAADATEAKNAHEAERIASAVQKATSTKAEAEARTFAEVTDLNNEVNNMLKQLEAEK 1440
Qy	1441 ELKRRQDDADDMMWAGWASQAQAEINARKAKNSVTSLSIINDLLEQLGQDVTVDLN 1500
Db	1441 ELKRRQDDADDMMWAGWASQAQAEINARKAKNSVTSLSIINDLLEQLGQDVTVDLN 1500
Qy	1501 KLINEIEGTLNKAKQEMKVSDDLDRKVSQDLENEAKKQEAAMQNDYNDIIEIMKDIRNLEDIR 1560
Db	1501 KLINEIEGTLNKAKQEMKVSDDLDRKVSQDLENEAKKQEAAMQNDYNDIIEIMKDIRNLEDIR 1560
Qy	1561 KTLPSGCGENTPSIEKP 1576
Db	1561 KTLPSGCGENTPSIEKP 1576
	RESULT 2
	AAB48453
ID	AAB48453 standard; proteoin; 1576 AA.
XX	AAB48453;
AC	02-MAR-2001 (first entry)
XX	Human laminin 8 polypeptide, SEQ ID NO: 24.
DE	Human; laminin 8; neuroprotective; angiogenic; osteopathic;
XX	antiartherosclerotic; glycoprotein; mesenchymal tissue injury;
KW	vascular tissue injury; neural injury; angiogenesis regulation.
OS	Homo sapiens.
XX	WO2000066732-A2.
PN	09-NOV-2000.
XX	28-APR-2000; 2000WO-US011543.
PD	
XX	
PF	
XX	



PR 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
PA Kortessmaa J, Tryggvason K;  
XX  
PI  
XX  
DR WPI. 2000-687539/67.  
DR N-PSDB; AAC83714.  
XX  
XX  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 214-218; 245pp; English.  
XX  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighboring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration  
XX  
SQ Sequence 1576 AA;  
Query Match 100.0%; Score 8544; DB 3; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QAAMDECTDEGRPQRCMEFNAAFNVTVATNTCGTPPEYCYVQTGVTGKSKCHLD 60  
DB 1 QAAMDECTDEGRPQRCMEFNAAFNVTVATNTCGTPPEYCYVQTGVTGKSKCHLD 60  
QY 61 AQOPHLOHGAFLTDYNNQADTTWQSQTLGAGVQPSINILTLHLGKAFDITYVRLKFX 120  
DB 61 AQOPHLOHGAFLTDYNNQADTTWQSQTLGAGVQPSINILTLHLGKAFDITYVRLKFX 120  
QY 121 TSRPESFAYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDFSDIS 180  
DB 121 TSRPESFAYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDFSDIS 180  
QY 181 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSY 240  
DB 181 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLKSY 240  
QY 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDPWRATA 300  
DB 241 YYAISDFAVGGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPFFNDPWRATA 300  
QY 301 ESASECLPCDCNCRGSOECYFDPPELYSTGHGHCNTCQNTDGAHCERENFFPLGNNE 360  
DB 301 ESASECLPCDCNCRGSOECYFDPPELYSTGHGHCNTCQNTDGAHCERENFFPLGNNE 360  
QY 361 ACSCHCSPVGLSLTQCDYSGRCCKPVGMDKDCRCQPGFHSLTEAGRCPCSDPSSGI 420  
DB 361 ACSCHCSPVGLSLTQCDYSGRCCKPVGMDKDCRCQPGFHSLTEAGRCPCSDPSSGI 420  
QY 421 DECNVETGRVCNDYEGNCRCKPFGNLESSNPRGCTPCFCGHSVCTNAGVSYVY 480  
DB 421 DECNVETGRVCNDYEGNCRCKPFGNLESSNPRGCTPCFCGHSVCTNAGVSYVY 480  
QY 481 SIGSTFQIDBDGWRABQRDGSSEASLEWSSERODIAVISDYFPRYFIAPAKFLGKQVLSY 540

DB 481 SIGSTFQIDBDGWRABQRDGSSEASLEWSSERODIAVISDYFPRYFIAPAKFLGKQVLSY 540  
QY 541 GQNLSPFSFRVDRDRTLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVRLHEATDY 600  
DB 541 GQNLSPFSFRVDRDRTLRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVRLHEATDY 600  
QY 601 PWRPALTPPEFQKLNLLNLSIKIRGYTSERSAGYLDVTLASARPGPGVPATWVESCTCP 660  
DB 601 PWRPALTPPEFQKLNLLNLSIKIRGYTSERSAGYLDVTLASARPGPGVPATWVESCTCP 660  
QY 661 VYGGOFCCEMCLSGYRRETPNLGYPSPCVLACNKGHSETCDPBTGYCNCRDNTAGPHCEK 720  
DB 661 VYGGOFCCEMCLSGYRRETPNLGYPSPCVLACNKGHSETCDPBTGYCNCRDNTAGPHCEK 720  
QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCTGTGTRKCELCDGVEG 780  
DB 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCTGTGTRKCELCDGVEG 780  
QY 781 DPLGRGNPVRCLRLCCQSDNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKDGFEGNEL 840  
DB 781 DPLGRGNPVRCLRLCCQSDNIDPNAVGNCRNLGTGELCKIYNTAGFYCDRCCKDGFEGNEL 840  
QY 841 APNPADKCKACNCPYGTWKKQSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGGCE 900  
DB 841 APNPADKCKACNCPYGTWKKQSSCNPVGTQCECLPHVTGQDCGACDPGFYNLQSGGCE 900  
QY 901 RCDCHALGSTNGQDRTGQCECPGIGTGOHCERCENHFGFGECKPCDCHPEGSLSL 960  
DB 901 RCDCHALGSTNGQDRTGQCECPGIGTGOHCERCENHFGFGECKPCDCHPEGSLSL 960  
QY 961 QCKDGRCECREGFGVGNRCQCEENFYNRSWPGQCEPCVRLVVKDVKADHVRKLOELE 1020  
DB 961 QCKDGRCECREGFGVGNRCQCEENFYNRSWPGQCEPCVRLVVKDVKADHVRKLOELE 1020  
QY 1021 SLIANLTGDMVTDOAFEDRLKEAREVMDLLAREADQVKDQNDMLDRQVNNLTSSQ 1080  
DB 1021 SLIANLTGDMVTDOAFEDRLKEAREVMDLLAREADQVKDQNDMLDRQVNNLTSSQ 1080  
QY 1081 ISRLQNRNTIEETGNLAEQARAHVENTERLIBIASRELEKAKVAAANSVTQPESTGDP 1140  
DB 1081 ISRLQNRNTIEETGNLAEQARAHVENTERLIBIASRELEKAKVAAANSVTQPESTGDP 1140  
QY 1141 NMTLLAEARKLAERHKQEADDIVRVAKTANDTSTEAVNLLRTLAGENCTAFEEELN 1200  
DB 1141 NMTLLAEARKLAERHKQEADDIVRVAKTANDTSTEAVNLLRTLAGENCTAFEEELN 1200  
QY 1201 RKYEOAKNIQDLEKQAAHVHEAKAGDKAVIYASVQLSPLDSETTLENEANNIKMEA 1260  
DB 1201 RKYEOAKNIQDLEKQAAHVHEAKAGDKAVIYASVQLSPLDSETTLENEANNIKMEA 1260  
QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKGTQEQOTADOLLARADAAKALAEAA 1320  
DB 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKGTQEQOTADOLLARADAAKALAEAA 1320  
QY 1321 KKGRTDLOEANDILNLLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTEAQAALG 1380  
DB 1321 KKGRTDLOEANDILNLLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTEAQAALG 1380  
QY 1381 SAAADATEAKNKAHEAERIAVQKNATSTKAEARTFAEVTOLDNEVNNMLKQLEAEK 1440  
DB 1381 SAAADATEAKNKAHEAERIAVQKNATSTKAEARTFAEVTOLDNEVNNMLKQLEAEK 1440  
QY 1441 ELKKEQDADODMMAGWASQAAQAEIINARKKNSVTSLSIINDLEQLGOLDVTDLN 1500  
DB 1441 ELKKEQDADODMMAGWASQAAQAEIINARKKNSVTSLSIINDLEQLGOLDVTDLN 1500  
QY 1501 KLINEIETGLNKADEKEMKVSDDLDRKVSLENEAKKQEAAMIDYNRDEIEEIMKDIRNLEDIR 1560  
DB 1501 KLINEIETGLNKADEKEMKVSDDLDRKVSLENEAKKQEAAMIDYNRDEIEEIMKDIRNLEDIR 1560  
QY 1561 KTLPSGCFNTPSTIEKP 1576  
DB 1561 KTLPSGCFNTPSTIEKP 1576

## RESULT 3

AB881595  
ID AB881595 standard; protein; 1576 AA.

XX AC AB881595;

XX XX 19-SEP-2002 (first entry)

DE Human laminin 10 third chain protein sequence SEQ ID NO:16.

XX Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialization; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.

XX OS Homo sapiens.

XX XX WO200250111-A2.

PN 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-0279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

DR N-PSDB; ABQ72913.

XX New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 177-182; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialization at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a third chain protein of laminin 10, from the present  
CC invention

XX Sequence 1576 AA;

XX Query Match 100.0%; Score 8544; DB 5; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAMDECTDEGRPCRCMPEFVNAFNVVATNTGTPPEYCVQGTGVTKSHCLCD 60

DB 1 QAMDECTDEGRPCRCMPEFVNAFNVVATNTGTPPEYCVQGTGVTKSHCLCD 60

QY 61 AQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITVRLKPH 120

DB 61 AQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYPPSSINLTLHLGKAFDITVRLKPH 120

QY 121 TSPSPFAIYKRTREDGWPVPIYQYSGSCENTYKANKRGFRTGDEQALCTDEPDSIS 180

DB 121 TSPSPFAIYKRTREDGWPVPIYQYSGSCENTYKANKRGFRTGDEQALCTDEPDSIS 180

QY 181 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY 240

181	PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSY	240
241	YYAISDFAVGGRCKCNHASECMKNEFDKLVNCKNHTYGVDCCKLPFFNDRPWRATA	300
241	YYAISDFAVGGRCKCNHASECMKNEFDKLVNCKNHTYGVDCCKLPFFNDRPWRATA	300
301	ESASECLPCDDNGRSQECYFDPPELYRSTGHGHCTNCODNTDGAHCRCRENFRLGNNE	360
301	ESASECLPCDDNGRSQECYFDPPELYRSTGHGHCTNCODNTDGAHCRCRENFRLGNNE	360
361	ACSSCHCSPVGLSTQCDSDSYGRCSCKPGWMDKCDRQCPGFHSLTEAGRCPCSDPGSGI	420
361	ACSSCHCSPVGLSTQCDSDSYGRCSCKPGWMDKCDRQCPGFHSLTEAGRCPCSDPGSGI	420
421	DECNVETGRVCYCKDNVEGNCERCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSVY	480
421	DECNVETGRVCYCKDNVEGNCERCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSVY	480
481	SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540
481	SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540
541	GONLSFSFRVDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSETTVKYVFLHEATDY	600
541	GONLSFSFRVDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSETTVKYVFLHEATDY	600
601	PWRPALTPFEFQKLNLLTSIKIRGTYSERSAGYLDVDTLASARPGPGVPATVWESCTCP	660
601	PWRPALTPFEFQKLNLLTSIKIRGTYSERSAGYLDVDTLASARPGPGVPATVWESCTCP	660
661	VYGGQFCFCEMCLSGYRRETNLGPYSPCVLCACNGHSETCDPBTGVCNCRDNTAGHCEK	720
661	VYGGQFCFCEMCLSGYRRETNLGPYSPCVLCACNGHSETCDPBTGVCNCRDNTAGHCEK	720
721	CSDGYGDSSTAGTSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGKRCCLCDDGYFG	780
721	CSDGYGDSSTAGTSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGKRCCLCDDGYFG	780
781	DPLGNGVRLCLCQSDNIDPNAVGNLRLTGECLKCIYNTAGFYCDKCKDGFNPL	840
781	DPLGNGVRLCLCQSDNIDPNAVGNLRLTGECLKCIYNTAGFYCDKCKDGFNPL	840
841	APNADKCKACNCPYGTMTQSSCNFVTQCECLPHVTQDCGACDPGFINYSQGGCE	900
841	APNADKCKACNCPYGTMTQSSCNFVTQCECLPHVTQDCGACDPGFINYSQGGCE	900
901	RDCHALGSTNGQCDITGQCECOPGITGOHCERCEVNHFGPGGCKPCDCHPEGSLSL	960
901	RDCHALGSTNGQCDITGQCECOPGITGOHCERCEVNHFGPGGCKPCDCHPEGSLSL	960
961	QCKDDGRCEBGFVGNRCQCEENYFYNSWFCQCEPCACYRLVKDKVADHRVKLQELE	1020
961	QCKDDGRCEBGFVGNRCQCEENYFYNSWFCQCEPCACYRLVKDKVADHRVKLQELE	1020
1021	SLIANLGTGDEWVTDOAFEDRLKEAREVMDLAREQDVKDQVNDLMDRLQRVNNTLSQ	1080
1021	SLIANLGTGDEWVTDOAFEDRLKEAREVMDLAREQDVKDQVNDLMDRLQRVNNTLSQ	1080
1081	ISRLQINRTIETGNLAQARAHVENTERLIIASRELEKAKAVAAANVSVTQPESTGDP	1140
1081	ISRLQINRTIETGNLAQARAHVENTERLIIASRELEKAKAVAAANVSVTQPESTGDP	1140
1141	NNMTLLAEARKLAERKQKQADDIRVAKTANTDTSTEAYNLLRLTLAGENQTAFAIEELN	1200
1141	NNMTLLAEARKLAERKQKQADDIRVAKTANTDTSTEAYNLLRLTLAGENQTAFAIEELN	1200
1201	KYISQAKNISODLEKQAAKVHBEAKAGDKAVIYASVAQLSPDSETELENNKMA	1260
1201	KYISQAKNISODLEKQAAKVHBEAKAGDKAVIYASVAQLSPDSETELENNKMA	1260
1261	ENLQOLIDQKLDYEDLREDMRGKLEVKLLSEKTEQOTADOLLARADAAKALAEAA	1320

Db	1261	ENLEQIDQKLKDYEDLREDMRCKELEVKNLLEKGTKEQTQADOLLARADAALAEAA	1322
QY	1321	KKGRDITLQEANDILNLLKQFDRVNDNKTAAEEALRKIPAINQITTEANEKTRTAQQAALG	1380
Db	1321	KKGRDITLQEANDILNLLKQFDRVNDNKTAAEEALRKIPAINQITTEANEKTRTAQQAALG	1380
QY	1381	SAAADATEAKVKAHEAEERIASAVQKNATSTKAAEAERTFAEVTDLDNVNNMLKQLEAEK	1440
Db	1381	SAAADATEAKVKAHEAEERIASAVQKNATSTKAAEAERTFAEVTDLDNVNNMLKQLEAEK	1440
QY	1441	ELKRRKDDADQDDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQLDVTVDLN	1500
Db	1441	ELKRRKDDADQDDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQLDVTVDLN	1500
QY	1501	KLNEIEGTLNKADEMKVSLDRKVSQLENEAKQAEAAIMDYNDRIEIMKQIRNLEDIR	1560
Db	1501	KLNEIEGTLNKADEMKVSLDRKVSQLENEAKQAEAAIMDYNDRIEIMKQIRNLEDIR	1560
QY	1561	KTLPSCGCFNTPSIEKP	1576
Db	1561	KTLPSCGCFNTPSIEKP	1576
RESULT 4			
AAB19804			
ID AAB19804 standard; protein; 1584 AA.			
XX	AAB19804;		
XX	05-MAR-2001 (first entry)		
DT	Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.		
DE	Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;		
KW	degenerative muscle disorder; muscular dystrophy; cell therapy.		
XX	Homo sapiens.		
XX	Key		
PH	Location/Qualifiers		
FT	1. .33		
FT	/label= Signal_peptide		
FT	34. .1609		
FT	/label= Mature_protein		
FT	1610. .1617		
FT	/label= FLAG		
XX	WC2000066730-A2.		
PN	09-NOV-2000.		
XX	28-APR-2000; 2000WO-US011378.		
XX	30-APR-1999; 99US-0131720P.		
PR	15-JUN-1999; 99US-0139198P.		
PR	12-JUL-1999; 99US-0143289P.		
PR	24-SEP-1999; 99US-0155945P.		
XX	(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.		
PA	Yurchenco P;		
XX	WPI; 2000-687537/67.		
DR	N-PSDB; AAA88904.		
XX	Purified laminin 2 protein, useful for research and therapeutic purposes		
PT	including peripheral nerve regeneration, treatment of degenerative muscle		
PT	disorders, angiogenesis regulation, and ex vivo cell therapy.		
XX	Claim 5; Page 275-280; 305pp; English.		
ES	The present sequence is that of the mature gamma-1 chain of human laminin		
XX	2, with an additional C-terminal FLAG epitope, resulting from expression		
CC	in transfected cells from mammalian expression vectors. Laminin 2 is		
CC			

QY 781 DPLGRNGPVRLCCLCOSENIDPNAVGNCRITGCECLKIYNTAGFYCDRCCKDGFNGNPL 840  
 Db 781 DPLGRNGPVRLCCLCOSENIDPNAVGNCRITGCECLKIYNTAGFYCDRCCKDGFNGNPL 840  
 QY 841 APNPADCKACACNPGYTMKQSSCNPTVTGQCECLPHVTGQDCGACDGFYNLQSGGCE 900  
 Db 841 APNPADCKACACNPGYTMKQSSCNPTVTGQCECLPHVTGQDCGACDGFYNLQSGGCE 900  
 QY 901 RCDCHALGSTNGQCDIRTCQCCQPGITGQHCERCEVNHFGPGCKPCDCHPEGSL 960  
 Db 901 RCDCHALGSTNGQCDIRTCQCCQPGITGQHCERCEVNHFGPGCKPCDCHPEGSL 960  
 QY 961 QCKDDGRCEGFGVGNRCDCQCEENYFYNRSPGQCEPCACVRLYKQKVDHRYKVLQELE 1020  
 Db 961 QCKDDGRCEGFGVGNRCDCQCEENYFYNRSPGQCEPCACVRLYKQKVDHRYKVLQELE 1020  
 QY 1021 SLIANLGTGDEWVTOAEDRLKEAREVMDLLREAOVDKVDQNDLMDRLQRVNNTLSSQ 1080  
 Db 1021 SLIANLGTGDEWVTOAEDRLKEAREVMDLLREAOVDKVDQNDLMDRLQRVNNTLSSQ 1080  
 QY 1081 ISRLQNRITIBETGNLABQARAHVENTERLIEIASRELEKAKVAAANVSVPQESTGDP 1140  
 Db 1081 ISRLQNRITIBETGNLABQARAHVENTERLIEIASRELEKAKVAAANVSVPQESTGDP 1140  
 QY 1141 NNMTLAERARKLAERHKEQADDIVRVAKTANDTSTAYNLLRLTAGENQTAPEIEELN 1200  
 Db 1141 NNMTLAERARKLAERHKEQADDIVRVAKTANDTSTAYNLLRLTAGENQTAPEIEELN 1200  
 QY 1201 RYEQAKNTSODLEKQAAVHEEAKRAGDKAVEIIVASVAQLSPDLSETLENEANNIKVEA 1260  
 Db 1201 RYEQAKNTSODLEKQAAVHEEAKRAGDKAVEIIVASVAQLSPDLSETLENEANNIKVEA 1260  
 QY 1261 ENLEQLIDOKLYEDREDMKGKLEVNKLLKGTQEQADQDOLLARADAALAEAA 1320  
 Db 1261 ENLEQLIDOKLYEDREDMKGKLEVNKLLKGTQEQADQDOLLARADAALAEAA 1320  
 QY 1321 KXGRDTLQANDILNNLKDFDRVNDNKTAAEALRKIPAINQITTEANEXTREAOQALG 1380  
 Db 1321 KXGRDTLQANDILNNLKDFDRVNDNKTAAEALRKIPAINQITTEANEXTREAOQALG 1380  
 QY 1381 SAAADATEAKNKAHEARIASAVQKNATSTKAEARTFAEYTDLDNEVNNMLKQLEAK 1440  
 Db 1381 SAAADATEAKNKAHEARIASAVQKNATSTKAEARTFAEYTDLDNEVNNMLKQLEAK 1440  
 QY 1441 ELKRKODDADQDMWAGMASQAQAEINAKAKNSVTSLLSIINDLEQLGQDVTDLN 1500  
 Db 1441 ELKRKODDADQDMWAGMASQAQAEINAKAKNSVTSLLSIINDLEQLGQDVTDLN 1500  
 QY 1501 KLNIEGTTLNKAKDEMYSDLDKVSVDLENEAKKQEAALNDYNDIEEIMKDINLEDIR 1560  
 Db 1501 KLNIEGTTLNKAKDEMYSDLDKVSVDLENEAKKQEAALNDYNDIEEIMKDINLEDIR 1560  
 QY 1561 KTLPSGCFNTPSIEKP 1576  
 Db 1561 KTLPSGCFNTPSIEKP 1576

## RESULT 5

AA19801  
 ID AA19801 standard; protein; 1609 AA.

XX AC AA19801;  
 XX DT 05-MAR-2001 (first entry)  
 XX DE Human laminin 2 gamma-1 chain.  
 XX KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
 XX OS degenerative muscle disorder; muscular dystrophy; cell therapy.  
 XX OS Homo sapiens.

PH Key Location/Qualifiers  
 FT Peptide 1..33  
 FT /label= Signal\_peptide  
 FT Protein 34..1609  
 FT /label= Mature\_protein  
 XX WO200006730-A2.  
 XX 09-NOV-2000.  
 XX 28-APR-2000; 2000WO-US011378.  
 XX 30-APR-1999; 99US-0131720P.  
 PR 15-JUN-1999; 99US-0139198P.  
 PR 12-JUL-1999; 99US-0143289P.  
 PR 24-SEP-1999; 99US-0155945P.  
 XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 PA Yurchenco P;  
 XX WPI; 2000-687537/67.  
 XX N-PSDB; AAA88901.  
 PT Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.  
 XX Claim 5; Page 239-244; 305pp; English.  
 XX The present sequence is that of the gamma-1 chain of human laminin 2. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AA19791-806) and the polynucleotides encoding them (see AA88891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, nerve regeneration, promoting cell attachment and migration, ex vivo angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media  
 XX Sequence 1609 AA;

Query Match 100.0%; Score 8544; DB 3; Length 1609;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QAAMDECTDEGGRPCRCMPFVNAAFNVTVVATNTGTPPEEYCVQTVGTGVTKSCHLCD 60  
 Db 34 QAAMDECTDEGGRPCRCMPFVNAAFNVTVVATNTGTPPEEYCVQTVGTGVTKSCHLCD 93  
 QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVOYVSSINLTLLHGKAFDITYVLEKSH 120  
 Db 94 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVOYVSSINLTLLHGKAFDITYVLEKSH 153  
 QY 121 TSRPESFAIKYRTREDGFWIPYQYISGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 180  
 Db 154 TSRPESFAIKYRTREDGFWIPYQYISGSCENTYSKANRGFIRTTGGDEQQAALCTDEFSDIS 213  
 QY 181 PLTGGNVAFSTLEGRPSAYNFDSPLQEWVATDTRVTLNRLNTGDEVDNDPKVLKSY 240  
 Db 214 PLTGGNVAFSTLEGRPSAYNFDSPLQEWVATDTRVTLNRLNTGDEVDNDPKVLKSY 273  
 QY 241 YYAISDFAVGGRCKNGHASECMKNEBFDKLVNCNKENTYGVDCCKLPFFNDRPWRATA 300  
 Db 274 YYAISDFAVGGRCKNGHASECMKNEBFDKLVNCNKENTYGVDCCKLPFFNDRPWRATA 333

QY 301 ESASECLPCDNGRQEQYFDPPELYRSTGHGHCCTNCQDNDGACRCRENFRLGNNE 360  
Db 334 ESASECLPCDNGRQEQYFDPPELYRSTGHGHCCTNCQDNDGACRCRENFRLGNNE 393  
QY 361 ACSSCHCSPVGLSTQCSYGRCSCKPGVMGKDCRCOPGHSILTEACRCSODPSGI 420  
Db 394 ACSSCHCSPVGLSTQCSYGRCSCKPGVMGKDCRCOPGHSILTEACRCSODPSGI 453  
QY 421 DSCNVTGRCVKDQNVGNCRCRCPGFNLESSNPRGCTPCFCFHHSSVCTNAVGYSY 480  
Db 454 DSCNVTGRCVKDQNVGNCRCRCPGFNLESSNPRGCTPCFCFHHSSVCTNAVGYSY 513  
QY 481 SISSTFQIDEDGWRAEQRCGSASLEWSSERODIAVISDSYPRYFIAPAKELGKQVLSY 540  
Db 514 SISSTFQIDEDGWRAEQRCGSASLEWSSERODIAVISDSYPRYFIAPAKELGKQVLSY 573  
QY 541 GQNLSPSFVRDRDRLSADLVLEAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 600  
Db 574 GQNLSPSFVRDRDRLSADLVLEAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 633  
QY 601 PWRPALTPPEFQKLLNNLTSIKIRGTYSRSAGYLDVTLASARPGVPATWVESCTCP 660  
Db 634 PWRPALTPPEFQKLLNNLTSIKIRGTYSRSAGYLDVTLASARPGVPATWVESCTCP 693  
QY 661 VYGGQFCMCLSGYRRETPNLGPYSPCVLCAQNGHSETCDPETGVNCRDNTAGPHCEK 720  
Db 694 VYGGQFCMCLSGYRRETPNLGPYSPCVLCAQNGHSETCDPETGVNCRDNTAGPHCEK 753  
QY 721 CSDGYTGDSTAGTSSDCQPCPCPGSSCAVVPKTEWCTNCTGTGKRCBLCDGDFG 780  
Db 754 CSDGYTGDSTAGTSSDCQPCPCPGSSCAVVPKTEWCTNCTGTGKRCBLCDGDFG 813  
QY 781 DPLGRNGPVLRLCQCSNIDPNAVGNCRNLGTGELCKCIYNTAGFYCDRCXGDFGNPL 840  
Db 814 DPLGRNGPVLRLCQCSNIDPNAVGNCRNLGTGELCKCIYNTAGFYCDRCXGDFGNPL 873  
QY 841 APNPADKCAKCNPNVTGTMKQSSCNVPTGQCECLPHVTGQCGADCPGFYNLQSGQCE 900  
Db 874 APNPADKCAKCNPNVTGTMKQSSCNVPTGQCECLPHVTGQCGADCPGFYNLQSGQCE 933  
QY 901 RCDCHALGSTNGQCDIRTGOCQCPGIGTQHCHERCENHFGPGECKDCCHPGRSLSL 960  
Db 934 RCDCHALGSTNGQCDIRTGOCQCPGIGTQHCHERCENHFGPGECKDCCHPGRSLSL 993  
QY 961 QCKDDGRCCEGFGVNRCDQCENYFYNRWPGQCEPCACVRLVKDVADHRVKLQELE 1020  
Db 994 QCKDDGRCCEGFGVNRCDQCENYFYNRWPGQCEPCACVRLVKDVADHRVKLQELE 1053  
QY 1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVQDVQDNLMDRLQVNTLSQ 1080  
Db 1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQDVQDVQDNLMDRLQVNTLSQ 1113  
QY 1081 ISRLQNRNTIETGNLAQARAHVENTERLIIASRELEKAKVAAANVSVPQESTGDP 1140  
Db 1114 ISRLQNRNTIETGNLAQARAHVENTERLIIASRELEKAKVAAANVSVPQESTGDP 1173  
QY 1141 NNWTLAEARKLAERHKOADDIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1200  
Db 1174 NNWTLAEARKLAERHKOADDIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1233  
QY 1201 RYVEQAKNISQDLKQARVHEAKRAGDKAVIYASVAQLSPDSEITLNEANNIKMEA 1260  
Db 1234 RYVEQAKNISQDLKQARVHEAKRAGDKAVIYASVAQLSPDSEITLNEANNIKMEA 1293  
QY 1261 ENLEQLIDQKLYEDLREDMRGKEVKNLLEKGTQEQTAQOLLARADAALAEAEA 1320  
Db 1294 ENLEQLIDQKLYEDLREDMRGKEVKNLLEKGTQEQTAQOLLARADAALAEAEA 1353  
QY 1321 KKGSDTLQEAANDILNLUKOFDRRVNDNKTAAEALRKIPAINOTITEANEKTRQAQALG 1380  
Db 1354 KKGSDTLQEAANDILNLUKOFDRRVNDNKTAAEALRKIPAINOTITEANEKTRQAQALG 1413

QY 1381 SAADATEAKVKAHEARIASAVOKNATSTKAEARTFAEVTDLONEVNNMLKQLOAEK 1440  
Db 1414 SAADATEAKVKAHEARIASAVOKNATSTKAEARTFAEVTDLONEVNNMLKQLOAEK 1473  
QY 1441 ELKRKQDDADQDMMAGMASQAAQAEAINARKAKNSVTSLLSIINDLLQLGOLDTVDLN 1500  
Db 1474 ELKRKQDDADQDMMAGMASQAAQAEAINARKAKNSVTSLLSIINDLLQLGOLDTVDLN 1533  
QY 1501 KLINEISGTINKAKDEMKVSDLDKESVLENEAKQAEAAIMDYNRDIEETMKDIRNLEDIR 1560  
Db 1534 KLINEISGTINKAKDEMKVSDLDKESVLENEAKQAEAAIMDYNRDIEETMKDIRNLEDIR 1593  
QY 1561 KTLPSGCFNTPSIEKP 1576  
Db 1594 KTLPSGCFNTPSIEKP 1609  
RESULT 6  
AAB48452  
ID AAB48452 standard; protein; 1609 AA.  
XX AAB48452;  
AC AAB48452;  
DT 02-MAR-2001 (first entry)  
XX Human laminin 8 polypeptide, SEQ ID NO: 22.  
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX Homo sapiens.  
XX WO200066732-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011543.  
XX 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
XX WPI: 2000-687539/67.  
XX N-P5DB; AAC83713.  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 202-207; 245pp; English.  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
XX migration  
XX Sequence 1609 AA;

Query Match 100.0%; Score 8544; DB 3; Length 1609;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QAAMDECTDEGRPORCMPEFVNAAPNTVATNTCGTPPEYCVQGTGVTGKSHCLCD	60	QY	1021	SLIANLTGDBMTVDQAFEDRLKEAREVMDLLAREAQDVKDVQDNLMRLQRVNNTLSQ	1080
DB	34	QAAMDECTDEGRPORCMPEFVNAAPNTVATNTCGTPPEYCVQGTGVTGKSHCLCD	93	DB	1054	SLIANLTGDBMTVDQAFEDRLKEAREVMDLLAREAQDVKDVQDNLMRLQRVNNTLSQ	1113
QY	61	ACQPHLQGAALFTDYNQADTTWQSQTMLAGVQYPSINLTLHLKAFDITVRLKPH	120	QY	1081	ISRLQNTNTTTEETGNLAEOARAHVENTERLIIASRELEKAKVAAANTSVTQPESTGDP	1140
DB	94	ACQPHLQGAALFTDYNQADTTWQSQTMLAGVQYPSINLTLHLKAFDITVRLKPH	153	DB	1114	ISRLQNTNTTTEETGNLAEOARAHVENTERLIIASRELEKAKVAAANTSVTQPESTGDP	1173
QY	121	TSRPSFALYKXETREDGWPVQYYSGSCENTYSKANRPFRTGDSQQAALCTDEPSDIS	180	QY	1141	NMWTLLAEARKLAERHKQBADDIRVAKTANTDTSTAYNLLRLTLAGENQTAFFEELN	1200
DB	154	TSRPSFALYKXETREDGWPVQYYSGSCENTYSKANRPFRTGDSQQAALCTDEPSDIS	213	DB	1174	NMWTLLAEARKLAERHKQBADDIRVAKTANTDTSTAYNLLRLTLAGENQTAFFEELN	1233
QY	181	PLTGNVAFSTLEGRPSAYNFNSVLQSWTATDIRVTLNRLNTFGDEVFNDPVLKSY	240	QY	1201	KRYEQAKNISDLKQKQARVHEEAKRAGDKAVEIYASVAOLSPLDSETLENEANNIKMEA	1260
DB	214	PLTGNVAFSTLEGRPSAYNFNSVLQSWTATDIRVTLNRLNTFGDEVFNDPVLKSY	273	DB	1234	KRYEQAKNISDLKQKQARVHEEAKRAGDKAVEIYASVAOLSPLDSETLENEANNIKMEA	1293
QY	241	YVAISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGYDCBKCLPFFNDPWRATA	300	QY	1261	ENLSQIDQKLYVEDIREDMRGHELEVKVNLLEKGTTEQQTADQLLARADAAKALAEAAA	1320
DB	274	YVAISDFAVGGRCKNGHASECMKNEFDKLVNCKHNTYGYDCBKCLPFFNDPWRATA	333	DB	1294	ENLSQIDQKLYVEDIREDMRGHELEVKVNLLEKGTTEQQTADQLLARADAAKALAEAAA	1353
QY	301	ESASECLPCDCNRSQEQYFDELYRSTGHGHCTNCODNTDGAHCBRCRENFRIGNNE	360	QY	1321	KKGRDTLQEAANDILNNLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRFAOQALG	1380
DB	334	ESASECLPCDCNRSQEQYFDELYRSTGHGHCTNCODNTDGAHCBRCRENFRIGNNE	393	DB	1354	KKGRDTLQEAANDILNNLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRFAOQALG	1413
QY	361	ACSSCHCSVGLSTQCSYGRCSCKPGVWGDKCDRCQPGPHSLTEAGCPSCDPSGSI	420	QY	1381	SAADATEAKVKAHEABRIASAVQKNATSTKABARTFAEVTDLDNVNNMLKQLEAEK	1440
DB	394	ACSSCHCSVGLSTQCSYGRCSCKPGVWGDKCDRCQPGPHSLTEAGCPSCDPSGSI	453	DB	1414	SAADATEAKVKAHEABRIASAVQKNATSTKABARTFAEVTDLDNVNNMLKQLEAEK	1473
QY	421	DECNVETGRVCXKDVGFNCRCKPFPNLESSNPRGCTPCFCFHSVSVCTNAVGYSVY	480	QY	1441	ELKKEKODDADODMMWAGWASQAQAEABINARKAKNSVTLSLSIINDLLQGLDQDVTDLN	1500
DB	454	DECNVETGRVCXKDVGFNCRCKPFPNLESSNPRGCTPCFCFHSVSVCTNAVGYSVY	513	DB	1474	ELKKEKODDADODMMWAGWASQAQAEABINARKAKNSVTLSLSIINDLLQGLDQDVTDLN	1533
QY	481	SISSTFOIDEDGWRAEQDGEASLEWSSERQDIAVISDSYFPIAPAKFLGKQVLSY	540	QY	1501	KLNEIEGTLNKADEMKVSOLDKRVSDLENEAKKQAAIMDYNRDIEEIMKDIRNLEDIR	1560
DB	514	SISSTFOIDEDGWRAEQDGEASLEWSSERQDIAVISDSYFPIAPAKFLGKQVLSY	573	DB	1534	KLNEIEGTLNKADEMKVSOLDKRVSDLENEAKKQAAIMDYNRDIEEIMKDIRNLEDIR	1593
QY	541	GQNLFSFRVDRRLRLAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKVYFRLHATDY	600	QY	1561	KTLPSGCGFNTPSIEKP	1576
DB	574	GQNLFSFRVDRRLRLAEDLVLEGAGLRVSVPLIAQGNYSYSETTVKVYFRLHATDY	633	DB	1594	KTLPSGCGFNTPSIEKP	1609
QY	601	PWRPALTPPEFQKLNNTSIRKGTYSERSAGVLDVTLASARPFGVPATWVESCTCP	660	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	634	PWRPALTPPEFQKLNNTSIRKGTYSERSAGVLDVTLASARPFGVPATWVESCTCP	693	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	661	VYGGQFCMCLSGVRRTPNLGPSPVLCACNGHSETCDPETGVNCRDNTAGPHCEK	720	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	694	VYGGQFCMCLSGVRRTPNLGPSPVLCACNGHSETCDPETGVNCRDNTAGPHCEK	753	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	721	CSDGYGDBTAGTSSDCQPCPCPGSSCAVVPKTKVVCNCPGTGTTGKRCCLCDDGYFG	780	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	754	CSDGYGDBTAGTSSDCQPCPCPGSSCAVVPKTKVVCNCPGTGTTGKRCCLCDDGYFG	813	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	781	DFLGNPVRICRLQCCSDNIDPNAVGNCLRTGECCLKIYNTAGFYCDRCCKDGFQNL	840	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	814	DFLGNPVRICRLQCCSDNIDPNAVGNCLRTGECCLKIYNTAGFYCDRCCKDGFQNL	873	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	841	APNPADKCKACNCPYGTWQSSCNVPTGQCECLPHVTGQDCCACDPGFYNIQSOGGCE	900	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	874	APNPADKCKACNCPYGTWQSSCNVPTGQCECLPHVTGQDCCACDPGFYNIQSOGGCE	933	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	901	RCDCHALGSTGQCDIRTGQCECPGTGQHCERCEVNHFGPEGCKPCDCHEPSLSL	960	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	934	RCDCHALGSTGQCDIRTGQCECPGTGQHCERCEVNHFGPEGCKPCDCHEPSLSL	993	QY	1609	KTLPSGCGFNTPSIEKP	1609
QY	961	QCKDDGRCEGREGFVGNRCDCQCEENYFYNRSWPCQCECPACRYLVKDKVADHRVKLQELE	1020	QY	1609	KTLPSGCGFNTPSIEKP	1609
DB	994	QCKDDGRCEGREGFVGNRCDCQCEENYFYNRSWPCQCECPACRYLVKDKVADHRVKLQELE	1053	QY	1609	KTLPSGCGFNTPSIEKP	1609

## RESULT 7

AB881594  
 ID AB881594 standard; protein; 1609 AA.

AC AB881594;

DT 19-SEP-2002 (first entry)

DE Human laminin 10 third chain protein sequence SEQ ID NO:14.

Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
 tissue repair development; laminin; healing; vascular tissue;  
 re-endothelialisation; vascular injury; cell attachment; cell stasis;  
 proliferation; migration.

OS Homo sapiens.

Key Location/Qualifiers

Peptide 1..33

Protein 34..1609

/label= laminin\_10\_third\_chain

WO200250111-A2.

27-JUN-2002.

21-DEC-2001; 2001WO-US051035.

21-DEC-2000; 2000US-0257449P.

28-MAR-2001; 2001US-0279282P.

13-NOV-2001; 2001US-00279282.

XX PA (BIOS-) BIOSTRATUM INC.

XX PI Tryggvason K, Doi M, Thyboll J;

XX DR WPI; 2002-557650/59.

XX DR N-PSDB; ABQ72912.

XX New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for

PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 165-170; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is

CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell

CC growth and differentiation in tissue repair development. Specifically,

CC laminin 10 can be used for accelerating the healing injuries of vascular

CC tissue, improving the biocompatibility of grafts useful for treating such

CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,

CC proliferation, differentiation, and/or migration. The present sequence

CC represents a third chain protein of laminin 10, from the present

CC invention

XX SQ Sequence 1609 AA;

Query Match 100.0%; Score 8544; DB 5; Length 1609;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGPQRCMEPEFNAENVTVAATNTCGTPPEYCVQGTGVTGKSLCHL 60

DB 34 QAAMDECTDEGGPQRCMEPEFNAENVTVAATNTCGTPPEYCVQGTGVTGKSLCHL 93

QY 61 AGQPHLQHGAAFLTDYNNQADTTWQSTMLAGVQVPSINLTLLGKAFDITYVRLKPH 120

DB 94 AGQPHLQHGAAFLTDYNNQADTTWQSTMLAGVQVPSINLTLLGKAFDITYVRLKPH 153

QY 121 TSPESFAYKRTREGDPPIPOYYSGSCENTYSKANRGFIETGGDEQALCTDFSDIS 180

DB 154 TSPESFAYKRTREGDPPIPOYYSGSCENTYSKANRGFIETGGDEQALCTDFSDIS 213

QY 181 PLTGGNVAFSTLEGPSAYNFNSPVLQEWATDITRVLTNLNTFGDEVFNDPKVLKSY 240

DB 214 PLTGGNVAFSTLEGPSAYNFNSPVLQEWATDITRVLTNLNTFGDEVFNDPKVLKSY 273

QY 241 YVAISDFAVGGRCCKNGHASECMKNFDFKLVNCKNTYGVDCCKLPFFNDRPWRATA 300

DB 274 YVAISDFAVGGRCCKNGHASECMKNFDFKLVNCKNTYGVDCCKLPFFNDRPWRATA 333

QY 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCENFFRLGNNE 360

DB 334 ESASECLPCDCNCRSQECYFDPPELYRSTGHGHCTNCQDNTDGAHCERCENFFRLGNNE 393

QY 361 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDCRCQCFHSLTAGCRPCSDPSGSI 420

DB 394 ACSSCHCSPVGSLSLSTQDSYGRCSCKPGVMGDKDCRCQCFHSLTAGCRPCSDPSGSI 453

QY 421 DECNVETGRVCCKDNVEGNCERCKPGFNLESNPRGCTPCFCFHSSVCTNAVGVSYV 480

DB 454 DECNVETGRVCCKDNVEGNCERCKPGFNLESNPRGCTPCFCFHSSVCTNAVGVSYV 513

QY 481 S1SSTFQIDEDGWAEQRDQSGSEASLWSSERQDIAVISDYPFRYFIAPAKFLGKVL 540

DB 514 S1SSTFQIDEDGWAEQRDQSGSEASLWSSERQDIAVISDYPFRYFIAPAKFLGKVL 573

QY 541 GQNLSTFRVDRDRTLRLSADLVLEGAGLVSVPLIAQGNVSEPTVTKVYVRLHEATDY 600

DB 574 GQNLSTFRVDRDRTLRLSADLVLEGAGLVSVPLIAQGNVSEPTVTKVYVRLHEATDY 633

QY 601 PWRPALTPEFQKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGVGPATVWESCTCP 660

Db 634 PWRPALTPEFQKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGVGPATVWESCTCP 693

QY 661 VYGGGFCEMCLSGYRRETNLGPYSCVLCACNHSSETCDPTGVCNCRDNTAGPHCEK 720

Db 694 VYGGGFCEMCLSGYRRETNLGPYSCVLCACNHSSETCDPTGVCNCRDNTAGPHCEK 753

QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWVCTNCTGTGKRCCLCDDGYFG 780

Db 754 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWVCTNCTGTGKRCCLCDDGYFG 813

QY 781 DPLGRNGPVRCLRCQCSDNIDENAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGFENPL 840

Db 814 DPLGRNGPVRCLRCQCSDNIDENAVGNCNRLTGECLKCIYNTAGFYCDRCCKDGFENPL 873

QY 841 APNADCKKACNPNYGTMTKQSSCNPTGQCCLPHVTGQDCGACDPGFYNLQSGGCE 900

Db 874 APNADCKKACNPNYGTMTKQSSCNPTGQCCLPHVTGQDCGACDPGFYNLQSGGCE 933

QY 901 RCDCHALGSTNGQCDIRTGQCEQCPGIGTGHCEVNHFGPQEGCKPCDCHPEGSLSL 960

Db 934 RCDCHALGSTNGQCDIRTGQCEQCPGIGTGHCEVNHFGPQEGCKPCDCHPEGSLSL 993

QY 961 QCKDDGRCBCEBGFVGNRCQCEENFYNSWFCQCECPACVLYKDKVADHRVKLQELE 1020

Db 994 QCKDDGRCBCEBGFVGNRCQCEENFYNSWFCQCECPACVLYKDKVADHRVKLQELE 1053

QY 1021 SLIANLTGDBMTDQAFEDRLKEAREVNDLLREAQDVNDQNLMDRLQRVNNTLSQ 1080

Db 1054 SLIANLTGDBMTDQAFEDRLKEAREVNDLLREAQDVNDQNLMDRLQRVNNTLSQ 1113

QY 1081 ISRLQIRNTIETGNLAEQARAHVENTERLIIIASRELEKAKVAAANVSVPQESTGDP 1140

Db 1114 ISRLQIRNTIETGNLAEQARAHVENTERLIIIASRELEKAKVAAANVSVPQESTGDP 1173

QY 1141 NMTLLAEARKLAERHKEQADDIVRVAKTANTDSTEAYNLLRTLAGEQTAFETIELN 1200

Db 1174 NMTLLAEARKLAERHKEQADDIVRVAKTANTDSTEAYNLLRTLAGEQTAFETIELN 1233

QY 1201 RYEQAKNIISQDLEKQAAARVHEEAKRAGDKAVIYASVAQLSPDSETLEANEANNIKMEA 1260

Db 1234 RYEQAKNIISQDLEKQAAARVHEEAKRAGDKAVIYASVAQLSPDSETLEANEANNIKMEA 1293

QY 1261 ENLEQLIDQKLYEDLREDMRGKLELVKNLLEKGTQQTADQOLLARADAAKALAEAA 1320

Db 1294 ENLEQLIDQKLYEDLREDMRGKLELVKNLLEKGTQQTADQOLLARADAAKALAEAA 1353

QY 1321 KKGRDITLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINOTITEANEKTRAQOALG 1380

Db 1354 KKGRDITLQEANDILNLLKDFRRVNDNKTAAEEALRKIPAINOTITEANEKTRAQOALG 1413

QY 1381 SAAADATEAKNKAHEAERIAAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLEAEK 1440

Db 1414 SAAADATEAKNKAHEAERIAAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLEAEK 1473

QY 1441 ELKEKQDADQDQMMAGWASQAQAEAEINARKAKNSVTSLSIINDLLEQLGQDVTVDLN 1500

Db 1474 ELKEKQDADQDQMMAGWASQAQAEAEINARKAKNSVTSLSIINDLLEQLGQDVTVDLN 1533

QY 1501 XLNBIETGLNKADEMKVSDLRKVSQLENEAKKQEAAMIDYNRDIEEIMKDRLNLEDIR 1560

Db 1534 XLNBIETGLNKADEMKVSDLRKVSQLENEAKKQEAAMIDYNRDIEEIMKDRLNLEDIR 1593

QY 1561 KTLPSGCFNTPSIEKP 1576

Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 8

ADC01887

ID ADC01887 standard; protein; 1609 AA.

XX AC

AC ADC01887;



XX DT 18-DEC-2003 (first entry)  
 XX DE Human laminin gamma 1 subunit.  
 XX KW Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;  
 XX KW gamma1 subunit; alpha4 subunit; angiogenesis.  
 XX OS Homo sapiens.  
 XX PN US2003103975-A1.  
 XX PD 05-JUN-2003.  
 XX PF 18-NOV-2002; 2002US-00299058.  
 XX PR 03-NOV-1999; 99US-0163199P.  
 XX PR 03-NOV-2000; 2000US-00706235.  
 XX PA (JONE/) JONES J C R.  
 XX PA (GONZ/) GONZALES M.  
 XX PI Jones JCR, Gonzales M;  
 XX PI WPI; 2003-755217/71.  
 XX DR N-PSDB; ADC01886.  
 XX PT Antigenic fragment of alpha4 laminin, useful for preparing a composition  
 XX PT for treating tumor.  
 XX PS Disclosure; Page 42-46; 52pp; English.  
 XX CC The invention relates to an antigenic fragment of the human alpha4  
 CC laminin subunit appearing as ADC01881. Also included are a chimeric  
 CC and/or fusion protein comprising the antigenic fragment, an antibody to  
 CC the antigenic fragment, a cell line that produces the antibody, an  
 CC isolated laminin complex (laminin-x, comprising an alpha4 subunit, a  
 CC beta3 subunit or gamma1 subunit), modulating angiogenesis and a method of  
 CC inducing tumours. The antigenic fragment of alpha4 laminin subunit is  
 CC useful for preparing a composition (e.g. the antibody 2A3) for treating a  
 CC tumour. The present sequence represents the human gamma 1 laminin  
 CC subunit.  
 XX SQ Sequence 1609 AA;  
 Query Match 100.0%; Score 8544; DB 7; Length 1609;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QAAMDECTDEGRPQRCMPEFVNAAFNVVVAITTCGTPPEEYCVQGVGTGKSHLCD 60  
 DB 34 QAAMDECTDEGRPQRCMPEFVNAAFNVVVAITTCGTPPEEYCVQGVGTGKSHLCD 93  
 QY 61 AGPHLQGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDIYVRLKXH 120  
 DB 94 AGPHLQGAFLTDYNNQADTTWQSTMLAGVQYPSINLTLHLGKAFDIYVRLKXH 153  
 QY 121 TSPSPFAIKYKRTREDGPMIYQYYSGSCENTYSKANRGFIRITGGDEQALCTDEFSDIS 180  
 DB 154 TSPSPFAIKYKRTREDGPMIYQYYSGSCENTYSKANRGFIRITGGDEQALCTDEFSDIS 213  
 QY 181 PLTGGNVAFTLEGPSAYNFDNSPVQEWATDIRVTLNRLNTGDEVFNDPKVLSY 240  
 DB 214 PLTGGNVAFTLEGPSAYNFDNSPVQEWATDIRVTLNRLNTGDEVFNDPKVLSY 273  
 QY 241 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKNTYGVDCCKLPFFNDRPWRATA 300  
 DB 274 YYAISDFAVGGRCKNGHASECMKNEFDKLVNCKNTYGVDCCKLPFFNDRPWRATA 333  
 QY 301 ESASECLPCDNGSQEYCFPELYRSTGCHGCTNCQDNTDGAHCERCHENFRLLGNNE 360  
 DB 334 ESASECLPCDNGSQEYCFPELYRSTGCHGCTNCQDNTDGAHCERCHENFRLLGNNE 393

QY 361 ACSSCHCSPVGLSTQCDYSYGRCSCKPQVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 420  
 DB 394 ACSSCHCSPVGLSTQCDYSYGRCSCKPQVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 453  
 QY 421 DECNVETCRVCYCKNVGFCNCRCKPGFFNLESSNPRGCTPCPCFGHSSVCTTNAVGYSVY 480  
 DB 454 DECNVETCRVCYCKNVGFCNCRCKPGFFNLESSNPRGCTPCPCFGHSSVCTTNAVGYSVY 513  
 QY 481 SISSTFQIDEDGWRAEORDGSEASLEWSSERQDIAVSDSYFFPYFAPAKFELGKQVLSY 540  
 DB 514 SISSTFQIDEDGWRAEORDGSEASLEWSSERQDIAVSDSYFFPYFAPAKFELGKQVLSY 573  
 QY 541 GQNLSPFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTKVYVFLHEATDY 600  
 DB 574 GQNLSPFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTKVYVFLHEATDY 633  
 QY 601 PWRPALTPFEFQKLLNLTSTIKIRGTYSERSAGVLDVTLASARPGPGVPATVWESCTCP 660  
 DB 634 PWRPALTPFEFQKLLNLTSTIKIRGTYSERSAGVLDVTLASARPGPGVPATVWESCTCP 693  
 QY 661 VQYGGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720  
 DB 694 VQYGGQFCMCLSGYRRETNLGPYSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753  
 QY 721 CSDGYIGDSTAGTSDQPCPCPGSSCAVVPKTKVWCTNCTPTGTTGKCELCDDGYFG 780  
 DB 754 CSDGYIGDSTAGTSDQPCPCPGSSCAVVPKTKVWCTNCTPTGTTGKCELCDDGYFG 813  
 QY 781 DPLGRNGPVLRLCRLCQCSNIDPNAVCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 840  
 DB 814 DPLGRNGPVLRLCRLCQCSNIDPNAVCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 873  
 QY 841 APNPADKCKACNPNYGTMTKQSSCNVPTGQCCELPHTVQDCGACDPGFYNLQSQGCE 900  
 DB 874 APNPADKCKACNPNYGTMTKQSSCNVPTGQCCELPHTVQDCGACDPGFYNLQSQGCE 933  
 QY 901 RCDCHALGSTNGQCDIITGQCEQCPGTTGQRCERCVNHPFGPGECKPCDCHPEGSLSL 960  
 DB 934 RCDCHALGSTNGQCDIITGQCEQCPGTTGQRCERCVNHPFGPGECKPCDCHPEGSLSL 993  
 QY 961 QCKDDGRCCEGREGVGNRCQCEBENYFNRSWPGCOECPACYRLVKDKVADHRVKLQELE 1020  
 DB 994 QCKDDGRCCEGREGVGNRCQCEBENYFNRSWPGCOECPACYRLVKDKVADHRVKLQELE 1053  
 QY 1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLREAGQVDQVQNDLMDRLQRVNNTLSQ 1080  
 DB 1054 SLIANLTGDEMVTDOAFEDRLKEAREVMDLREAGQVDQVQNDLMDRLQRVNNTLSQ 1113  
 QY 1081 ISRLQNRNTEETGNLAEQARHVENTERLIEIASRELEKAKVAAANYSVTQPESTGDP 1140  
 DB 1114 ISRLQNRNTEETGNLAEQARHVENTERLIEIASRELEKAKVAAANYSVTQPESTGDP 1173  
 QY 1141 NMVTLLEAEARKLAERHKEADDIIRVAKTANDTSTEAYNLLRTLAGEHOTAFEELN 1200  
 DB 1174 NMVTLLEAEARKLAERHKEADDIIRVAKTANDTSTEAYNLLRTLAGEHOTAFEELN 1233  
 QY 1201 RYEQAKNIQSQLEKQAARVHEAKKAGKAVIYASVAQLSPDSEITLSEANNIKMEA 1260  
 DB 1234 RYEQAKNIQSQLEKQAARVHEAKKAGKAVIYASVAQLSPDSEITLSEANNIKMEA 1293  
 QY 1261 ENLEQLIDOKLYEDLREDMRGKELVKNLLEKGTQEQDADOLLARADAKALAEAEA 1320  
 DB 1294 ENLEQLIDOKLYEDLREDMRGKELVKNLLEKGTQEQDADOLLARADAKALAEAEA 1353  
 QY 1321 KKGSDTLQEBANDILNLLKOPDREVNNDKTAABEALAKI PAINTQITPEANEKTRQAQALG 1380  
 DB 1354 KKGSDTLQEBANDILNLLKOPDREVNNDKTAABEALAKI PAINTQITPEANEKTRQAQALG 1413  
 QY 1381 SAAADATEAKNKAHEARTASAVOKNATSTKAABETFAEVTDLDNEVNNMLKQLEAEK 1440  
 DB 1414 SAAADATEAKNKAHEARTASAVOKNATSTKAABETFAEVTDLDNEVNNMLKQLEAEK 1473  
 QY 1441 ELKEKQDQDDQDMMWAGMASQAQAEAINARKAKNSVTLSLSIINDLLEQLQQLDVTDLN 1500

DB 1474 ELKRIKQDDADQDMWAGMASQAQAEINARKAKNSVTSLSIINDLLEQLGQDVTDLN 1533  
QY 1501 KLNIEGTANKAKDEMKVSDLRKVSLENEAKQBAALMDYNRDIEETMKDIRNLEDIR 1560  
DB 1534 KLNIEGTANKAKDEMKVSDLRKVSLENEAKQBAALMDYNRDIEETMKDIRNLEDIR 1593  
QY 1561 KTLPSGCFNTPSIEKP 1576  
DB 1594 KTLPSGCFNTPSIEKP 1609  
RESULT 9  
ID AAB19803  
AA19803 standard; protein; 1617 AA.  
XX  
AC AAB19803;  
XX  
DT 05-MAR-2001 (first entry)  
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.  
DE  
DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..33 /label= Signal\_peptide  
FT 34..1609 /label= Mature\_protein  
FT Peptide 1610..1617 /label= FLAG  
FT  
XX WO20066730-A2.  
PN  
XX 09-NOV-2000.  
PD  
XX 28-APR-2000; 2000WO-USO11378.  
PP  
XX 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
DR WPI; 2000-687537/67.  
DR N-PSDB; AAA88903.  
XX  
PT Purified laminin 2 protein, useful for research and therapeutic purposes  
FT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
XX Claim 5; Page 263-268; 305pp; English.  
PS  
XX The present sequence is that of the gamma-1 chain of human laminin 2,  
XX with an additional C-terminal FLAG epitope, resulting from expression in  
CC transfected cells from mammalian expression vectors. Laminin 2 is  
CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)  
CC chains. It is thought to be specifically required for stabilizing  
CC myotubes during skeletal muscle development, and for preventing  
CC apoptosis. Genetic defects in its structure or expression are associated  
CC with a major type of congenital muscular dystrophy. Laminin 2 is also  
CC thought to be important in Schwann cell/basal lamina interactions. The  
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain  
CC polypeptides (see AAB19791-806) and the polynucleotides encoding them  
CC (see AAA88891-906), methods for making recombinant laminin 2, cells that  
CC express recombinant laminin 2, and methods for using purified laminin 2  
CC for research and therapeutic purposes including peripheral nerve

CC regeneration, treatment of degenerative muscle disorders, angiogenesis  
CC regulation, promoting cell attachment and migration, ex vivo cell  
CC therapy, improving the take of grafts, improving the biocompatibility of  
CC medical devices and preparing improved culture devices and media  
XX  
SQ Sequence 1617 AA;  
Query Match 100.0%; Score 8544; DB 3; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QAAMDECTDEGGRPCRCMPEFVNAAPNVTVVANTGCTPPEEYCVQGTGVTKSHCLCD 60  
DB 34 QAAMDECTDEGGRPCRCMPEFVNAAPNVTVVANTGCTPPEEYCVQGTGVTKSHCLCD 93  
QY 61 AQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLHLGKAFDITVRLKPH 120  
DB 94 AQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQYFSSINLTLHLGKAFDITVRLKPH 153  
QY 121 TSRPESFALYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGGBQQAALCTDEFSDIS 180  
DB 154 TSRPESFALYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGGBQQAALCTDEFSDIS 213  
QY 181 PLTGNVAFSTLEGRPSAYNFDSNPSVLOEWWTATDITVTLNRLNTGDEVNDPKVLKSY 240  
DB 214 PLTGNVAFSTLEGRPSAYNFDSNPSVLOEWWTATDITVTLNRLNTGDEVNDPKVLKSY 273  
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFFNDFRWRATA 300  
DB 274 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFFNDFRWRATA 333  
QY 301 ESASECLPCDCNGRSQBCYFDPPELYRSTGHGHCTNCDNTDGAHCRCRENFRNLGNE 360  
DB 334 ESASECLPCDCNGRSQBCYFDPPELYRSTGHGHCTNCDNTDGAHCRCRENFRNLGNE 393  
QY 361 ACSSCHCSFVGSLSLTQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 420  
DB 394 ACSSCHCSFVGSLSLTQCDSDYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSI 453  
QY 421 DECNVETGRCVKDNVGEFNCERCKPGFFNLESNPRGCTPCFCFHSSVCTNAGVSVY 480  
DB 454 DECNVETGRCVKDNVGEFNCERCKPGFFNLESNPRGCTPCFCFHSSVCTNAGVSVY 513  
QY 481 SISSTFQIDEDGWAEORDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540  
DB 514 SISSTFQIDEDGWAEORDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573  
QY 541 GQNLFSFPRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKVFRLHEATDY 600  
DB 574 GQNLFSFPRVDRDTRLASAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKVFRLHEATDY 633  
QY 601 PWRPALTPFEQKLNILNLTSTKIRGTYSERAGYLDVTLASARPGVGPATWVESCTCP 660  
DB 634 PWRPALTPFEQKLNILNLTSTKIRGTYSERAGYLDVTLASARPGVGPATWVESCTCP 693  
QY 661 VGYGQFCFCEMCLSGYRRETNLPNGYSPCVLCACNGHSETCDPETGVNCNCRDNTAGPHCEK 720  
DB 694 VGYGQFCFCEMCLSGYRRETNLPNGYSPCVLCACNGHSETCDPETGVNCNCRDNTAGPHCEK 753  
QY 721 GSDGYGSTAGTSDSDQPCPCPGSSCAVVPKTEVVCNTNCTGTTGKRCCLDDGVYFG 780  
DB 754 GSDGYGSTAGTSDSDQPCPCPGSSCAVVPKTEVVCNTNCTGTTGKRCCLDDGVYFG 813  
QY 781 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFFGNPL 840  
DB 814 DPLGRNGPVRCLRCQCSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDRCCKDGFFGNPL 873  
QY 841 ANPADKAKACNCPYGMKQSSCNPNVTGQCECLPHVTGQDCCACDPGFVNLQSGQCE 900  
DB 874 ANPADKAKACNCPYGMKQSSCNPNVTGQCECLPHVTGQDCCACDPGFVNLQSGQCE 933  
QY 901 RCDCHALGSTGQCDIRTGQCECOPGITGQHCERCEVNHFGFEGCKPCDCHPEGSLSL 960

Db	934	RDCHALGSTNGQCDIRITGQCEQPGITGQHCERCEVNHFGFPGEGCKPCDCHPEGSLSL	993
Qy	961	QCXDDGRCCEGREGVGNRCQCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLQELE	1020
Db	994	QCXDDGRCCEGREGVGNRCQCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLQELE	1053
Qy	1021	SLIANLTGDMVTQDAFEDRLKEAREVMDLREAOVDKVDQNLMDRLQRVNTLSQ	1080
Db	1054	SLIANLTGDMVTQDAFEDRLKEAREVMDLREAOVDKVDQNLMDRLQRVNTLSQ	1113
Qy	1081	ISRLQNTIRNTEETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1140
Db	1114	ISRLQNTIRNTEETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP	1173
Qy	1141	NNMTLLAEAEKLAERHKQADDIRVAKTANDTSTTEAYNLLRTLAGENQTAPEIEELN	1200
Db	1174	NNMTLLAEAEKLAERHKQADDIRVAKTANDTSTTEAYNLLRTLAGENQTAPEIEELN	1233
Qy	1201	RKYEQAANI SODLEKQARVHEEAKRAGDKAVETIYASVAQLSPDSETLENEANNIKQEA	1260
Db	1234	RKYEQAANI SODLEKQARVHEEAKRAGDKAVETIYASVAQLSPDSETLENEANNIKQEA	1293
Qy	1261	ENLEQLIDQKLKQYEDLREDMRGKELEVKNLLEKGTQEQQTADQLARADAAKALAEAEA	1320
Db	1294	ENLEQLIDQKLKQYEDLREDMRGKELEVKNLLEKGTQEQQTADQLARADAAKALAEAEA	1353
Qy	1321	KKGEDTLOEANDILNLLKDFDRVNDKNTAAEBALRKIPAINOTITTEANEKTRQAQALG	1380
Db	1354	KKGEDTLOEANDILNLLKDFDRVNDKNTAAEBALRKIPAINOTITTEANEKTRQAQALG	1413
Qy	1381	SAAADATEAKNAHEAERIASAVOKNATSTKAAEAERTFAEVTDLNDEVNNMLKQLOPAEK	1440
Db	1414	SAAADATEAKNAHEAERIASAVOKNATSTKAAEAERTFAEVTDLNDEVNNMLKQLOPAEK	1473
Qy	1441	ELKKEQDADDDMMWAGSQAQAEINARKAKNSVTSLLSINDLLEQLGQDITVDLN	1500
Db	1474	ELKKEQDADDDMMWAGSQAQAEINARKAKNSVTSLLSINDLLEQLGQDITVDLN	1533
Qy	1501	KLNEIEGLTNKAKDEMKSVDLDRKVSLENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIR	1560
Db	1534	KLNEIEGLTNKAKDEMKSVDLDRKVSLENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIR	1593
Qy	1561	KTLPSGCFNTPSIEKP	1576
Db	1594	KTLPSGCFNTPSIEKP	1609
RESULT 10			
AAW50898			
ID	AAW50898 standard; protein; 1609 AA.		
XX	AAW50898;		
XX	07-DEC-1998 (first entry)		
DT	Human laminin G1 chain.		
XX			
DE			
XX	Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;		
KW	Down's syndrome; hereditary cerebral haemorrhage; inflammation;		
KW	malignancy; Familial Mediterranean Fever; multiple myeloma;		
KW	type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;		
KW	Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;		
KW	carpal tunnel syndrome; senile cardiac amyloid polynuropathy;		
KW	Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;		
therapy.			
XX			
OS	Homo sapiens.		
XX			
PN	WO9815179-A1.		
XX			
PD	16-APR-1998.		
XX			
PF	08-OCT-1997; 97WO-US018145.		

XX	08-OCT-1996;	96US-0027981P.
PR	(UNIW ) UNIV WASHINGTON.	
PA	Castillo G, Snow AD;	
XX	WPI; 1998-240534/21.	
DR	Use of laminin and fragments - for developing products for use in the	
PT	diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or	
XX	CJD.	
PS	Claim 15; Page 106-109; 132pp; English.	
CC	This is the amino acid sequence of the human laminin G1 chain. The	
CC	primary object of the invention is to use laminin, laminin-derived	
CC	protein fragments and/or laminin-derived polypeptides as potent	
CC	inhibitors of amyloid formation, deposition, accumulation and/or	
CC	persistence in Alzheimer's disease and other amyloidoses. The laminin	
CC	products (see AAWS0888-98) may include mouse or human laminin A or A1	
CC	chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1	
CC	chain, the globular repeats of the laminin A1 chain and the beta-amyloid	
CC	binding domain of the laminin A chain. A claimed method for treating an	
CC	amyloid disease comprises administering a polypeptide having a	
CC	conformational similarity to a fragment of a laminin protein. A method	
CC	for diagnosing an amyloid disease involves determining levels of laminin	
CC	in a sample. Production of laminin or its fourth globular repeat in vivo	
CC	provides a method for in vivo inhibition of beta-amyloid amyloidosis. The	
CC	products and methods can be used for the diagnosis, prognosis, monitoring	
CC	and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome	
CC	and hereditary cerebral haemorrhage with amyloidosis of the Dutch type	
CC	(where the specific amyloid is the beta-amyloid protein), the amyloidosis	
CC	associated with chronic inflammation, various forms of malignancy and	
CC	familial Mediterranean Fever (AA amyloid or inflammation-association	
CC	amyloidosis), the amyloidosis associated with multiple myeloma and other	
CC	B-cell abnormalities (AL amyloid), the amyloidosis associated with type	
CC	II diabetes (amylin or islet amyloid), the amyloidosis associated with	
CC	prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler	
CC	syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis	
CC	associated with long-term haemodialysis and carpal tunnel syndrome (beta	
CC	2-microglobulin amyloid), the amyloidosis associated with senile cardiac	
CC	amyloid and Familial Amyloidotic Polynuropathy (prealbumin or	
CC	transthyretin amyloid), and the amyloidosis associated with endocrine	
CC	tumours such as medullary carcinoma of the thyroid (variant of	
CC	procalcitonin)	
XX	Sequence 1609 AA;	

Query Match	100.0%;	Score 8540;	DB 2;	Length 1609;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1575;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;	
QY	1	QAAMDECTDEGRPORCMPEFVNAFNVTVATNTCGTPPEECVQGTGVTGTSCHLCD	60	
Db	34	QAAMDECTDEGRPORCMPEFVNAFNVTVATNTCGTPPEECVQGTGVTGTSCHLCD	93	
QY	61	ACQPHLQGAAPLTDDYNQADTTWQSQTMLAGVQPPSSINLTLLHKGAFDITYVRLKXFH	120	
Db	94	ACQPHLQGAAPLTDDYNQADTTWQSQTMLAGVQPPSSINLTLLHKGAFDITYVRLKXFH	153	
QY	121	TSRPESFALYKTRTDGWPVQYVYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDIS	180	
Db	154	TSRPESFALYKTRTDGWPVQYVYSGSCENTYSKANRGFIRTTGGDEQQAALCTDFSDIS	213	
QY	181	PLTGNVAFSTLEGPPSAYNFNDNSPVLQEWATDITRVTLNRLNTFGDEVNDPKVLKSY	240	
Db	214	PLTGNVAFSTLEGPPSAYNFNDNSPVLQEWATDITRVTLNRLNTFGDEVNDPKVLKSY	273	
QY	241	YYAISDFAVGGCKCNHGASECMKNEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA	300	
Db	274	YYAISDFAVGGCKCNHGASECMKNEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA	333	

301 ESASECLPCDCNCRSGQCYFDPDELVRSTGHGHCNCQDNTDGAHCERCRENFFRLGNNE 360  
334 ESASECLPCDCNCRSGQCYFDPDELVRSTGHGHCNCQDNTDGAHCERCRENFFRLGNNE 393  
361 ACSSCHCSVSGLSSTOCDYSGCSCKPGVGMKDCRCQGFHSLTEAGRCPCSDPSGSI 420  
394 ACSSCHCSVSGLSSTOCDYSGCSCKPGVGMKDCRCQGFHSLTEAGRCPCSDPSGSI 453  
421 DECNVETGRCVCKNDVEGNCERCKPGFFNLESSNPRGCTPCFCFHHSVCTNAGVYSY 480  
454 DECNVETGRCVCKNDVEGNCERCKPGFFNLESSNPRGCTPCFCFHHSVCTNAGVYSY 513  
481 SISSTFOIDEDGWRABQRGDSASLEWSSERODIAVISDYPFRYFIAPAKELGQVLSY 540  
514 SISSTFOIDEDGWRABQRGDSASLEWSSERODIAVISDYPFRYFIAPAKELGQVLSY 573  
541 GQNLSPSFVRDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 600  
574 GQNLSPSFVRDRDTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 633  
601 PWRPALTPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPQGVPAWVESCCTCP 660  
634 PWRPALTPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPQGVPAWVESCCTCP 693  
661 VYGGGFCBMCCLSGYRRETNLPSPCVLCAENGHSETCDPETGVNCNCRDNTAGPHEX 720  
694 VYGGGFCBMCCLSGYRRETNLPSPCVLCAENGHSETCDPETGVNCNCRDNTAGPHEX 753  
721 CSDGYVGDSTAGTSRCQPCPCPGGSCAVVPKTEWVCTNPTGTTGRCBLCDGDFG 780  
754 CSDGYVGDSTAGTSRCQPCPCPGGSCAVVPKTEWVCTNPTGTTGRCBLCDGDFG 813  
781 DPLGRNGPVLRLCLCOCSNIDNVCNRLTGECLKCIYNTAGFYCDRCXKDFGPNPL 840  
814 DPLGRNGPVLRLCLCOCSNIDNVCNRLTGECLKCIYNTAGFYCDRCXKDFGPNPL 873  
841 APNPADKCAKCNPNYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPOFYNLQSGQCE 900  
874 APNPADKCAKCNPNYGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPOFYNLQSGQCE 933  
901 RCDCHALGSTNGOCDRTGQCECPGIGTGHCEBCEVNHFGPGECKPCDCHPGSLSL 960  
934 RCDCHALGSTNGOCDRTGQCECPGIGTGHCEBCEVNHFGPGECKPCDCHPGSLSL 993  
961 QCKDDGRCREGVNCRDQCEENFYNRSWPGQCEPCACVRLVKDKVADHRVKLQBLE 1020  
994 QCKDDGRCREGVNCRDQCEENFYNRSWPGQCEPCACVRLVKDKVADHRVKLQBLE 1053  
1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLEAODVKVDONLMDLQRVNNTLSQ 1080  
1054 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLEAODVKVDONLMDLQRVNNTLSQ 1113  
1081 ISRLQIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140  
1114 ISRLQIRNTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173  
1141 NNMTLLAEARKLAERHKEADDIVRVAKTANDTSTEANLLRLTAGENQAFIEHLN 1200  
1174 NNMTLLAEARKLAERHKEADDIVRVAKTANDTSTEANLLRLTAGENQAFIEHLN 1233  
1201 RYEOQAKNISDLEKQAAKVHEAKRAGDKAVEIYASVAQLSPDLSETLENNIKMEA 1260  
1234 RYEOQAKNISDLEKQAAKVHEAKRAGDKAVEIYASVAQLSPDLSETLENNIKMEA 1293  
1261 ENLEQIDQKLDYEDLRDMRGKLELVKNLLEKGTQEQTDQDLARADAKALAEBA 1320  
1294 ENLEQIDQKLDYEDLRDMRGKLELVKNLLEKGTQEQTDQDLARADAKALAEBA 1353  
1321 KGRDRTLQANDLILNNKDFDRVNDKNTAAEELRKIPAINQTTIEANEKTRBAQALG 1380  
1354 KGRDRTLQANDLILNNKDFDRVNDKNTAAEELRKIPAINQTTIEANEKTRBAQALG 1413  
1381 SAAADATEAKNKAHEABRIASAVQKNATSTKAEARTFAEVTDLQNEVNNMLKQLQEA 1440

1414 SAAADATEAKNKAHEABRIASAVQKNATSTKAEARTFAEVTDLQNEVNNMLKQLQEA 1473  
1441 ELKKEKQDDAQDDMMMACWASQAQAEAEINARKAKNSVTSLSIINDLLEQLGQDVTDLN 1500  
1474 ELKKEKQDDAQDDMMMACWASQAQAEAEINARKAKNSVTSLSIINDLLEQLGQDVTDLN 1533  
1501 KLNIEGTILNKADEMKVSDLRKVSLENEAKQEAAMNDYNRDIEEIMKDIRNLEDIR 1560  
1534 KLNIEGTILNKADEMKVSDLRKVSLENEAKQEAAMNDYNRDIEEIMKDIRNLEDIR 1593  
1561 KTLPSGCGFNTPSIEKP 1576  
1594 KTLPSGCGFNTPSIEKP 1609

RESULT 11  
AAB19805  
ID AAB19805 standard; protein; 1605 AA.  
XX  
AC AAB19805;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Mouse laminin 2 gamma-1 chain.  
XX  
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Mus musculus.  
XX  
FH Key  
FT Peptide 1. .33 Location/Qualifiers  
FT Protein 34. .1605 /label= Signal\_peptide  
FT /label= Mature\_protein  
XX  
PN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
PS WPI; 2000-687537/67.  
DR N-PSDB; AAA88905.  
XX  
PT Purified laminin 2 protein, useful for research and therapeutic purposes  
including peripheral nerve regeneration, treatment of degenerative muscle  
disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 288-294; 305pp; English.  
XX  
CC The present sequence is that of the gamma-1 chain of mouse laminin 2.  
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
CC (100 kDa) chains. It is thought to be specifically required for  
CC stabilizing myotubes during skeletal muscle development, and for  
CC preventing apoptosis. Genetic defects in human laminin 2 structure or  
CC expression are associated with a major type of congenital muscular  
CC dystrophy. Laminin 2 is also thought to be important in Schwann  
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
CC polynucleotides encoding them (see AAA88891-906), methods for making  
CC recombinant laminin 2, cells that express recombinant laminin 2, and  
CC methods for using purified laminin 2 for research and therapeutic

CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX  
SQ Sequence 1605 AA;

Query Match 94.1%; Score 8043; DB 3; Length 1605;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 1 QAANDCTDEGRQRCMPPEVNAFNTVATNTCGTPPEEVCQVGTGKSHCLCD 60  
DB 32 RAANDCADEGRQRCMPPEVNAFNTVATNTCGTPPEEVCQVGTGKSHCLCD 91  
QY 61 AGQHLGHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLHLGKAFDIYVRLKPH 120  
DB 92 AGQHLGHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLHLGKAFDIYVRLKPH 151  
QY 121 TSRPESFAIYRTREDGFWIPYQYSGSCENTYSKANRGFIRGGDEQQALCTDEFSDIS 180  
DB 152 TSRPESFAIYRTREDGFWIPYQYSGSCENTYSKANRGFIRGGDEQQALCTDEFSDIS 211  
QY 181 PLTGNVAFSTLEGRPSAYNFDNPSVLQEWATDIDRVTLNRLNTFGDEVFNDPKVLSY 240  
DB 212 PLTGNVAFSTLEGRPSAYNFDNPSVLQEWATDIDRVTLNRLNTFGDEVFNDPKVLSY 271  
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCBKLPFFNDPWRATA 300  
DB 272 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCBKLPFFNDPWRATA 331  
QY 301 ESASBCLPCDCNGRSOECYFPELYRSTGHGCHTNCQDNTDGAHCRERENFRLGNE 360  
DB 332 ESASBCLPCDCNGRSOECYFPELYRSTGHGCHTNCQDNTDGAHCRERENFRLGNE 391  
QY 361 ACSSCHCSFVGLSTQDCSYGRCSKPGWMDKCDRCQPGFHSLTEAGRCPCSDPSGI 420  
DB 392 ACSPCHCSFVGLSTQDCSYGRCSKPGWMDKCDRCQPGFHSLTEAGRCPCSDPSGI 451  
QY 421 DECVETGRVCVKNDVEGFNCRCKPFPNLESNPRGCTPCFCFHSVCTNAGYSVY 480  
DB 452 DECVETGRVCVKNDVEGFNCRCKPFPNLESNPRGCTPCFCFHSVCTNAGYSVY 511  
QY 481 SISSTFOIDECWRAEQDGSSEASLEWSSERQDIASVSDSYFPRYFAPAKFLGKQVLSY 540  
DB 512 DISSTFOIDECWRAEQDGSSEASLEWSSERQDIASVSDSYFPRYFAPAKFLGKQVLSY 571  
QY 541 GONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFLRHEATDY 600  
DB 572 GONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFLRHEATDY 631  
QY 601 PWRPALTPPEFQKLNLLNTSKIRGTYSERSAGYLDVTLASARPGVGPATVWESCTCP 660  
DB 632 PWRPALTPPEFQKLNLLNTSKIRGTYSERSAGYLDVTLASARPGVGPATVWESCTCP 691  
QY 661 VYGGQFCMCLSGYRRTPNLGYPSPVLCAHNGHSETCDPFGVNCNDRNTAGPCEK 720  
DB 692 VYGGQFCMCLSGYRRTPNLGYPSPVLCAHNGHSETCDPFGVNCNDRNTAGPCEK 751  
QY 721 CSDGYVGGSTAGTSDCQPCPCGSSCAVVPKTEVVTCTGTTGKRCCLCDDGYFG 780  
DB 752 CSDGYVGGSTAGTSDCQPCPCGSSCAVVPKTEVVTCTGTTGKRCCLCDDGYFG 811  
QY 781 DPLGRNGPVRLCRLQCCSDNIDPNVAGNCRLTGCECLKIYNTAGFYCDRCCKGFFGNPL 840  
DB 812 DPLGRNGPVRLCRLQCCSDNIDPNVAGNCRLTGCECLKIYNTAGFYCDRCCKGFFGNPL 871  
QY 841 APNPADKCKACNCPYGTQKQSSCNVYTGQCECLPHVYTGQCCGACDPCGPFYVNLQSGGCE 900  
DB 872 APNPADKCKACNCPYGTQKQSSCNVYTGQCECLPHVYTGQCCGACDPCGPFYVNLQSGGCE 930  
QY 901 RCDCHALGSTNGQCDIRTGQCEQPGITGQHCEVNHFGFPGGCKPCDCHPEGSLSL 960

DB 931 RCDCHALGSTNGQCDIRTGQCEQPGITGQHCEVNHFGFPGGCKPCDCHPEGSLSL 990  
QY 961 QCKDDGRCECEGFGVGNRCQCEENYFYNRSWPGQCEPCACRYLVKQKADHRVVKLQELE 1020  
DB 991 QCKDDGRCECEGFGVGNRCQCEENYFYNRSWPGQCEPCACRYLVKQKADHRVVKLQELE 1050  
QY 1021 SLIANLGTGDEWVTDOAFEDRLKEAREHVMILLREAOQVKDQNDMLDRQVNTLSQ 1080  
DB 1051 SLIANLGTGDEWVTDOAFEDRLKEAREHVMILLREAOQVKDQNDMLDRQVNTLSQ 1110  
QY 1081 ISRLQNIQNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSTQPESTGDP 1140  
DB 1111 ISRLQNIQNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSTQPESTGDP 1169  
QY 1141 NNMTLLABEARKLAEHVKQADDDIVRVAKTANDSTSEYNNLLRTLAGENOTAFIEELN 1200  
DB 1170 NNMTLLABEARKLAEHVKQADDDIVRVAKTANDSTSEYNNLLRTLAGENOTAFIEELN 1229  
QY 1201 RYVEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKEA 1260  
DB 1230 RYVEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKEA 1289  
QY 1261 ENLEQLIQKLYEDLREDMRGKELEVKNLLEKQTEQQTADQLLARADAAKALAEAA 1320  
DB 1290 ADLRLIQKLYEDLREDMRGKELEVKNLLEKQTEQQTADQLLARADAAKALAEAA 1349  
QY 1321 KKGRTLOEANDILNNLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRAQQAALG 1380  
DB 1350 KKGRTLOEANDILNNLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRAQQAALG 1409  
QY 1381 SAADATEAKNKAHEAERIASAVQKNATSTKAEABERTFAEVTDLNNEVNNMLKQLEBAEK 1440  
DB 1410 NAADATEAKNKAHEAERIASAVQKNATSTKAEABERTFAEVTDLNNEVNNMLKQLEBAEK 1469  
QY 1441 ELKRRDODADODMMWAGWASQAQAEAEINARKAKNSVLSLSIINDLLEQLGQDVTVDLN 1500  
DB 1470 ELKRRDODADODMMWAGWASQAQAEAEINARKAKNSVLSLSIINDLLEQLGQDVTVDLN 1529  
QY 1501 KLINEIEGTLNKAEMKVSDDLDRKVSYLENEAKQEAAMNDYNDIEEIMKDINLEDIR 1560  
DB 1530 KLINEIEGTLNKAEMKVSDDLDRKVSYLENEAKQEAAMNDYNDIEEIMKDINLEDIR 1589  
QY 1561 KTLPGCFNTPSIEKP 1576  
DB 1590 KTLPGCFNTPSIEKP 1605

RESULT 12  
AAB48454  
ID AAB48454 standard; protein; 1605 AA.  
XX AAB48454;  
AC AAB48454;  
DT 02-MAR-2001 (first entry)  
XX Mouse laminin 8 polypeptide, SEQ ID NO: 26.  
DE Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
OS Mus musculus.  
XX WO2000066732-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011543.  
XX 30-APR-1999; 99US-0131720P.  
XX 21-AUG-1999; 99US-0149738P.  
XX 24-SEP-1999; 99US-0155945P.

PR 11-FEB-2000; 2000US-0182012P.  
 PA (BIOS-) BIOSTRATUM INC.  
 XX Kortessmaa J, Tryggvason K;  
 PI WPI; 2000-687539/67.  
 XX N-PSDB; AAC83715.  
 DR Purified laminin 8 protein, useful for research and therapeutic purposes  
 XX including peripheral nerve regeneration, treatment of degenerative muscle  
 PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
 PT Claim 5; Page 227-232; 245pp; English.  
 XX  
 CC The present sequence is a laminin 8 polypeptide chain. Laminins are a  
 CC family of heterotrimeric glycoproteins that function via binding  
 CC interactions with neighbouring cell receptors and by forming laminin  
 CC networks. They are signalling molecules which influence cellular  
 CC function. Laminin 8 is useful for treating injuries to tissue of  
 CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
 CC treating injuries to vascular tissue, promoting cell attachment and  
 CC migration, ex vivo cell therapy, improving the biocompatibility of  
 CC medical devices, and preparing improved cell culture devices and media.  
 CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
 CC of vascular injuries, improving the take of grafts, improving the  
 CC biocompatibility of medical devices, treating neural injuries (neural  
 CC regeneration), regulating angiogenesis, and promoting cell attachment and  
 CC migration  
 XX  
 XX Sequence 1605 AA;  
 SQ  
 Query Match 94.1%; Score 8043; DB 3; Length 1605;  
 Best Local Similarity 93.3%; Pred. No. 0;  
 Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;  
 QY 1 QAMDCSTDEGRPQRCMPPEFNAAPNVVATNCTGTPPEYCVQTGVTKSCHLCD 60  
 DB 32 RAMDCABEGRPQRCMPPEFNAAPNVVATNCTGTPPEYCVQTGVTKSCHLCD 91  
 QY 61 AGOPHLOHGAFLTDYNNQADTTWQSTMLAGVQYPSINILTLHLKAFDITYRLKPH 120  
 DB 92 AGOCHLOHGAFLTDYNNQADTTWQSTMLAGVQYPSINILTLHLKAFDITYRLKPH 151  
 QY 121 TSRPESFALKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDBQOALCTDFSDIS 180  
 DB 152 TSRPESFALKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDBQOALCTDFSDIS 211  
 QY 181 PLTGGNVAFSTLEGPSAYNFDNSPVLQSWVTATDIRVTNLNLTFGDEVFNDPVLKSY 240  
 DB 212 PLTGGNVAFSTLEGPSAYNFDNSPVLQSWVTATDIRVTNLNLTFGDEVFNDPVLKSY 271  
 QY 241 YYAISDFAVGGRCCKNGHASECKKNEPDKLVCKNCKHNTYGVDCCKLPFFNDRPWRATA 300  
 DB 272 YYAISDFAVGGRCCKNGHASECKKNEPDKLVCKNCKHNTYGVDCCKLPFFNDRPWRATA 331  
 QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTNCOQNTDGAHCERENFFRLGNNE 360  
 DB 332 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTNCRDNTDGAHCERENFFRLGNTE 391  
 QY 361 ACSSCHCSPVGLSTQCDYGRCKCKPVGWGDRCQPFHSLTEAGRCPCSDPSSGI 420  
 DB 392 ACSPCHCSPVGLSTQCDYGRCKCKPVGWGDRCQPFHSLTEAGRCPCSDPSSGI 451  
 QY 421 DECNVETGRVCKDNVGEFNCRCRCKPFPNLESSNPRGCTPCFCFHSVSVCTNAVGVSVY 480  
 DB 452 DECNVETGRVCKDNVGEFNCRCRCKPFPNLESSNPRGCTPCFCFHSVSVCTNAVGVSVY 511  
 QY 481 SISSTFQIDEDGWRABQRDGSSEASLEWSSERODIAVISDYPFRPIAPKFLGQVLSY 540  
 DB 512 DISSFTQIDEDGWRABQRDGSSEASLEWSSERODIAVISDYPFRPIAPKFLGQVLSY 571  
 QY 541 GQNLSPFRVDRDRTLSDLEVLLEGAGLRVSVPLIAQGNVSPSETTVKYIFRLHEATDY 600

DB 572 GQNLSPFRVDRDRTLSDLEVLLEGAGLRVSVPLIAQGNVSPSETTVKYIFRLHEATDY 631  
 QY 601 PWRPALTPFPQKLLNNLTISKIRGYYSERSAGYLDVTLASARPGPGVPAWVESCCTCP 660  
 DB 632 PWRPALSPFPQKLLNNLTISKIRGYYSERSAGYLDVTLASARPGPGVPAWVESCCTCP 691  
 QY 661 VVGGOFCMCLSGYRRETNLGPYSPVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720  
 DB 692 VVGGOFCMCLSGYRRETNLGPYSPVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 751  
 QY 721 CSDGYGDSSTAGTSSDQPCPCPGSSCAVVPKTKVVCNCTGTGTGKRCCLCDGYFG 780  
 DB 752 CSDGYGDSSTAGTSSDQPCPCPGSSCAVVPKTKVVCNCTGTGTGKRCCLCDGYFG 811  
 QY 781 DPLGRNGPVRCLCQCQSDNIDPNAVCNRLTGECLKCIYNTAGFYCDCKDGFENPL 840  
 DB 812 DPLGSNGPVRCLCQCQSDNIDPNAVCNRLTGECLKCIYNTAGFYCDCKDGFENPL 871  
 QY 841 APNPADCKACACNPNYGTMKQSSCNFVTCQCECLPHVTGQDCGADPGFYNLSQSGCE 900  
 DB 872 APNPADCKACACNPNYGTMKQSSCNFVTCQCECLPHVTGQDCGADPGFYNLSQSGCE 930  
 QY 901 RCDCHALGSTNGQCDINTGOCRCQPGITGOCRCCEVNHFGPGECKPCDCHPEGSLSL 960  
 DB 931 RCDCHALGSTNGQCDINTGOCRCQPGITGOCRCCEVNHFGPGECKPCDCHPEGSLSL 990  
 QY 961 QCKDDGRCECREGFGVGNRCQCEENFYNSWFGQCECPACYRLVKDKVADHRVKLQELE 1020  
 DB 991 QCKDDGRCECREGFGVGNRCQCEENFYNSWFGQCECPACYRLVKDKVADHRVKLQELE 1050  
 QY 1021 SLIANLTGDBMTVDQAFEDRLKEABREVMDLREABQDVKDQVNDQNLMDRLQRVNLTSSQ 1080  
 DB 1051 SLIANLTGDBMTVDQAFEDRLKEABREVMDLREABQDVKDQVNDQNLMDRLQRVNLTSSQ 1110  
 QY 1081 ISRLQNTIRNTIEETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVTVOPESTGDP 1140  
 DB 1111 ISRLQNTIRNTIEETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVTVOPESTGDP 1169  
 QY 1141 NNMTLLAEARKLAERHKQABDDIVRVAKTANTDTSTAYNLLRTLAGENQTAFAIEELN 1200  
 DB 1170 NNMTLLAEARKLAERHKQABDDIVRVAKTANTDTSTAYNLLRTLAGENQTAFAIEELN 1229  
 QY 1201 RYBEOAKNIQDLEKQAAHVHEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260  
 DB 1230 RYBEOAKNIQDLEKQAAHVHEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1289  
 QY 1261 ENLEQLIDQKLDYEDLREDMRGKELEVKNLLEKGTQOQTADQOLLARADAALAEAEA 1320  
 DB 1290 ADLRLIDQKLDYEDLREDMRGKELEVKNLLEKGTQOQTADQOLLARADAALAEAEA 1349  
 QY 1321 KKGSDTLQEAANDILNLLKDFDRVNDKNTAAEALRKIPAINOTITEANEKTEAQAALG 1380  
 DB 1350 KKGSDTLQEAANDILNLLKDFDRVNDKNTAAEALRKIPAINOTITEANEKTEAQAALG 1409  
 QY 1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAAERTFAEVTOLDNEVNNMLKQLEAEK 1440  
 DB 1410 NAAADATEAKNKAHEAERIASAVQKNATSTKAAERTFAEVTOLDNEVNNMLKQLEAEK 1469  
 QY 1441 ELKXKQDADQDMMAGMASQAQAEAINAKKAKSVTSLSIINDLLBQLGOLDTVDLN 1500  
 DB 1470 ELKXKQDADQDMMAGMASQAQAEAINAKKAKSVTSLSIINDLLBQLGOLDTVDLN 1529  
 QY 1501 KLANIEGTLNKAKDEMVKVSLDRKVSLENEAKKQAEAIMDYNRDIIEEMKDIRNLEDIR 1560  
 DB 1530 KLANIEGTLNKAKDEMVKVSLDRKVSLENEAKKQAEAIMDYNRDIIEEMKDIRNLEDIR 1589  
 QY 1561 KTLPSGCFNTPSTIEKP 1576  
 DB 1590 KTLPSGCFNTPSTIEKP 1605

RESULT 13

ABBA1596	DB	152	TSRPESFAIYKRTREDDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDQEQALCTDEPDSIS	211
ID ABB81596 standard; protein; 1605 AA.	QY	181	PLTGNVAFSTLEGRPSAYNFDSNVLQEWWTATDTRVTLNRLNTFGDEVNPKVLKSY	240
AC ABB81596;	DB	212	PLTGNVAFSTLEGRPSAYNFDSNVLQEWWTATDTRVTLNRLNTFGDEVNPKVLKSY	271
DT 19-SEP-2002 (first entry)	QY	241	YYAISDFAVGRCRCNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFFNDFRRRATA	300
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.	DB	272	YYAISDFAVGRCRCNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFFNDFRRRATA	331
XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;	QY	301	BSASECLPCDNGRSQCYDPPELYRSTGHGCHCTNCDNTDGAHCERCENPRLGNNE	360
KW tissue repair development; laminin; healing; vascular tissue;	DB	332	BSASECLPCDNGRSQCYDPPELYRSTGHGCHCTNCDNTDGAHCERCENPRLGNNE	391
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;	QY	361	ACSSCHSPVGSLSLSTQCDSYGRCSCKPVGMDKCDRCQPGFHSILTEAGCRPCSDPSGSI	420
XX proliferation; migration.	DB	392	ACSPCHSPVGSLSLSTQCDSYGRCSCKPVGMDKCDRCQPGFHSILTEAGCRPCSDPSGSI	451
OS Mus musculus.	QY	421	DECNVTGRCVKDNVEGFNCRCCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSVY	480
XX Key Location/Qualifiers	DB	452	DECNVTGRCVKDNVEGFNCRCCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSVY	511
FT Peptide 1..33 /label= signal	QY	481	SISSTFQIDEDGWEAKORDGSEASLEWSSRRQDIAVISDSYFFPRYFIAPAKFLGKQVLSY	540
FT Protein 34..1605 /label= laminin_10_third_chain	DB	512	SISSTFQIDEDGWEAKORDGSEASLEWSSRRQDIAVISDSYFFPRYFIAPAKFLGKQVLSY	571
XX WO2002050111-A2.	QY	541	GQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNISYSETTVKVFRLHEATDY	600
PD 27-JUN-2002.	DB	572	GQNLFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNISYSETTVKVFRLHEATDY	631
XX 21-DEC-2001; 2001WO-US051035.	QY	601	PWRPALTPFEFOKLLNLTSTIKIRGTYSERSAGVLDVTLASARPGVGPATVWESCTCP	660
PR 21-DEC-2000; 2000US-0257449P.	DB	632	PWRPALTPFEFOKLLNLTSTIKIRGTYSERSAGVLDVTLASARPGVGPATVWESCTCP	691
PR 28-MAR-2001; 2001US-0279822P.	QY	661	VGYGGQFCMCLSGYRRETPNLGYSVPCVLCACNHSSETCDPETGVCNCRDNTAGPHCEK	720
PR 13-NOV-2001; 2001US-00279282.	DB	692	VGYGGQFCMCLSGYRRETPNLGYSVPCVLCACNHSSETCDPETGVCNCRDNTAGPHCEK	751
XX (BIOS-) BIOSTRATUM INC.	QY	721	CSDYGYDSTAGTSSDCPCPCGGSSCAVVPKTKVCTNCTGTGKCELCDDGVFG	780
XX Tryggvason K, Doi M, Thyboll J;	DB	752	CSDYGYDSTAGTSSDCPCPCGGSSCAVVPKTKVCTNCTGTGKCELCDDGVFG	811
DR WPI; 2002-557650/59.	QY	781	DPLGRNGPVRLCRLCQCDNIDPNAVGNLCNRLTGCECLKIYNTAGFYCDRCCKGFFGNPL	840
XX N-PSDB; ABQ72914.	DB	812	DPLGRNGPVRLCRLCQCDNIDPNAVGNLCNRLTGCECLKIYNTAGFYCDRCCKGFFGNPL	871
XX New human laminin-10 proteins, useful for accelerating the healing of	QY	841	APNPADKCAKACNPNYGTMOQSSCNVPTGQCECLPHVTQDQDQACDPGNLQSGGCE	900
PT vascular tissue, improving the biocompatibility of grafts, or for	DB	872	APNPADKCAKACNPNYGTMOQSSCNVPTGQCECLPHVTQDQDQACDPGNLQSGGCE	930
PT promoting re-endothelialization at the site of vascular injuries.	QY	901	RCDCHALGSTNGQCDIRTGQCECPGIGTGOHCERCEVNHFGFPGEGCKPCDCHPEGSLSL	960
XX Claim 9; Page 191-195; 21pp; English.	DB	931	RCDCHALGSTNGQCDIRTGQCECPGIGTGOHCERCEVNHFGFPGEGCKPCDCHPEGSLSL	990
XX The present invention describes human laminin alpha 5. Also described is	QY	961	QCKDDGRCCEGREGVGNRCDCENYFYNRSWPCQCPACIYRLVKDQVADHRVKLOELE	1020
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are	DB	991	QCKDDGRCCEGREGVGNRCDCENYFYNRSWPCQCPACIYRLVKDQVADHRVKLOELE	1050
CC useful in maintaining cell/tissue phenotype as well as promoting cell	QY	1021	SLIANLGTGDSMTDQAFEDRLKEAREVMDLLREADQVDVNDONLMDRLQRVNNTLSQ	1080
CC growth and differentiation in tissue repair development. Specifically,	DB	1051	SLIANLGTGDSMTDQAFEDRLKEAREVMDLLREADQVDVNDONLMDRLQRVNNTLSQ	1110
CC laminin 10 can be used for accelerating the healing injuries of vascular	QY	1081	ISRLQINRTIETGNTLAQARAHVENTERLIEIASRELEKAKVAAANVSUTQPESTGDP	1140
CC tissue, improving the biocompatibility of grafts useful for treating such	DB	1111	ISRLQINRTIETGNTLAQARAHVENTERLIEIASRELEKAKVAAANVSUTQPESTGDP	1169
CC injuries, for promoting re-endothelialisation at the site of vascular	QY	1141	NNMTLLAEAEARKLAERKQKQADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIIBELN	1200
CC proliferates, and promote cell attachment and subsequent cell stasis,	DB	1170	NNMTLLAEAEARKLAERKQKQADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIIBELN	1229
CC represents a third chain protein of laminin 10, from the present	QY	1201	RKYEQAKNISQDLKQAKARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKWEA	1260
CC invention	DB	1230	RKYEQAKNISQDLKQAKARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEA	1289

Query Match 94.1%; Score 8043; DB 5; Length 1605;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 1 QANDECTDGGRCQRCWPFVNAFNVVATNTGTPPEEYCVOTGVTKSCHLCD 60  
DB 32 RAANDECADEGGRQRCWPFVNAFNVVATNTGTPPEEYCVOTGVTKSCHLCD 91  
QY 61 AGQPHLGHAFLDYNNQADTTWQSQOTMLAGVQVPSSINLTLHLGKAFDITYVLKXTH 120  
DB 92 AGQPHLGHAFLDYNNQADTTWQSQOTMLAGVQVPSSINLTLHLGKAFDITYVLKXTH 151  
QY 121 TSRPESFAIYKRTREDDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDQEQALCTDEPDSIS 180





Db 632 FWRPALSPFFQKLNLLNTLSIKRGTSERTAGYLDVTLQSAKPGGVPATWVESCTCP 691  
Qy 661 VYGGQFCMCLSGYRRETNLPYSPVLCACNGHSETCDPBTGVCNCRDNTAGPHCEK 720  
Db 692 VYGGQFCETCLPGYRRETSPLGYSVCLCTCNHGHSETCDPBTGVCDCRDNTAGPHCEK 751  
Qy 721 CSDDGYGDSGTAGSSDCCPCPCGGSSCAVPTKKEVWCTNCPGTGTRCBLCDGDFG 780  
Db 752 CSDDGYGDSGTAGSSDCCPCPCGGSSCAVPTKKEVWCTNCPGTGTRCBLCDGDFG 811  
Qy 781 DPLGRNGPVLRLCRLCQSDNDIDNAGVNCNRLTGECLKCIYNTAGYCDRCCKDGFPGNPL 840  
Db 812 DPLGSNGPVLRLCPCQCNNDIDNAGVNCNRLTGECLKCIYNTAGYCDRCCKEGFGNPL 871  
Qy 841 APNPADKCKACNCPYGTMKQSSCNPTVGOCECLPHVTGDCGACDPCGFYNLQSGQCE 900  
Db 872 APNPADKCKACNCPYGTMKQSSCNPTVGOCECLPHVTGDCGACDPCGFYNLQSGQCE 931  
Qy 901 RCDHALGSTNGQDINTGQCEQPGITGQHCERCERNHFGPGEGCKPCDCHPGSGLSL 960  
Db 932 RCDHALGSTNGQDINTGQCEQPGITGQHCERCERNHFGPGEGCKPCDCHPGSGLSL 991  
Qy 961 QCKDDGCECEGFGVGNRCDOCEENFYNRSWPGQCECPACVRLVKDVADHRVYKQBLE 1020  
Db 992 QCKDDGCECEGFGVGNRCDOCEENFYNRSWPGQCECPACVRLVKDVADHRVYKQBLE 1051  
Qy 1021 SLIANLTGDMVTDOAFEDRLKEAREVMDLRLRAQDVQKVDQNLMDRLQVNNLTSSQ 1080  
Db 1052 SLIANLTGDMVTDOAFEDRLKEAREVMDLRLRAQDVQKVDQNLMDRLQVNNLTSSQ 1111  
Qy 1081 ISRLQNTNRTIETGNLQARAHVENTERLEIASRELEKAKAAVANSVTOPESTGDP 1140  
Db 1112 ISRLQNTNRTIETGNLQARAHVENTERLEIASRELEKAKAAVANSVTOPESTGDP 1171  
Qy 1141 NNMTLLAEARKLAERHKEQADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFEIEBLN 1200  
Db 1172 NNMTLLAEARKLAERHKEQADDIVRVAKTANDTSTEAYNLLRLTAGENQTAFEIEBLN 1231  
Qy 1201 RYEQAKNISQDLEKQARVHEEAKGAGDKAVEIYASVAQLSPDSETLEANEANNIWEA 1260  
Db 1232 RYEQAKNISQDLEKQARVHEEAKGAGDKAVEIYASVAQLSPDSETLEANEANNIWEA 1291  
Qy 1261 ENLEQLIDQKDYEDLREDMRGKELEVNLLLEKQTEQQTADQLARADAAKALABEAA 1320  
Db 1292 ADLRLIDQKDYEDLREDMRGKELEVNLLLEKQTEQQTADQLARADAAKALABEAA 1351  
Qy 1321 KKGRTLOEANDILNKKDFDRVNDKNTAAEALRKTPAINQTTTEANEKTRAQOALG 1380  
Db 1352 KKGRTLOEANDILNKKDFDRVNDKNTAAEALRKTPAINQTTTEANEKTRAQOALG 1411  
Qy 1381 SAAADATEAKNKAHEARIASAVOKNATSTKAEARTFAEVTDLNENYNNMLKQLEAEK 1440  
Db 1412 NAAADATEAKNKAHEARIASAVOKNATSTKAEARTFAEVTDLNENYNNMLKQLEAEK 1471  
Qy 1441 ELKRGKODDADQMMAGMASQAQAEABINARKKNSVTSLSIINDLEQLGQDQTDVLDN 1500  
Db 1472 ELKRGKODDADQMMAGMASQAQAEABINARKKNSVTSLSIINDLEQLGQDQTDVLDN 1531  
Qy 1501 KLNIEGTNLKAKDEMKVSDLRKYSVLENEAKKQEAAMIDYNDRIEIMKDINRLIEDIR 1560  
Db 1532 KLNIEGTNLKAKDEMKVSDLRKYSVLENEAKKQEAAMIDYNDRIEIMKDINRLIEDIR 1591  
Qy 1561 KTLPSGCENTPTSEK 1576  
Db 1592 KTLPSGCENTPTSEK 1607

RESULT 15  
AAB19806  
ID AAB19806 standard; protein; 1572 AA.  
XX  
AC AAB19806;

XX 05-MAR-2001 (first entry)  
XX Mouse laminin 2 mature gamma-1 chain.  
XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
XX degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX Mus musculus.  
XX WO200066730-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011378.  
XX 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
XX 12-JUL-1999; 99US-0143289P.  
XX 24-SEP-1999; 99US-0155945P.  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA86906.  
XX Purified laminin 2 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 302-306; 305pp; English.  
XX The present sequence is that of mouse laminin 2 gamma-1 chain mature  
XX protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and  
XX gamma-1 (100 kDa) chains. It is thought to be specifically required for  
XX stabilizing myotubes during skeletal muscle development, and for  
XX preventing apoptosis. Genetic defects in human laminin 2 structure or  
XX expression are associated with a major type of congenital muscular  
XX dystrophy. Laminin 2 is also thought to be important in Schwann  
XX cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
XX beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
XX polynucleotides encoding them (see AAA8891-906), methods for making  
XX recombinant laminin 2, cells that express recombinant laminin 2, and  
XX methods for using purified laminin 2 for research and therapeutic  
XX purposes including peripheral nerve regeneration, treatment of  
XX degenerative muscle disorders, angiogenesis regulation, promoting cell  
XX attachment and migration, ex vivo cell therapy, improving the take of  
XX grafts, improving the biocompatibility of medical devices and preparing  
XX improved culture devices and media  
XX Sequence 1572 AA;

Query Match 94.1%; Score 8038; DB 3; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
Qy 3 AMDECTDGGPQRCMPFVNAFNVTVATNTCGTPPEYCVQTVGTGKTSCHLCDAG 62  
Db 1 AMDECAEGGRPQRCMPFVNAFNVTVATNTCGTPPEYCVQTVGTGKTSCHLCDAG 60  
Qy 63 QPHLGHGAFLTDVNNQADTTWQSQOTMLAGVQVPSINLTLLHGKAFDITYVRLKPHTS 122  
Db 61 QPHLGHGAFLTDVNNQADTTWQSQOTMLAGVQVPSINLTLLHGKAFDITYVRLKPHTS 120  
Qy 123 RPESFAIYKTRDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 182  
Db 121 RPESFAIYKTRDGPWIPYQYSGSCENTYSKANRGFIRTTGGDEQQALCTDFSDISPL 180  
Qy 183 TCGNVAFSTLEGRPSAYNFONS PVLQEWVATDIRVTNLNTEGDEVNDPKVLKSYV 242  
Db 181 TCGNVAFSTLEGRPSAYNFONS PVLQEWVATDIRVTNLNTEGDEVNDPKVLKSYV 240

QY 243 AISDFAVGGRCKNGHASECKWNEFDKLVNCKHNTYGVDCCKLFFFNDRPWRATAES 302  
DB 241 AISDFAVGGRCKNGHASECKWNEFDKLVNCKHNTYGVDCCKLFFFNDRPWRATAES 300  
QY 303 ASECLPCDCNCRSGOEYDFDELVRSTGHGHCNTCNDTDGACERCRNFRLGNNEAC 362  
DB 301 ASECLPCDCNCRSGOEYDFDELVRSTGHGHCNTCNDTDGACERCRNFRLGNTEAC 360  
QY 363 SSCSCPSVGLSTOCDYGRCSCKPGVWGDCKDRCPGHSLTEACRSCDPPSGSIDE 422  
DB 361 SPCHSCPSVGLSTOCDYGRCSCKPGVWGDCKDRCPGHSLTEACRSCDPPSGSIDE 420  
QY 423 CNVETGRVCVKDNVEGFCNCRKPGFFNLESSNPRGCTPCFCFCHGSSVCTNAVGSYVSI 482  
DB 421 CNVETGRVCVKDNVEGFCNCRKPGFFNLESSNPKGCTPCFCFCHGSSVCTNAVGSYVDI 480  
QY 483 SSTFOIDEDGWRABORCGSASLEWSSERQDIAVISDSYPPRYFIAPAKFLCKQVLSYCO 542  
DB 481 SSTFOIDEDGWRABORCGSASLEWSSERQDIAVISDSYPPRYFIAPAKFLCKQVLSYCO 540  
QY 543 NLSFSFVRDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSTTVKYVFRLHEATDYPW 602  
DB 541 NLSFSFVRDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSTTVKYVFRLHEATDYPW 600  
QY 603 RPAUTPFEFOKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCPVG 662  
DB 601 RPAUTPFEFOKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVPATWVESCTCPVG 660  
QY 663 YGGQFCMCLSGVRETPNLPYSPCVLACNCHSETCDPETGVCNCRONTAGPCHCKCS 722  
DB 661 YGGQFCMCLSGVRETPNLPYSPCVLACNCHSETCDPETGVCNCRONTAGPCHCKCS 720  
QY 723 DGYGDSSTAGTSSDCPCPCPGSSSCAVVPKTEVVCNCTPTGTTOKRCELDDGDFGDP 782  
DB 721 DGYGDSSTAGTSSDCPCPCPGSSSCAVVPKTEVVCNCTPTGTTOKRCELDDGDFGDP 780  
QY 783 LGRNGPVRCLRLCOCSDNIDPNVAGNRLTGELCKIYNTAGFYCDRCCKGFFGNPLAP 842  
DB 781 LGRNGPVRCLRLCOCSDNIDPNVAGNRLTGELCKIYNTAGFYCDRCCKGFFGNPLAP 840  
QY 843 NPADKCKACNPNYGTWKQSSCNVPTGQCECLPHVTGQDCGACDPGFYNLQSGGQCERC 902  
DB 841 NPADKCKACNPNYGTWKQSSCNVPTGQCECLPHVTGQDCGACDPGFYNLQSGGQCERC 899  
QY 903 DCHALGSTNGQCDIRTGQCECPGIGQHCHERCEVNHFGPBGCKPCDCHPEGSLSLQC 962  
DB 900 DCHALGSTNGQCDIRTGQCECPGIGQHCHERCEVNHFGPBGCKPCDCHPEGSLSLQC 959  
QY 963 KDDGRCECRGFGVGNRCDCQCEENFYFNRSWPGQCECPACVRLVKQVADHRVKLOELBSL 1022  
DB 960 KDDGRCECRGFGVGNRCDCQCEENFYFNRSWPGQCECPACVRLVKQVADHRVKLOELBSL 1019  
QY 1023 IANLGTGDMVTDOAFEDRLKEAREVMDLREAOQVMDVQNDLMDRLORVNNLTSSQIS 1082  
DB 1020 IANLGTGDMVTDOAFEDRLKEAREVMDLREAOQVMDVQNDLMDRLORVNNLTSSQIS 1079  
QY 1083 RLQNRNTIETGNLABQARAHVENTERLIEIASRELEKAKVAANVSVPQESTGDPNN 1142  
DB 1080 RLQNRNTIETGNLABQARAHVENTERLIEIASRELEKAKVAANVSVPQESTGDPNN 1138  
QY 1143 MTLAEERARKLABRHKOEADDIVRVAKTANDTSTAYNLLRLTAGENOTAFIEBELNRK 1202  
DB 1139 MTLAEERARKLABRHKOEADDIVRVAKTANDTSTAYNLLRLTAGENOTAFIEBELNRK 1198  
QY 1203 YEQAKNTISQLEKQAAVHEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKOEARN 1262  
DB 1199 YEQAKNTISQLEKQAAVHEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKOEARN 1258  
QY 1263 LEQLIDOKLYEDLREDMGKELEVNKLEKTEQOOTADOLARADAAKALAEBAKK 1322  
DB 1259 LDRLLIDOKLYEDLREDMGKELEVNKLEKTEQOOTADOLARADAAKALAEBAKK 1318

QY 1323 GRDTLOEANDILNNLKDFDRVNDNKTAAEEALRKIPAINOTITTEANEKTRAQOALGSA 1382  
DB 1319 GRSTLOEANDILNNLKDFDRVNDNKTAAEEALRRIPALNRTIAEANEKTRAQOALGNA 1378  
QY 1383 AADATEAKNKAHEAERIAAVQKNATSTKAEAEERTFAEYTDLDNEVNNMLKQLOAEKEL 1442  
DB 1379 AADATEAKNKAHEAERIAAVQKNATSTKAEAEERTFAEYTDLDNEVNNMLKQLOAEKEL 1438  
QY 1443 KKKODDADODMMWAGWASQAAQAEENAKKNSVTLSLSIINDLLLEQLGQJDTVDLNLK 1502  
DB 1439 KKKODDADODMMWAGWASQAAQAEENAKKNSVTLSLSIINDLLLEQLGQJDTVDLNLK 1498  
QY 1503 NEIEGTLINKAKEMKVSDDLDRKVSLENEAKQOEAAIMDYNRDIEBEIMKIDINLEDIRKT 1562  
DB 1499 NEIEGTLINKAKEMKVSDDLDRKVSLENEAKQOEAAIMDYNRDIEBEIMKIDINLEDIRKT 1558  
QY 1563 LPSCCENTPSTIEKP 1576  
DB 1559 LPTGCFNTPSTIEKP 1572

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Job time : 48.8526 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 11.9221 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-16  
Perfect score: 8544  
Sequence: 1 QAMDECTDEGRPCRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*  
5: /cgn2\_5/ptodata/2/iaa/PTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8544	100.0	1576	US-09-562-702A-24	Sequence 24, Appl
2	8544	100.0	1576	US-09-561-818A-24	Sequence 24, Appl
3	8544	100.0	1584	US-09-562-702A-28	Sequence 28, Appl
4	8544	100.0	1609	US-09-562-702A-22	Sequence 22, Appl
5	8544	100.0	1609	US-09-561-818A-22	Sequence 22, Appl
6	8544	100.0	1617	US-09-562-702A-26	Sequence 26, Appl
7	8043	94.1	1605	US-09-562-702A-30	Sequence 30, Appl
8	8043	94.1	1605	US-09-561-818A-26	Sequence 26, Appl
9	8038	94.1	1572	US-09-562-702A-32	Sequence 32, Appl
10	8038	94.1	1572	US-09-561-818A-28	Sequence 28, Appl
11	3600	42.1	1587	US-09-845-583A-10	Sequence 10, Appl
12	3600	42.1	1587	US-09-561-709B-3	Sequence 3, Appl
13	2637	30.9	1193	US-08-317-450B-13	Sequence 13, Appl
14	2637	30.9	1193	US-08-800-593-13	Sequence 13, Appl
15	2516.5	29.5	1111	US-08-317-450B-15	Sequence 15, Appl
16	2516.5	29.5	1111	US-08-800-593-15	Sequence 15, Appl
17	2355.5	27.6	1171	US-08-445-135-1	Sequence 1, Appl
18	1776	20.8	3088	US-09-562-702A-8	Sequence 8, Appl
19	1776	20.8	3089	US-09-562-702A-4	Sequence 4, Appl
20	1776	20.8	3110	US-09-562-702A-2	Sequence 2, Appl
21	1776	20.8	3110	US-09-562-702A-6	Sequence 6, Appl
22	1776	20.8	3110	US-09-561-709B-7	Sequence 7, Appl
23	1775.5	20.8	3111	US-08-460-309-4	Sequence 4, Appl
24	1775.5	20.8	3111	US-08-125-077-4	Sequence 4, Appl
25	1774.5	20.8	3106	US-09-562-702A-10	Sequence 10, Appl
26	1768.5	20.7	3084	US-09-562-702A-12	Sequence 12, Appl
27	1704	19.9	3075	US-08-460-309-5	Sequence 5, Appl

28	1704	19.9	3075	2	US-08-125-077-5	Sequence 5, Appl
29	1673	19.6	1765	4	US-09-562-702A-16	Sequence 16, Appl
30	1673	19.6	1765	4	US-09-561-818A-16	Sequence 16, Appl
31	1673	19.6	1786	4	US-09-562-702A-14	Sequence 14, Appl
32	1673	19.6	1786	4	US-09-561-818A-14	Sequence 14, Appl
33	1673	19.6	1786	4	US-09-561-709B-9	Sequence 9, Appl
34	1652	19.3	1761	4	US-09-561-709B-1	Sequence 1, Appl
35	1643	19.2	1786	4	US-09-562-702A-18	Sequence 18, Appl
36	1643	19.2	1786	4	US-09-561-818A-18	Sequence 18, Appl
37	1622.5	19.0	1725	4	US-09-562-702A-20	Sequence 20, Appl
38	1622.5	19.0	1725	4	US-09-561-818A-20	Sequence 20, Appl
39	1554	18.2	1799	4	US-09-845-583A-6	Sequence 6, Appl
40	1494	17.5	1798	4	US-09-561-709B-11	Sequence 11, Appl
41	1492	17.5	1798	4	US-09-845-583A-8	Sequence 8, Appl
42	1371	16.0	252	2	US-08-460-309-12	Sequence 12, Appl
43	1371	16.0	252	2	US-08-125-077-12	Sequence 12, Appl
44	1367	16.0	252	1	US-08-152-019A-38	Sequence 38, Appl
45	1346	15.8	251	1	US-08-152-019A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1  
US-09-562-702A-24  
; Sequence 24, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-24

Query Match	100.0%;	Score	8544;	DB	4;	Length	1576;
Best Local Similarity	100.0%;	Pred. No.	0;				
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						Gaps	0;
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Db	1	QAA	MDCTDEGRPCRCMPEFVNAAFNVTVVATNTCGTPEEYCVQGTGVTGK	SCHL	CD	60	
Qy	61	AGQ	PHLQHGAAFLTDYNNQADTTWQSO	TMLAGVOYESSINLT	HLGKAFDITVRLKEH	120	
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Qy	121	TSR	PESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFI	RTGGDEQQALCTDEFSDIS	180		
Db	121	TSR	PESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFI	RTGGDEQQALCTDEFSDIS	180		
Qy	181	PLT	CGNVAFSTLEGRPSAYFNDSNVLQEW	TATDIRVTNLNLTFGDEVNDPKV	KSY	240	
Db	181	PLT	CGNVAFSTLEGRPSAYFNDSNVLQEW	TATDIRVTNLNLTFGDEVNDPKV	KSY	240	
Qy	241	YYA	ISDFAVGRCCKNGHASECMKNEFDKLV	CNCKHNTYGVDC	CKLPFFNDRPWR	RATA	300
Db	241	YYA	ISDFAVGRCCKNGHASECMKNEFDKLV	CNCKHNTYGVDC	CKLPFFNDRPWR	RATA	300

301 ESASECLPCDNGRQBCYFDPBLYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 360  
301 ESASECLPCDNGRQBCYFDPBLYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 360  
361 ACSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKDCRCQPGFHSULTAGRCPCSCDPSGSI 420  
361 ACSCHCSPVGSLSLTCDSYGRCSCKPGVMGDKDCRCQPGFHSULTAGRCPCSCDPSGSI 420  
421 DECNVETGRVCCKDNVGFNCRCRCKPGFNLBSNPRGCTPCFCFGHSSVCTNAVGSYV 480  
421 DECNVETGRVCCKDNVGFNCRCRCKPGFNLBSNPRGCTPCFCFGHSSVCTNAVGSYV 480  
481 SISSTFOIDEGWEABORDGSEASLEWSERODIAVSDSYFPRYFIAPAKFLGKQVLSY 540  
481 SISSTFOIDEGWEABORDGSEASLEWSERODIAVSDSYFPRYFIAPAKFLGKQVLSY 540  
541 QNLSPFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKVFRLHEATDY 600  
541 QNLSPFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKVFRLHEATDY 600  
601 PWRPALTPFEFQKLNNTSIRKGTYSERSAGVLDVTLASARPGGVPATWVESCTCP 660  
601 PWRPALTPFEFQKLNNTSIRKGTYSERSAGVLDVTLASARPGGVPATWVESCTCP 660  
661 VYGQGFCEMCLSGYRRETNLGPSPCVLCACNHSETCDPETGVNCRDNTAGPHEK 720  
661 VYGQGFCEMCLSGYRRETNLGPSPCVLCACNHSETCDPETGVNCRDNTAGPHEK 720  
721 CSDGYGDSITAGTSSDQPCPCPGSSCAVPTKVVCTNCPTGTGKRCCLCDGPGYF 780  
721 CSDGYGDSITAGTSSDQPCPCPGSSCAVPTKVVCTNCPTGTGKRCCLCDGPGYF 780  
781 DPLGRNGFVRLCRCLQCQSDNIDPNAVCNRLTGECCLKIYNTAGFYCDRCCKDGFNGPL 840  
781 DPLGRNGFVRLCRCLQCQSDNIDPNAVCNRLTGECCLKIYNTAGFYCDRCCKDGFNGPL 840  
841 APNPADCKACNPNYGTMKQSSCNVPTGCECLPHVTGQDGCADPGYNIQSGQGE 900  
841 APNPADCKACNPNYGTMKQSSCNVPTGCECLPHVTGQDGCADPGYNIQSGQGE 900  
901 RCDCHALGSTNGQDITGQCECPGITGQHCERCEVNHFGFPGCKPCDCHPEGSLSL 960  
901 RCDCHALGSTNGQDITGQCECPGITGQHCERCEVNHFGFPGCKPCDCHPEGSLSL 960  
961 QCKDGRCEGREGVGNRCQCEYFNYSWPGQCEPCACRYLVKDKVADHRVKLQELE 1020  
961 QCKDGRCEGREGVGNRCQCEYFNYSWPGQCEPCACRYLVKDKVADHRVKLQELE 1020  
1021 SLIANLGTGDMVTDQAFEDLKEAREVMDLLREAOVDKVDQNLMDRLQRVNNLTSSQ 1080  
1021 SLIANLGTGDMVTDQAFEDLKEAREVMDLLREAOVDKVDQNLMDRLQRVNNLTSSQ 1080  
1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140  
1081 ISRLQNRNTIETGNLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140  
1141 NNMTLLABEARKLAEKHQAEADIVRVAKTANDTSTAYNLLRLTAGENQTAPEIELN 1200  
1141 NNMTLLABEARKLAEKHQAEADIVRVAKTANDTSTAYNLLRLTAGENQTAPEIELN 1200  
1201 RKYEQAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260  
1201 RKYEQAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEA 1260  
1261 ENLSQIDQKDYEDLREDMRGKELEVONLLEKGTQEQTAQDLARADAANKALAEBA 1320  
1261 ENLSQIDQKDYEDLREDMRGKELEVONLLEKGTQEQTAQDLARADAANKALAEBA 1320  
1321 KKGRTLOEANDILNNLKDFRRVNDNKTAAEALRKIPAINQITTEANEKTRAEQAALG 1380  
1321 KKGRTLOEANDILNNLKDFRRVNDNKTAAEALRKIPAINQITTEANEKTRAEQAALG 1380  
1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAEARTFAEVTDLQDNEVNNMLKQLEAEK 1440

1381 SAAADATEAKNKAHEAERIASAVQKNATSTKAEARTFAEVTDLQDNEVNNMLKQLEAEK 1440  
1441 ELKRRQDDADQDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500  
1441 ELKRRQDDADQDMMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500  
1501 KLINEIEGTINKAKDEMVKVSDLDKRVSDLENEAKQOEAAMINDYNDIEBEIMKDIRLEDIR 1560  
1501 KLINEIEGTINKAKDEMVKVSDLDKRVSDLENEAKQOEAAMINDYNDIEBEIMKDIRLEDIR 1560  
1561 KTLPSGCFTPSIEKP 1576  
1561 KTLPSGCFTPSIEKP 1576

## RESULT 2

US-09-561-818A-24  
; Sequence 24, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-24

Query Match 100.0%; Score 8544; DB 4; Length 1576;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGRPCRCMPEFVNAAFNVVATTCGTPPEEYCVQTVGTGTSKCHLCD 60

DB 1 QAAMDECTDEGRPCRCMPEFVNAAFNVVATTCGTPPEEYCVQTVGTGTSKCHLCD 60

QY 61 AQPHLQHGAAFLTDYNNQADTTWQSMLAGVQYSSINLTLHLKAPDITTVRLKHF 120

DB 61 AQPHLQHGAAFLTDYNNQADTTWQSMLAGVQYSSINLTLHLKAPDITTVRLKHF 120

QY 121 TSRPESFAIKRTRDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 180

DB 121 TSRPESFAIKRTRDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 180

QY 181 PUTGNVAFSTLEGRPSAYNFNDSPVLOEWVTATDIRVTNLRLATFGDEVNDPKVLKSY 240

DB 181 PUTGNVAFSTLEGRPSAYNFNDSPVLOEWVTATDIRVTNLRLATFGDEVNDPKVLKSY 240

QY 241 YVAISDPAVGRCKCNHSHASECMKNEFDKVCNCKHNTYGVDCCKLPFFFNDRPWRATA 300

DB 241 YVAISDPAVGRCKCNHSHASECMKNEFDKVCNCKHNTYGVDCCKLPFFFNDRPWRATA 300

QY 301 ESASECLPCDNGRQBCYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 360

DB 301 ESASECLPCDNGRQBCYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRNFRLGNNE 360

QY 361 ACSSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKDCRCQPGFHSULTAGRCPCSCDPSGSI 420

DB 361 ACSSCHCSPVGSLSLTCQDSYGRCSCKPGVMGDKDCRCQPGFHSULTAGRCPCSCDPSGSI 420

QY 421 DECNVETGRVCCKDNVGFNCRCRCKPGFNLBSNPRGCTPCFCFGHSSVCTNAVGSYV 480

DB 421 DECNVETGRVCCKDNVGFNCRCRCKPGFNLBSNPRGCTPCFCFGHSSVCTNAVGSYV 480

QY 481 SISSTFOIDEGWEABORDGSEASLEWSERODIAVSDSYFPRYFIAPAKFLGKQVLSY 540

DB 481 SISSTFOIDEGWEABORDGSEASLEWSERODIAVSDSYFPRYFIAPAKFLGKQVLSY 540

Db 481 SISSTFQIDEDGWRAEQRDGSSEASLEWSSERODIAVISDSYFPRFPIAPAKFLGKQVLSY 540  
QY 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFLRHEATDY 600  
Db 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFLRHEATDY 600  
QY 601 PWRPALTPPEFQKLNLLNLSIKIRTYSEBSAGYLLDDVTLASARPGVPAWESCTCP 660  
Db 601 PWRPALTPPEFQKLNLLNLSIKIRTYSEBSAGYLLDDVTLASARPGVPAWESCTCP 660  
QY 661 VGYGQFCFCEMCLSGYRRRETNLPNPGSPCVLACACNGHSETCPETGVCNCRONTAGPHCEK 720  
Db 661 VGYGQFCFCEMCLSGYRRRETNLPNPGSPCVLACACNGHSETCPETGVCNCRONTAGPHCEK 720  
QY 721 CSBGYYGSTAGTSDCQPCPCGSSCAVVPKTEVVCTNCTPTGTRKRCBELCDDGVFG 780  
Db 721 CSBGYYGSTAGTSDCQPCPCGSSCAVVPKTEVVCTNCTPTGTRKRCBELCDDGVFG 780  
QY 781 DPLGNGPVRCLRLCQCSNIDPNVAGNCNRLTGELCKIYNTAGFYCDRCCKDGFPGNPL 840  
Db 781 DPLGNGPVRCLRLCQCSNIDPNVAGNCNRLTGELCKIYNTAGFYCDRCCKDGFPGNPL 840  
QY 841 APNPADKACNCPYGTMKQSSCNPVGTGQCECLPHVTGQDCAACDPGFYNLQSGQCE 900  
Db 841 APNPADKACNCPYGTMKQSSCNPVGTGQCECLPHVTGQDCAACDPGFYNLQSGQCE 900  
QY 901 RDCCHALSTNGQCDIRTGQCECQPGITGQHCECEVNHFGFPGCKPCDCHPEGSLSL 960  
Db 901 RDCCHALSTNGQCDIRTGQCECQPGITGQHCECEVNHFGFPGCKPCDCHPEGSLSL 960  
QY 961 QCKDDGRCCEGFGVGNRCDOCEENFYNNRWPQCECPACVRLVKDVAHVRKVLQELE 1020  
Db 961 QCKDDGRCCEGFGVGNRCDOCEENFYNNRWPQCECPACVRLVKDVAHVRKVLQELE 1020  
QY 1021 SLIANLGTGDMVTQAFEDRLKEAREVMOLLREAQDVKDQNDQMLRQVNTLSQ 1080  
Db 1021 SLIANLGTGDMVTQAFEDRLKEAREVMOLLREAQDVKDQNDQMLRQVNTLSQ 1080  
QY 1081 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAANVSTQPESTGDP 1140  
Db 1081 ISRLQIRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAANVSTQPESTGDP 1140  
QY 1141 NMNTLLABEARKLARHKEADDIIVRAKTANDTSTEAYNLLRLTAGENQTAFEIENL 1200  
Db 1141 NMNTLLABEARKLARHKEADDIIVRAKTANDTSTEAYNLLRLTAGENQTAFEIENL 1200  
QY 1201 RYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLEANNIKMEA 1260  
Db 1201 RYEQAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLEANNIKMEA 1260  
QY 1261 ENLEQLIDQKLDYEDLREDWRGKELEVNLLKKGTEQQTADQILARADAALABEAA 1320  
Db 1261 ENLEQLIDQKLDYEDLREDWRGKELEVNLLKKGTEQQTADQILARADAALABEAA 1320  
QY 1321 KKGRTLOEANDILNNLKDFFRRVNDNKTAAEALRKIPALNQITTEANEXTREAOQALG 1380  
Db 1321 KKGRTLOEANDILNNLKDFFRRVNDNKTAAEALRKIPALNQITTEANEXTREAOQALG 1380  
QY 1381 SAAADATEAKNAHAEERIASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAK 1440  
Db 1381 SAAADATEAKNAHAEERIASAVQKNATSTKAEARTFAEVTDLNNEVNNMLKQLOEAK 1440  
QY 1441 ELKRQDDADODMMAGASQAQAEINAKKNVSTLSLIIINDLLEQLGQDLDVLDN 1500  
Db 1441 ELKRQDDADODMMAGASQAQAEINAKKNVSTLSLIIINDLLEQLGQDLDVLDN 1500  
QY 1501 KLNIEGTLNKAKEMKVSDDLDRKVSJDLNENAKKQEAALMDYNRDIEEIKMDIRNLEDIR 1560  
Db 1501 KLNIEGTLNKAKEMKVSDDLDRKVSJDLNENAKKQEAALMDYNRDIEEIKMDIRNLEDIR 1560  
QY 1561 KTLPSGCCNTPSIEKP 1576  
Db 1561 KTLPSGCCNTPSIEKP 1576

## RESULT 3

US-09-562-702A-28  
; Sequence 28, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 1584  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-28

Query Match 100.0%; Score 8544; DB 4; Length 1584;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAWDECTEGGRCPCMPPEFVNAAFNVTVAINTCGTPPEYCVQTVGTGTSKCHLCD 60  
Db 1 QAAWDECTEGGRCPCMPPEFVNAAFNVTVAINTCGTPPEYCVQTVGTGTSKCHLCD 60  
QY 61 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVYPPSSINLTHLGKAFDIYVRLKPH 120  
Db 61 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVYPPSSINLTHLGKAFDIYVRLKPH 120  
QY 121 TSPESFALYKRTREDGPWIPYQYISGSCENTYSKANRGFIETGDEQALCTDEPSDIS 180  
Db 121 TSPESFALYKRTREDGPWIPYQYISGSCENTYSKANRGFIETGDEQALCTDEPSDIS 180  
QY 181 PLTGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLSY 240  
Db 181 PLTGGNVAFTLEGRPSAYNFDNSPVLQEWVTATDIRVTNLNLTFGDEVFNDPKVLSY 240  
QY 241 YYAISDFAYGGRCKNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFPNDRPHRRATA 300  
Db 241 YYAISDFAYGGRCKNGHASECMKNEFDKLVCKNCKNTYGVDCCKLPFPNDRPHRRATA 300  
QY 301 ESASECLPCDCNRSOECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRENFRLGNNE 360  
Db 301 ESASECLPCDCNRSOECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRENFRLGNNE 360  
QY 361 ACSSCHSPVGLSTQCDISYGRCSCKPGVMGDKDRCPQPGHSLTEAGRCPCDPSGSI 420  
Db 361 ACSSCHSPVGLSTQCDISYGRCSCKPGVMGDKDRCPQPGHSLTEAGRCPCDPSGSI 420  
QY 421 DECNVETGRVCVKDNVGEFNCERCKPFPNLESSNPRGCTPCFCFHSVCTNAVGSYVY 480  
Db 421 DECNVETGRVCVKDNVGEFNCERCKPFPNLESSNPRGCTPCFCFHSVCTNAVGSYVY 480  
QY 481 SISSTFQIDEDGWRAEQRDGSSEASLEWSSERODIAVISDSYFPRFPIAPAKFLGKQVLSY 540  
Db 481 SISSTFQIDEDGWRAEQRDGSSEASLEWSSERODIAVISDSYFPRFPIAPAKFLGKQVLSY 540  
QY 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFLRHEATDY 600  
Db 541 GQNLFSFRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNSSYPSETTVKYVFLRHEATDY 600  
QY 601 PWRPALTPPEFQKLNLLNLSIKIRTYSEBSAGYLLDDVTLASARPGVPAWESCTCP 660

Db	601	W P W P A L T P P F B F O K L L N N L T S I K R G T T Y S E R S A G Y L D D V T T L A S A R P G P G V P A T W V E S C T C P	660
Qy	661	V Y G G O F C E M C L S G Y R R E T P N L G P S P C V L C A C N G H S E T C D P E T G V C N C R D N T A G P H C E K	720
Db	661	V Y G G O F C E M C L S G Y R R E T P N L G P S P C V L C A C N G H S E T C D P E T G V C N C R D N T A G P H C E K	720
Qy	721	C S D G Y Y G D S T A G T S S D C Q P C P C P G G S S C A V P K T K E V V C T N C P T G T T G K E C E L C D D G Y F G	780
Db	721	C S D G Y Y G D S T A G T S S D C Q P C P C P G G S S C A V P K T K E V V C T N C P T G T T G K E C E L C D D G Y F G	780
Qy	781	D P L G R N G P V R L C R L C Q C S D N I D P N A V G C N R L T G E C L K C I Y N T A G F Y C D R C K D G F G C N P L	840
Db	781	D P L G R N G P V R L C R L C Q C S D N I D P N A V G C N R L T G E C L K C I Y N T A G F Y C D R C K D G F G C N P L	840
Qy	841	A P N P A D K C K A C N P Y T M T K Q Q S C N P V T G C E C L P H V T Q D C G A C D P P G Y N I Q S G G C E	900
Db	841	A P N P A D K C K A C N P Y T M T K Q Q S C N P V T G C E C L P H V T Q D C G A C D P P G Y N I Q S G G C E	900
Qy	901	R C D C H A L G S T N G C D I R T G O C E Q P G I T G O H C E R C E V N H F G P E G C K P C D C H P E G S L S L	960
Db	901	R C D C H A L G S T N G C D I R T G O C E Q P G I T G O H C E R C E V N H F G P E G C K P C D C H P E G S L S L	960
Qy	961	Q C K D D G R C E R G F V G N R C Q C E N Y F Y N R S W F G C Q C P A C Y R L V K D K V A D H R V K L Q E L E	1020
Db	961	Q C K D D G R C E R G F V G N R C Q C E N Y F Y N R S W F G C Q C P A C Y R L V K D K V A D H R V K L Q E L E	1020
Qy	1021	S L T A N I L G T G E M V T D Q A F E D R L K E A E R V M D L R E A O D V K D V D N L M D R L Q R V N N T L S Q	1080
Db	1021	S L T A N I L G T G E M V T D Q A F E D R L K E A E R V M D L R E A O D V K D V D N L M D R L Q R V N N T L S Q	1080
Qy	1081	I S R L Q N I R N T I E E T G N L A E Q A R A H V E N T E R L I E I A S R E L E K A K V A A N V S V T O P E S T G D P	1140
Db	1081	I S R L Q N I R N T I E E T G N L A E Q A R A H V E N T E R L I E I A S R E L E K A K V A A N V S V T O P E S T G D P	1140
Qy	1141	N N M T L L A E A R K U A E R H K Q B A D I V R V A K T A N D T S T E A Y N L L R T L A G E N Q T A F E I E E L N	1200
Db	1141	N N M T L L A E A R K U A E R H K Q B A D I V R V A K T A N D T S T E A Y N L L R T L A G E N Q T A F E I E E L N	1200
Qy	1201	R K Y E Q A K N I S O D L E K Q A A R V H E A K R A G D K A V E I Y A S V A O L S P L D S E T L E N E A N N I K W E A	1260
Db	1201	R K Y E Q A K N I S O D L E K Q A A R V H E A K R A G D K A V E I Y A S V A O L S P L D S E T L E N E A N N I K W E A	1260
Qy	1261	E N I E Q L I D Q K L K O Y E D I R E D M R G K E L E V K N L L E K G K T E Q O T A O L L A R A D A A K A L A B E A A	1320
Db	1261	E N I E Q L I D Q K L K O Y E D I R E D M R G K E L E V K N L L E K G K T E Q O T A O L L A R A D A A K A L A B E A A	1320
Qy	1321	K K G R D T L Q E A N D I L A N N L K D F R R V N D N K T A A E B A L R K I P A I N O T I T E A N E K T E A Q O A L G	1380
Db	1321	K K G R D T L Q E A N D I L A N N L K D F R R V N D N K T A A E B A L R K I P A I N O T I T E A N E K T E A Q O A L G	1380
Qy	1381	S A A A D A T E A K N K A H E A E R I A S A V O K N A T S T K A B A E R T F A E V T D L D N E V N N M L K Q L Q E A E K	1440
Db	1381	S A A A D A T E A K N K A H E A E R I A S A V O K N A T S T K A B A E R T F A E V T D L D N E V N N M L K Q L Q E A E K	1440
Qy	1441	E L K E K O D D A Q D M M M A G S Q A A Q E A B I N A R K A K N S V T S I L S I I N D L L E Q L G O L D T V D L N	1500
Db	1441	E L K E K O D D A Q D M M M A G S Q A A Q E A B I N A R K A K N S V T S I L S I I N D L L E Q L G O L D T V D L N	1500
Qy	1501	K L N E I G T L N K A D E M K V S D L D R K V S D L E N A E K K Q E A A I M D Y N R D I E E I M K D I R N L E D I R	1560
Db	1501	K L N E I G T L N K A D E M K V S D L D R K V S D L E N A E K K Q E A A I M D Y N R D I E E I M K D I R N L E D I R	1560
Qy	1561	K T L P S G C F N T P S I E K P	1576
Db	1561	K T L P S G C F N T P S I E K P	1576

## RESULT 4

RESULT 4  
US-09-562-702A-22

US-09-562-702A-22  
; Sequence 22, Application US/09562702A

; sequence 22, Applicant  
; Patent No. 6632790

GENERAL INFORMATION:



721 CSDGYGDSGTAGTSSDCQPCPGSSCAVVKTEVCTNCTGTGTRKRCCLDDGYFG 780  
754 CSDGYGDSGTAGTSSDCQPCPGSSCAVVKTEVCTNCTGTGTRKRCCLDDGYFG 813  
781 DPLGRNGPVRCLRLCCSNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCXGDFGNPL 840  
814 DPLGRNGPVRCLRLCCSNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCXGDFGNPL 873  
841 APNPADKCAKNCNPYGTWKQSSCNPTVGOCECLPHVTGQCGACDPCFYNLQSGQCE 900  
874 APNPADKCAKNCNPYGTWKQSSCNPTVGOCECLPHVTGQCGACDPCFYNLQSGQCE 933  
901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPGECKPCDCHPGSLSL 960  
934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPGECKPCDCHPGSLSL 993  
961 QCKDGRCEGREGVGNRCQCEENFYRSPGCECPACVRLVKDVKADHRVKLOELE 1020  
994 QCKDGRCEGREGVGNRCQCEENFYRSPGCECPACVRLVKDVKADHRVKLOELE 1053  
1021 SLTANLGTGDMYTDOAFEDRLKEAREVMDLLREAOQVDQVNDLMDRLQVNTLSQ 1080  
1054 SLTANLGTGDMYTDOAFEDRLKEAREVMDLLREAOQVDQVNDLMDRLQVNTLSQ 1113  
1081 ISRLQIRNTIETGNLAEQARHVENTERLIEIASRELEKAKVAANVSVTQPESTGDP 1140  
1114 ISRLQIRNTIETGNLAEQARHVENTERLIEIASRELEKAKVAANVSVTQPESTGDP 1173  
1141 NNWTLAERKAEARKHQEADDIIVRAKTANDTSTEAYNLLRLTLAGENQTAPELELN 1200  
1174 NNWTLAERKAEARKHQEADDIIVRAKTANDTSTEAYNLLRLTLAGENQTAPELELN 1233  
1201 RKEQAKNISQDLEKQARVHEBAKAGDKAVEIYASVAQLSPDSETLNEBANNIKMEA 1260  
1234 RKEQAKNISQDLEKQARVHEBAKAGDKAVEIYASVAQLSPDSETLNEBANNIKMEA 1293  
1261 ENLEQIDQKDYEDLREDMRKELEVKULLKKGTEQOTADOLLARADAKALAEBA 1320  
1294 ENLEQIDQKDYEDLREDMRKELEVKULLKKGTEQOTADOLLARADAKALAEBA 1353  
1321 KGRDITLQEAANDILNLLKDFDRVNVNKTAAEALRKIPAINOTITEANEKTRQAQALG 1380  
1354 KGRDITLQEAANDILNLLKDFDRVNVNKTAAEALRKIPAINOTITEANEKTRQAQALG 1413  
1381 SAAADATEAKNKAHEAERIASAVQKATSTKABAEFTFAEVTDLDEVNMLKQLOEAEK 1440  
1414 SAAADATEAKNKAHEAERIASAVQKATSTKABAEFTFAEVTDLDEVNMLKQLOEAEK 1473  
1441 ELKRQDDADQDMMAGASQAAQAEABINAKKNSVTSLLSIINDLLEQLGOLDIVDLN 1500  
1474 ELKRQDDADQDMMAGASQAAQAEABINAKKNSVTSLLSIINDLLEQLGOLDIVDLN 1533  
1501 KLANIEGTNLKAKDEMKSVDLRKVSLENEAKKQEAAMIDYNRDIEEIKDIRNLEDIR 1560  
1534 KLANIEGTNLKAKDEMKSVDLRKVSLENEAKKQEAAMIDYNRDIEEIKDIRNLEDIR 1593  
1561 KTLPSGCFNTPSTEKP 1576  
1594 KTLPSGCFNTPSTEKP 1609

RESULT 5

US-09-561-818A-22  
; Sequence 22 Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Korttesmaa, Jari  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99, 274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-22

Query Match 100.0%; Score 8544; DB 4; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGRPQRCMPEFVNAAFNVTVVATNTGCTPPEEYCVQGTGVTKSCHLCD 60  
DB 34 QAAMDECTDEGRPQRCMPEFVNAAFNVTVVATNTGCTPPEEYCVQGTGVTKSCHLCD 93  
QY 61 AQPHLOHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLHLKAFDITVRLKHF 120  
DB 94 AQPHLOHGAFLTDYNNQADTTWQSQOTMLAGVQYPSINLTLHLKAFDITVRLKHF 153  
QY 121 TSREPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRITGDDQCALCTDEFSDIS 180  
DB 154 TSREPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRITGDDQCALCTDEFSDIS 213  
QY 181 PLTGNVAFSTLEGRPSAYNFDSNPLVQEWATDIRVTNLNRLNTFGDEVFNDPKVLKSY 240  
DB 214 PLTGNVAFSTLEGRPSAYNFDSNPLVQEWATDIRVTNLNRLNTFGDEVFNDPKVLKSY 273  
QY 241 YYAISDFAVGRCCKNGHSCMKNBEFDKLVNCKHNTYGVDCCKLPFFNDPWRREATA 300  
DB 274 YYAISDFAVGRCCKNGHSCMKNBEFDKLVNCKHNTYGVDCCKLPFFNDPWRREATA 333  
QY 301 ESASECLPCDCNGRSQSCYDPPELYRSTGHGCTNCDNTDGAHCRCRCRNFRLGNE 360  
DB 334 ESASECLPCDCNGRSQSCYDPPELYRSTGHGCTNCDNTDGAHCRCRCRNFRLGNE 393  
QY 361 ACSSCHSPVSGSLSTQCDSDYGRCKPVGMDKCDRCQPGFHSILTEAGCRPCSDPSSGI 420  
DB 394 ACSSCHSPVSGSLSTQCDSDYGRCKPVGMDKCDRCQPGFHSILTEAGCRPCSDPSSGI 453  
QY 421 DECNVETGRCVCKDNVGFNCERCKPGFNLESNPRGCTPCPCFCHSSVCTNAGVSVY 480  
DB 454 DECNVETGRCVCKDNVGFNCERCKPGFNLESNPRGCTPCPCFCHSSVCTNAGVSVY 513  
QY 481 SISSTFQIDEDGWAERQDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGQVLSY 540  
DB 514 SISSTFQIDEDGWAERQDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGQVLSY 573  
QY 541 GONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYVRLHEATDY 600  
DB 574 GONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYVRLHEATDY 633  
QY 601 PWRPALTPFEFQKLNLLNTSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660  
DB 634 PWRPALTPFEFQKLNLLNTSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 693  
QY 661 VYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVNCNCRONTAGPHECK 720  
DB 694 VYGGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPETGVNCNCRONTAGPHECK 753  
QY 721 CSDGYGDSGTAGTSSDCQPCPGSSCAVVKTEVCTNCTGTGTRKRCCLDDGYFG 780  
DB 754 CSDGYGDSGTAGTSSDCQPCPGSSCAVVKTEVCTNCTGTGTRKRCCLDDGYFG 813  
QY 781 DPLGRNGPVRCLRLCCSNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCXGDFGNPL 840  
DB 814 DPLGRNGPVRCLRLCCSNDIPNAGVNCNRLTGECLKCIYNTAGFYCDRCXGDFGNPL 873  
QY 841 APNPADKCAKNCNPYGTWKQSSCNPTVGOCECLPHVTGQCGACDPCFYNLQSGQCE 900  
DB 874 APNPADKCAKNCNPYGTWKQSSCNPTVGOCECLPHVTGQCGACDPCFYNLQSGQCE 933  
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPGECKPCDCHPGSLSL 960



Db 1054 SLTANLGTGDMVTDQAFEDRLKEAREVMDLLREAQDKVDQNDLMDRLQRVNNLTSSQ 1113  
Qy 1081 ISRLQNRINTIETGNLAEOARAHVENTERLIIASRELEKAKVAANVSVPQESTGDP 1140  
Db 1114 ISRLQNRINTIETGNLAEOARAHVENTERLIIASRELEKAKVAANVSVPQESTGDP 1173  
Qy 1141 NNWTLAAEARKLAERHKQADDIIVRAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200  
Db 1174 NNWTLAAEARKLAERHKQADDIIVRAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233  
Qy 1201 RYEQAKNISODLEKQARVHEEAKRAGDKAVIYASVAQLSPDSETLENEANNIKMEA 1260  
Db 1234 RYEQAKNISODLEKQARVHEEAKRAGDKAVIYASVAQLSPDSETLENEANNIKMEA 1293  
Qy 1261 ENLEQLDQKLKDYEDLREDMRGKELEVKVNLLEKGTQEQQTADQLLARADAARALAEAAA 1320  
Db 1294 ENLEQLDQKLKDYEDLREDMRGKELEVKVNLLEKGTQEQQTADQLLARADAARALAEAAA 1353  
Qy 1321 KKGRTDLOEANDILNNUKDFDRRVNDNKTAAEALRKIPAINOTITTEANEKTRBAQOALG 1380  
Db 1354 KKGRTDLOEANDILNNUKDFDRRVNDNKTAAEALRKIPAINOTITTEANEKTRBAQOALG 1413  
Qy 1381 SAAADATEAKNKAHEAERIASAVOKNATSTKAAERTFAEVTDLDEVNMMKLOEABEK 1440  
Db 1414 SAAADATEAKNKAHEAERIASAVOKNATSTKAAERTFAEVTDLDEVNMMKLOEABEK 1473  
Qy 1441 ELKEKQDADQDMMWAGSQAQAEAEINARKAKNSVTSLLSINDLLEOLGOLDTVVDLN 1500  
Db 1474 ELKEKQDADQDMMWAGSQAQAEAEINARKAKNSVTSLLSINDLLEOLGOLDTVVDLN 1533  
Qy 1501 KLINEIETLNKAKDEMKSOLDKRVSDLENEAKKQEAAMNDYNRDIEEIMKDIRNLEDIR 1560  
Db 1534 KLINEIETLNKAKDEMKSOLDKRVSDLENEAKKQEAAMNDYNRDIEEIMKDIRNLEDIR 1593  
Qy 1561 KTLPSGCFNTPSIEKP 1576  
Db 1594 KTLPSGCFNTPSIEKP 1609

RESULT 7

US-09-562-702A-30  
; Sequence 30, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-30

Query Match 94.1%; Score 8043; DB 4; Length 1605;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

Qy 1 QAAEMDCTDEGRQRCMPEFVNAFNVVATNTCGTPPEEYCVQGVGVTKSCHLCD 60  
Db 32 RAANDECADEGRQRCMPEFVNAFNVVATNTCGTPPEEYCVQGVGVTKSCHLCD 91

Qy 61 AGQPHLQHGAAFLTDYNNQADTTWWSQOTMLAGVQYPSINLTLHLGKAFDITVRLKPH 120  
Db 92 AGQPHLQHGAAFLTDYNNQADTTWWSQOTMLAGVQYPSINLTLHLGKAFDITVRLKPH 151  
Qy 121 TSRESFAIYKRTREDGPMIPIYQYSGSCENTYKANGFIRTCGDEQALCTDEFSDIS 180  
Db 152 TSRESFAIYKRTREDGPMIPIYQYSGSCENTYKANGFIRTCGDEQALCTDEFSDIS 211  
Qy 181 PLTGNVAFSTLEGRPSAYNFDNSFVLQEWWTATDIRVTLNRLNTFGDEVNDPKVLKSY 240  
Db 212 PLTGNVAFSTLEGRPSAYNFDNSFVLQEWWTATDIRVTLNRLNTFGDEVNDPKVLKSY 271  
Qy 241 YTAISDFAVGRCCKNGHASECMKNEFDKVCNCKENTYGVDCCKLPPFFNDRPWRATA 300  
Db 272 YTAISDFAVGRCCKNGHASECMKNEFDKVCNCKENTYGVDCCKLPPFFNDRPWRATA 331  
Qy 301 ESASECLPCDCNCRSGOEYFDPYELRSTGHGHCCTNCODNTDGAHCRCRENFRLGNNE 360  
Db 332 ESASECLPCDCNCRSGOEYFDPYELRSTGHGHCCTNCODNTDGAHCRCRENFRLGNNE 391  
Qy 361 ACSSCHCPVSGSLSTQCDYSYGRCSCKPGVMDKDCRCOPGPHSLTEAGRCSCDPSGSI 420  
Db 392 ACSPCHCPVSGSLSTQCDYSYGRCSCKPGVMDKDCRCOPGPHSLTEAGRCSCDPSGSI 451  
Qy 421 DECNVETGRVCCKNVEGFNCERCKPFPNLESSNPRGCTPCFCFPGHSSVCTNAVGVSVY 480  
Db 452 DECNVETGRVCCKNVEGFNCERCKPFPNLESSNPRGCTPCFCFPGHSSVCTNAVGVSVY 511  
Qy 481 STSSTFQIDEDGWRAEQRDGEASLEWSSERQDIAVISDSYPPRYFIAPALFKQVLSY 540  
Db 512 STSSTFQIDEDGWRAEQRDGEASLEWSSERQDIAVISDSYPPRYFIAPALFKQVLSY 571  
Qy 541 GQNLSPSRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNYPSETTVKYVFLRHEATDY 600  
Db 572 GQNLSPSRVDRDRRLSAEDLVLEGAGLRVSVPLIAQGNYPSETTVKYVFLRHEATDY 631  
Qy 601 PWRPALTPFEFOKLNNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660  
Db 632 PWRPALTPFEFOKLNNLTSTIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 691  
Qy 661 VGYGQFCETCLPFGYRRRETPSLGYPSCVLCNCHSETCDPFGVCDRCNRTAGPHEK 720  
Db 692 VGYGQFCETCLPFGYRRRETPSLGYPSCVLCNCHSETCDPFGVCDRCNRTAGPHEK 751  
Qy 721 CSDGYGDSSTAGTSDCQPCPCGSSCAVVPKTEVVCTNCTPTGTTGKRCCLCDDGYFG 780  
Db 752 CSDGYGDSSTAGTSDCQPCPCGSSCAVVPKTEVVCTNCTPTGTTGKRCCLCDDGYFG 811  
Qy 781 DPLGNGPVRCLRCQCSNDIDPNAVGNCRLTGECLKCIYNTAGFYCDCKDGFNGPL 840  
Db 812 DPLGNGPVRCLRCQCSNDIDPNAVGNCRLTGECLKCIYNTAGFYCDCKDGFNGPL 871  
Qy 841 APNADKCKACNCPYGTMKQSSCNVPTGOCCLPHVTGQDCGACDPFYNLQSGQCE 900  
Db 872 APNADKCKACNCPYGTMKQSSCNVPTGOCCLPHVTGQDCGACDPFYNLQSGQCE 930  
Qy 901 RCDHALGSTNGQCDIRTCQCECQPGITGQHCECEVNHFGPBGCKPCDCHPEGSLSL 960  
Db 931 RCDHALGSTNGQCDIRTCQCECQPGITGQHCECEVNHFGPBGCKPCDCHPEGSLSL 990  
Qy 961 QCKDDGRCEGREGFYGNBDCOEENYFYNRSPGQCEPCACVRLVKDVADHRVKLE 1020  
Db 991 QCKDDGRCEGREGFYGNBDCOEENYFYNRSPGQCEPCACVRLVKDVADHRVKLE 1050  
Qy 1021 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAQDKVDQNDLMDRLQRVNNLTSSQ 1080  
Db 1051 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAQDKVDQNDLMDRLQRVNNLTSSQ 1110  
Qy 1081 ISRLQNRINTIETGNLAEOARAHVENTERLIIASRELEKAKVAANVSVPQESTGDP 1140  
Db 1111 ISRLQNRINTIETGNLAEOARAHVENTERLIIASRELEKAKVAANVSVPQESTGDP 1169

QY 1141 NMNTLLAEEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1200  
 DB 1170 NMNTLLAEEARKLAERHKEADDDIVRVAKTANETSAEYNNLLRTLAGENQTAPEIEELN 1229  
 QY 1201 RKYEQAKNISODLEKQAAARVHEEAKAGDKAVEIYASVAQLSPDSTLEANEANNIKKEA 1260  
 DB 1230 RKYEQAKNISODLEKQAAARVHEEAKAGDKAVEIYASVAQLTPVDSEALEANEANKKEA 1289  
 QY 1261 ENLEQLODKLQYEDLREDNRGKELEVNLLKNGKTEQOQTADOLLARADAALAEBA 1320  
 DB 1290 ADLRLIDQKLUKQYEDLREDNRGKEHEVNLLKNGKAEQOQTADOLLARADAALAEBA 1349  
 QY 1321 KKGRTDLOEANDILNNLKDFRRVNDNKTAAEEALRIPAINQITITBEANEKTRAEQAALG 1380  
 DB 1350 KKGRTDLOEANDILNNLKDFRRVNDNKTAAEEALRIPAINRITIAEANEKTRAEQAALG 1409  
 QY 1381 SAAADATEAKNAHEAEEIASAVOKNATSTKAEARTFAEVTDLNENNNMLKQLEAEK 1440  
 DB 1410 NAAADATEAKNAHEAEEIASAOKNATSTKAEARTFAEVTDLNENNNMLKQLEAEK 1469  
 QY 1441 ELKRQDDADQDMMWAGMASQAQAEAEINARKAKNSVTSLSIIINDLEQLGQDVTVDLN 1500  
 DB 1470 ELKRQDDADQDMMWAGMASQAQAEAEINARKAKNSVSSLSIQLNNLLDQGLDVTVDLN 1529  
 QY 1501 KLINEGTGLNKADEMVKVSDLRKVSLENEAKKQEAINDYNDRIEINKDIRNLEDIR 1560  
 DB 1530 KLINEGTGLNKADEMVKVSDLRKVSLENEAKKQEAINDYNDRIEINKDIRNLEDIR 1589  
 QY 1561 KTLFGGCFNTPSIEKP 1576  
 DB 1590 KTLFGGCFNTPSIEKP 1605  
 RESULT 8  
 US-09-561-818A-26  
 ; Sequence 26, Application US/09561818A  
 ; Patent No. 6638907  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kortessmaa, Jarkko  
 ; APPLICANT: Tryggvason, Karl  
 ; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
 ; FILE REFERENCE: 99,274-D  
 ; CURRENT APPLICATION NUMBER: US/09/561,818A  
 ; CURRENT FILING DATE: 2000-04-28  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 1605  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-561-818A-26  
 Query Match 94.1%; Score 8043; DB 4; Length 1605;  
 Best Local Similarity 93.3%; Pred. No. 0;  
 Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;  
 QY 1 QAAMDECTDEGGRPORCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTKSHCLCD 60  
 DB 32 RAAMDECADEGGRPORCMPEFVNAFNVVATNTCGTPPEYCVQGTGVTKSHCLCD 91  
 QY 61 AGQPHLQGAFLTDYNNQADTTWQSQTMLAGVQYSSINLTLHLKAFDITYVLKHF 120  
 DB 92 AGQOHLQGAFLTDYNNQADTTWQSQTMLAGVQYSSINLTLHLKAFDITYVLKHF 151  
 QY 121 TSPSPFAIYKRTREDGFWIPYQYSGSENTYSKANRGFIRTCGDQQAALCTDEFSDIS 180  
 DB 152 TSPSPFAIYKRTREDGFWIPYQYSGSENTYSKANRGFIRTCGDQQAALCTDEFSDIS 211  
 QY 181 PLTGNVAFSTLEGSPSYNFDNSPVLOEHWATATDIRVTLNRLNTPGDEVFNDPKVLKSY 240  
 DB 212 PLTGNVAFSTLEGSPSYNFDNSPVLOEHWATATDIRVTLNRLNTPGDEVFNDPKVLKSY 271  
 QY 241 YYAISDFAVGGKCKNGHASECMKNEFDKLCVNCCKHNTYGVDCCKLPFFNDRPWRATA 300

DB 272 YYAISDFAVGGKCKNGHASECMKNEFDKLCVNCCKHNTYGVDCCKLPFFNDRPWRATA 331  
 QY 301 ESASECLPCDCNCRSQBCYFDPPELYRSTGHGHCCTNCDNTDGAHCRCRENFPLGNNE 360  
 DB 332 ESASECLPCDCNCRSQBCYFDPPELYRSTGHGHCCTNCDNTDGAHCRCRENFPLGNNE 391  
 QY 361 ACSSCHCSFVSGSLSTQCDISYGRCSCKPGVMGDKDRCPGPHSLTEAGRCPCSCDPSGSI 420  
 DB 392 ACSFCHCSFVSGSLSTQCDISYGRCSCKPGVMGDKDRCPGPHSLTEAGRCPCSCDPSGSI 451  
 QY 421 DSCNVETRCVCKNVGFCNCRCKPFPFNLESSNPRGCTPCFCFHSVCTNAGVSYV 480  
 DB 452 DSCNVETRCVCKNVGFCNCRCKPFPFNLESSNPRGCTPCFCFHSVCTNAGVSYV 511  
 QY 481 STSSTFQIDEDCWRAEQDSEASLEWSESDIAVIISDSYFPRYFIAPKPLGQVLSY 540  
 DB 512 DISSYFQIDEDCWRAEQDSEASLEWSESDIAVIISDSYFPRYFIAPKPLGQVLSY 571  
 QY 541 GQNLFSFPRVDRDRTRLAEADLVLEGAGLRVSVPLIAAGNSYPSSTTTVKYVRLHEATDY 600  
 DB 572 GQNLFSFPRVDRDRTRLAEADLVLEGAGLRVSVPLIAAGNSYPSSTTTVKYVRLHEATDY 631  
 QY 601 PWRPALTPPEFQKLNNTLSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 660  
 DB 632 PWRPALTPPEFQKLNNTLSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCTCP 691  
 QY 661 VYGGQFCCEMLCSYRRRTPNLPYSPVLCACNHSSETCPETGVCNCRONTAGPHCEK 720  
 DB 692 VYGGQFCETCLPYRRRTPSLGYPSPVLCNCHSETCPETGVCNCRONTAGPHCEK 751  
 QY 721 CSDGYGDSSTAGTSSDCQPCPCGSSCAVVPKTVCTNCTGTTCKRCCELCDGDFYF 780  
 DB 752 CSDGYGDSSTAGTSSDCQPCPCGSSCAVVPKTVCTNCTGTTCKRCCELCDGDFYF 811  
 QY 781 DPLGRNGPVRCLRCQCSNDIDPNVAGNCNLITGELCKIYNTAGFYCDRCXGDFGNNPL 840  
 DB 812 DPLGSGNPVRLCRPCQCNNDIDPNVAGNCNLITGELCKIYNTAGFYCDRCXGDFGNNPL 871  
 QY 841 APNADKCKACNCPYGMKQSSCNVPTGOCCLPHVTGDCGACDGFVNLGSGQCE 900  
 DB 872 APNADKCKACACN-YGTVQOQSSCNVPTGOCCLPHVTGDCGACDGFVNLGSGQCE 930  
 QY 901 RCDCHALASTNGQCDIRTCQCECQPGITGQHCERCEVNHFGFEGCKPCDCHPEGSLSL 960  
 DB 931 RCDCHALASTNGQCDIRTCQCECQPGITGQHCERCEVNHFGFEGCKPCDCHPEGSLSL 990  
 QY 961 QCKDORCECREGFGVNRCDQCEENYFYNRSPGQCEPCYRLVKDKVADHRVKQLE 1020  
 DB 991 QCKDORCECREGFGVNRCDQCEENYFYNRSPGQCEPCYRLVKDKVADHRVKQLE 1050  
 QY 1021 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAOQVXDVDQNLMDLQRVNNTLSQ 1080  
 DB 1051 SLIANLGTGDEMVTQAFEDRLKEAREVMDLLREAOQVXDVDQNLMDLQRVNNTLSQ 1110  
 QY 1081 ISRLQNRNTIETGNLAEOQARAHVENTERLIEIASRLEKAKVAANVSITQPESTGCP 1140  
 DB 1111 ISRLQNRNTIETGNLAEOQARAHVENTERLIEIASRLEKAKVAANVSITQPESTGCP 1169  
 QY 1141 NMNTLLAEEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRTLAGENQTAPEIEELN 1200  
 DB 1170 NMNTLLAEEARKLAERHKEADDDIVRVAKTANETSAEYNNLLRTLAGENQTAPEIEELN 1229  
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 DB 1230 RKYEQAKNISODLEKQAAARVHEEAKAGDKAVEIYASVAQLTPVDSEALEANEANKKEA 1289  
 QY 1261 ENLEQLODKLQYEDLREDNRGKELEVNLLKNGKTEQOQTADOLLARADAALAEBA 1320  
 DB 1290 ADLRLIDQKLUKQYEDLREDNRGKEHEVNLLKNGKAEQOQTADOLLARADAALAEBA 1349  
 QY 1321 KKGRTDLOEANDILNNLKDFRRVNDNKTAAEEALRIPAINQITITBEANEKTRAEQAALG 1380

Db 1350 KGRSTLQEAANDILNNLKDFDRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALG 1409  
Qy 1381 SAADATEAKKAHEAERIASAVQKNATSTKAAERTFAEYTDLDNEVNNMLKQLOEAEK 1440  
Db 1410 NAAADATEAKKAHEAERIASAQKNATSTKAAERTFGEVTDLDNEVNNMLKQLOEAEK 1469  
Qy 1441 ELARKODDADQDDMMAGWASQAQAEABINARKAKNSVTSLLSIINDLLQLGQDLDVLDN 1500  
Db 1470 ELARKODDADQDDMMAGWASQAQAEABINARKAKNSVTSLLSIINDLLQLGQDLDVLDN 1529  
Qy 1501 KLNEIEGTLNKADEMKSVDLDRKVSLENEAKQAEAAIMDYNRDIIEIMKDINLEDIR 1560  
Db 1530 KLNEIEGSLNKADEMKSVDLDRKVSLESEARKQAEAAIMDYNRDIIEIMKDINLEDIR 1589  
Qy 1561 KTLPSGCFNTPSIEKP 1576  
Db 1590 KTLPTGCFNTPSIEKP 1605

RESULT 9  
US-09-562-702A-32  
; Sequence 32, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-32

Query Match 94.1%; Score 8038; DB 4; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 3 AMDCTDEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKTSCHLCDAG 62  
Db 1 AMDECADEGGRPQRCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGKTSCHLCDAG 60  
Qy 63 QPHLOHGAFLTDYNNQADITWQSQTLAGVQYPSSINLTLLGKAFDITYYRLKPHTS 122  
Db 61 QOHLQHGAAFLTDYNNQADITWQSQTLAGVQYPSSINLTLLGKAFDITYYRLKPHTS 120  
Qy 123 RPESFALYKRTREDGPIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDFSDISPL 182  
Db 121 RPESFALYKRTREDGPIPYQYSGSCENTYSKANRGFIRTGDEQOALCTDFSDISPL 180  
Qy 183 TGGNVAFTLEGRPSAYNFONSPLQEWVATDITRVTLNRLNLTGDEVFNDPKVLSYYY 242  
Db 181 TGGNVAFTLEGRPSAYNFONSPLQEWVATDITRVTLNRLNLTGDEVFNDPKVLSYYY 240  
Qy 243 AISDPFVGGRCCKNGHASECMKNEFDKLVGNCKHNTYGVCEKLPFFNDRPWRRTAES 302  
Db 241 AISDPFVGGRCCKNGHASECMKNEFDKLVGNCKHNTYGVCEKLPFFNDRPWRRTAES 300  
Qy 303 ASECLPCDCNCRSQECYFDPBELYSTGHGHCNTQDNTGACRCERENFFLGNNEAC 362  
Db 301 ASECLPCDCNCRSQECYFDPBELYSTGHGHCNTQDNTGACRCERENFFLGNTEAC 360

Qy 363 SSCHCSPVGSISTQDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSDIE 422  
Db 361 SPCHCSPVGSISTQDSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPSGSDIE 420  
Qy 423 CNVETGRVCNDVGEFNCERCKPGFNLBNSSNPGCTPCFCFCHSSVCTNAVGSYVSI 482  
Db 421 CNVETGRVCNDVGEFNCERCKPGFNLBNSSNPGCTPCFCFCHSSVCTNAVGSYVSI 480  
Qy 483 SSTFOIDDGHRAEQDGESEASLEWSSERQDIAVISDSYFFRYPIAPKFLGKOVLSYXG 542  
Db 481 SSTFOIDDGHRAEQDGESEASLEWSSERQDIAVISDSYFFRYPIAPKFLGKOVLSYXG 540  
Qy 543 NLSFSFRVDRDRLSADIVLEGAGLRVSVPLTAQNSYPSSETTVKVFFLHATDYPW 602  
Db 541 NLSFSFRVDRDRLSADIVLEGAGLRVSVPLTAQNSYPSSETTVKVFFLHATDYPW 600  
Qy 603 RPALTFEFOKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVGPATVVECTCPVG 662  
Db 601 RPALTFEFOKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVGPATVVECTCPVG 660  
Qy 663 YGGQFCMCLSGYRRETNLPYSPCVLCAANGHSETCDPTGVCNCRDNTAGHCEKCS 722  
Db 661 YGGQFCMCLSGYRRETNLPYSPCVLCAANGHSETCDPTGVCNCRDNTAGHCEKCS 720  
Qy 723 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLDGDYFGDP 782  
Db 721 DGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCPTGTTGKRCCLDGDYFGDP 780  
Qy 783 LGRNQPVRLCRLCQCSNDIDENAVGNCNRLTCECLKCIYNTAGPYCORCKDGFNGNLIAP 842  
Db 781 LGRNQPVRLCRLCQCSNDIDENAVGNCNRLTCECLKCIYNTAGPYCORCKDGFNGNLIAP 840  
Qy 843 NPADKCKACNPNVTGKMQSSCNPVTCQCLPHVTGQDCGACDPGYNLQSGGCRCC 902  
Db 841 NPADKCKACNPNVTGKMQSSCNPVTCQCLPHVTGQDCGACDPGYNLQSGGCRCC 899  
Qy 903 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPQEGCKPCDCHPEGSLSLQC 962  
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGPQEGCKPCDCHPEGSLSLQC 959  
Qy 963 KDDGRCCEGFGVGNRCDOCEENYFYNRSWPGCECPACVLYKDKVADHVKLOELES 1022  
Db 960 KDDGRCCEGFGVGNRCDOCEENYFYNRSWPGCECPACVLYKDKVADHVKLOELES 1019  
Qy 1023 IANLGTGDMVTDOAFEDRLXEAEREVMDLLEAQQDVKDQVNDQNLMDRLQRVNNLTSSQIS 1082  
Db 1020 IANLGTGDMVTDOAFEDRLXEAEREVMDLLEAQQDVKDQVNDQNLMDRLQRVNNLTSSQIS 1079  
Qy 1083 RLQNTIRNTEETGNLAQARAHVENTERLIEIASRELEKAKVAANVSVTQPESTGDPNN 1142  
Db 1080 RLQNTIRNTEETGNLAQARAHVENTERLIEIASRELEKAKVAANVSVTQPESTGDPNN 1138  
Qy 1143 MTLLEAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELNRK 1202  
Db 1139 MTLLEAEARKLAERHKEADDIRVAKTANDTSTEAYNLLRLTLAGENQTAPEIEELNRK 1198  
Qy 1203 YEQAKNIQDLEKQAAARVHEBAKAGDKAVIYASVAQLSPDSETLENEANNIMEAEN 1262  
Db 1199 YEQAKNIQDLEKQAAARVHEBAKAGDKAVIYASVAQLSPDSETLENEANNIMEAEN 1258  
Qy 1263 LBOLTDQKLKDYEDLPEDMRGKEVKNLEKGTQEQOTADQLLARADAALAEAEAAK 1322  
Db 1259 LBOLTDQKLKDYEDLPEDMRGKEVKNLEKGTQEQOTADQLLARADAALAEAEAAK 1318  
Qy 1323 GRDTLQEAANDILNNLKDFDRVNDNKTAAEEALRRIPAINOTITTEANEKTRQAQALGSA 1382  
Db 1319 GRDTLQEAANDILNNLKDFDRVNDNKTAAEEALRRIPAINOTITTEANEKTRQAQALGSA 1378  
Qy 1383 AADATEAKKAHEAERIASAVQKNATSTKAAERTFAEYTDLDNEVNNMLKQLOEAEK 1442  
Db 1379 AADATEAKKAHEAERIASAVQKNATSTKAAERTFAEYTDLDNEVNNMLKQLOEAEK 1436  
Qy 1443 KRQDQDADQDDMMAGWASQAQAEABINARKAKNSVTSLLSIINDLLQLGQDLDVLDNKL 1502

Db 1439 KRQDDADQDMVAGWASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDLDVNLK 1498  
QY 1503 NEIEGTINKAKDSMKVSDLDKRVSDLENEAKQAEAAIMDYNDIEIEMKDITNLEDIKT 1562  
Db 1499 NEIEGSLNKADEMKASDLDRKVSDESEARKQAEAAIMDYNDIAIIBIIKQIHNELEDIKT 1558  
QY 1563 LPSGCFNTPSIEKP 1576  
Db 1559 LPTGCFNTPSIEKP 1572

## RESULT 10

US-09-561-818A-28  
; Sequence 28, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-28

Query Match 94.1%; Score 8038; DB 4; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
QY 3 AMDECTDEGRPORCMPEFVNAFNVVATNTCTTPPEYCVGTGVTKSKCHLCDAG 62  
Db 1 AMDECADEGRPORCMPEFVNAFNVVATNTCTTPPEYCVGTGVTKSKCHLCDAG 60  
QY 63 QPHLQGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKPTS 122  
Db 61 QPHLQGAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYVRLKPTS 120  
QY 123 RPSFAIYKTRDEGPWIPYQYSGSCNTYSKANRGFIRTGDEQALCTDESDISPL 182  
Db 121 RPSFAIYKTRDEGPWIPYQYSGSCNTYSKANRGFIRTGDEQALCTDESDISPL 180  
QY 183 TGNVAFSTLEGRPSAYNPDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLSYYY 242  
Db 181 TGNVAFSTLEGRPSAYNPDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLSYYY 240  
QY 243 AISDFAVGRCKNGHASECMNEFDKLVCKKNTYGVDCCKLPFNDEPWRATAES 302  
Db 241 AISDFAVGRCKNGHASECMNEFDKLVCKKNTYGVDCCKLPFNDEPWRATAES 300  
QY 303 ASECLPCDCNGRSQECYDPPELYRSTGHGCTWCQDNTGACRCRENFFRLGNNEAC 362  
Db 301 ASECLPCDCNGRSQECYDPPELYRSTGHGCTWCQDNTGACRCRENFFRLGNNEAC 360  
QY 363 SSCCHSPVGLSTQCDYSVCRCKPVGWMDKCDRCQCPGFSHLTEAGRCPCSCPSSIDE 422  
Db 361 SPCHSPVGLSTQCDYSVCRCKPVGWMDKCDRCQCPGFSHLTEAGRCPCSCPSSIDE 420  
QY 423 CNVETGRVCYKDNVEGFNCRCCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSYYSI 482  
Db 421 CNVETGRVCYKDNVEGFNCRCCKPGFFNLESNPRGCTPCPCFGHSSVCTNAVGSYYSI 480  
QY 483 SSTFQIDEDGWAERDSEASLEWSSERDIAVISYFPYFIAKPTLKGQVLSYQG 542  
Db 481 SSTFQIDEDGWAERDSEASLEWSSERDIAVISYFPYFIAKPTLKGQVLSYQG 540  
QY 543 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSYPSSETTVKYIFRLHEATDYPW 602

Db 541 NLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSYPSSETTVKYIFRLHEATDYPW 600  
QY 603 RALTPFPFOKLNNLNTSIKIRGTYSERSAGYLDVLTASARPQGPVATWESCTCPVG 662  
Db 601 RALTPFPFOKLNNLNTSIKIRGTYSERSAGYLDVLTASARPQGPVATWESCTCPVG 660  
QY 663 YGQFCCEMLSGYRRETNLGPYPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCS 722  
Db 661 YGQFCCEMLSGYRRETNLGPYPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEKCS 720  
QY 723 DGYGDSSTAGTSSDCQPCPCPGSSCAVPRTKVWCTNCTGTGKRCCLCDDGYGDP 782  
Db 721 DGYGDSSTAGTSSDCQPCPCPGSSCAVPRTKVWCTNCTGTGKRCCLCDDGYGDP 780  
QY 783 LGRNGPVLRLCQLCQSDNIDENAVGNCNRLTGECLKIYNTAGFYCDRCXGDFGPNLAP 842  
Db 781 LGRNGPVLRLCQLCQSDNIDENAVGNCNRLTGECLKIYNTAGFYCDRCXGDFGPNLAP 840  
QY 843 NPADCKKACNPNYCTMKQSSCNPVTCOCCECLPHVTGDCGCDPFPYNLQSGQCERC 902  
Db 841 NPADCKKACNPNYCTMKQSSCNPVTCOCCECLPHVTGDCGCDPFPYNLQSGQCERC 899  
QY 903 DCHALGSTNGQCDINTGQCECQPGITGQHCHERCENHFGPESGCKPCDCHPESLSLQ 962  
Db 900 DCHALGSTNGQCDINTGQCECQPGITGQHCHERCENHFGPESGCKPCDCHPESLSLQ 959  
QY 963 KDDGCECEGREGVGNRCDOCEENYFNRSWPGCOCEPCACYRLVKDKVADHRVKLOELES 1022  
Db 960 KDDGCECEGREGVGNRCDOCEENYFNRSWPGCOCEPCACYRLVKDKVADHRVKLOELES 1019  
QY 1023 IANLGTGDEMVTQDAFEDRLKEAREVMDLLREAQDVKQVQDNLMDRLQVNNLSSQIS 1082  
Db 1020 IANLGTGDEMVTQDAFEDRLKEAREVMDLLREAQDVKQVQDNLMDRLQVNNLSSQIS 1079  
QY 1083 RLQNRINTIETGNLAQARAHVENTERLTIASRELEKAKAAANVSVTQPESTGDPNN 1142  
Db 1080 RLQNRINTIETGNLAQARAHVENTERLTIASRELEKAKAAANVSVTQPESTGDPNN 1138  
QY 1143 MTLAEBARKLAERKHQEAADDIVRAKNTANDTSTAYNLLRLTAGENOTAFIIBELNRK 1202  
Db 1139 MTLAEBARKLAERKHQEAADDIVRAKNTANDTSTAYNLLRLTAGENOTAFIIBELNRK 1198  
QY 1203 YEQAKNISODLEKQAAVHBEAKGADKAVIIVASVAQLSPDSELTLENNIKWEAEN 1262  
Db 1199 YEQAKNISODLEKQAAVHBEAKGADKAVIIVASVAQLSPDSELTLENNIKWEAEN 1258  
QY 1263 LEQLIDQKLXDYEDLREDMRGKELEVNLLLEKGTQEQTADQLLARADAKALAEBAAK 1322  
Db 1259 LEQLIDQKLXDYEDLREDMRGKELEVNLLLEKGTQEQTADQLLARADAKALAEBAAK 1318  
QY 1323 GRDTLQANDLILNKLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRAQOALGSA 1382  
Db 1319 GRDTLQANDLILNKLKDFDRVNDNKTAAEEALRKIPAINOTITEANEKTRAQOALGSA 1378  
QY 1383 AADATEAKNKAHEAERIASAVQKNATSKABERTFAEVTDLNNEVNNMLKQLEAEKEL 1442  
Db 1379 AADATEAKNKAHEAERIASAVQKNATSKABERTFAEVTDLNNEVNNMLKQLEAEKEL 1438  
QY 1443 KRKQDDADQDMWAGMASQAQAEAINARKAKSVTSLSIINDLLEQGLQDLDVNLK 1502  
Db 1439 KRKQDDADQDMWAGMASQAQAEAINARKAKSVTSLSIINDLLEQGLQDLDVNLK 1498  
QY 1503 NEIEGTINKAKDSMKVSDLDKRVSDLENEAKQAEAAIMDYNDIEIEMKDITNLEDIKT 1562  
Db 1499 NEIEGSLNKADEMKASDLDRKVSDESEARKQAEAAIMDYNDIAIIBIIKQIHNELEDIKT 1558  
QY 1563 LPSGCFNTPSIEKP 1576  
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 11  
US-09-845-583A-10

; Sequence 10, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ IDS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-845-583A-10

Query Match 42.1%; Score 3600; DB 4; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 1.4e-200;  
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

QY 2 AAMDECTDGGRCORCMPEFVNAAPNVTVVATNTCGTPPEEYCVOTGVTVTKSCHLDA 61  
DB AGMACYDAGRCORCLPVEFNAAPFORLAQASHTCSPDEFCPHVGAAGAGACQRCDA 79  
QY 62 GOPHLOHGAFLDYNNQADTTWQSQTMLAGVQYPSNINLHLGKAPDIIVYRLKFT 121  
DB 80 ADPQRHNASYLTDFHSQDESTWQSPSMAFVQYPTSVNITRLGKAYEITYVRLKFT 139  
QY 122 SRPESAIYKSTEDGPMYQYVSGSCENTYSKANRGRTGGDEQOALCTDESDISP 181  
DB 140 SRPESAIYKSRADGPWEPIYASCKTYRPEGQYLRGDEDERVAFCTSESDISP 199  
QY 182 LTGCVNAFSTLEGRPSAYPNDSPLVQLQWVTAIDIRVTLNRLNTFGDEVNDFPKVLKSY 241  
DB 200 LSGVNAFSTLEGRPSAYPNDSPLVQLQWVTAIDIRVTLNRLNTFGDEVNDFPKVLQSY 259  
QY 242 YALSDFAVGRCKNGHASECMNEFDKLVCKNCHNTYGVCEKCLPFPENDPWRATAE 301  
DB 260 YAVSDFSVGRCKNGHASECGPDVAGQACRCQHNNTGDCRCCLPFFQDRPWAGTAE 319  
QY 302 SASCELPDCNCRSQBECYFPELYRSTGGHCTNCQDNTDGAHCRCRENFRFLGNNEA 361  
DB 320 AAHECLPCNCSGRSECTFDRFLFRSTGGGRCHCRDHTAGPHCERCQENFYHMDPRMP 379  
QY 362 CSSCHCSPVGSLSTQDYSYGRCSCKGVMGDKDCRCOPGFHSLTEAGRCPCSDPSGSD 421  
DB 380 COPDCQASGLHQCDDTGTCAKPTVTGWKCDRLPGFHSUSEGGCRPCTCNPGSLD 439  
QY 422 ECVNTRGVCKDNVEGFCNCRCKPGFFNLESNPRGCTPCFCFGRHSSVCTNAVGSYVS 481  
DB 440 TCDPRGRCPCKENVEGNLDCRCPTFNLPHPNAGCSCFCYGHSKVCASTAQOVHH 499  
QY 482 ISFTFQIDEGWRAERDGEASLEWSSERQDIAVSDSYFPRYFAPAKFLGKQVLSYG 541  
DB 500 ILSDFHQAGEGWARSYGGSEHSPQSPN---GVLLSPDEBELTAPGLFGDQRPFSYG 555  
QY 542 QNLSFSRVRDRTRLSAEDLVLEGALRVSVPLIAQGNPSYBETTVKVYVRLH---EAT 598  
DB 556 QPILITFRVPGDPLPVQ-LRLEGTLALS--LRHSSLSGPQDARASQGGRAQVLPQET 612  
QY 599 DYPWRPALTPFEQKLNNTSIRKITYSERAG--YLDVTLGARPGPGVPATWVES 656  
DB 613 SEDVAPLPFPFHFORLLANTLSLRVSPGSPAGPVFLTEVRLTSARPGLSPSPASWVEI 672  
QY 657 CTCPVGVGGFCFECNLSGIRETNPGLPYSPCVLCACNGHSECTCDPTGVNCRDNTAGP 716  
DB 673 CSCPVTGTGFCSCAPGYKREMPQGGFYASCVPCTCNQHG-TCDPNTGLVCVSHHTEGP 731

QY 717 HCEKSDGYGDDTAGTSSDQPCPCPGGGSSCAVVPKTEVVTCTGTTGKRCBELCDD 776  
DB 732 SCERCLPGFVGNFFAQADDCQPCPCPGGACITTIPESEGVVCTHCPGQGRRCVCCDD 791  
QY 777 GYFGDPLGRNGPVRLCRLOCCSDNIDPNVGNCRNLTGCECLKIYNTAGFYCDRCXGDF 836  
DB 792 GFPGDPLGLFGHPQCHQCOCGSGNVDPNVGNCDPLSGHCLRLCHNTTGDHCEHCEGFX 851  
QY 837 GNPLAPNADKACACNPNYGTMTKQSSCNPTVGTQCECLPHVTGQDCGACDGFYNLQSG 896  
DB 852 GSALAPRPADKCMPCSCHPGSVSEQWPCDPVTGQSCSLPHVTARDCSRVCPGFFDLQPG 911  
QY 897 QGCERCDCHALGSTNGQCDIITQCEBQPGITQCHERCENVHHPGFGPECKPCDCHPEG 956  
DB 912 RGCRCCKCHPLGSOEDQCHPKTGCTCRPGVTGQACDRCOLGFFGSSIKGCACRCSPLG 971  
QY 957 SLSLOKXDDGRCRCREGFVGNRCDOCEENFYNRSPGCOECPACVYELVKDVADHEVKL 1016  
DB 972 AASAQCHYNGTCVCRPGFEGYKCDRCCHYNFFLADGTHCQCFSCVALVEETAKUKARL 1031  
QY 1017 QELESILANLGTGDEMVTDOAFEDRLKEAREVMDLLREADYKVDVQNDLMDRLQRVNT 1076  
DB 1032 TLTEGMLQSSDCGSPW---GPLDILLGEAPRG--DVYQGHLLPGAREAFLEQMMGLEGA 1086  
QY 1077 LSSQISRLQINRTIETGNLAQARAHVENTEELTEIASRELEKAKVAANAVSVTQPE 1136  
DB 1087 VKAAREQLORLNGARCAQAGSQKTCQLADLAEVLESSEEEILHAAAILASLEIPO-EG 1145  
QY 1137 TGDNNNTLLAEAREKLAERHKOEADDIRVAKTANDTSTEAYNLLRLTLRITLAGNQTA 1196  
DB 1146 PSQTKWHLAIEARALARSHRDATKIAATAWALLASNTSYALLWNLL--EGRVALET 1203  
QY 1197 E-ELNRKYEQAKNTSQDLEKQAAVHBEAKRAGDKAVEIYASVAQSLPDLSETL----- 1249  
DB 1204 QRDLEDYQVEYQAAQKALRTAVAEVLPEAE-----SVLATVQVGADTAPYLLALASP 1256  
QY 1250 -----ENEANNIKMEANLEQLIDQKDYEDLREDMRGKELEYKNLLEKGTQEQOT--- 1301  
DB 1257 GALPQKRAEDLGLKAKALEKTV---ASQHWATE--AARTLQTAQATLRLQTEPLTMA 1311  
QY 1302 -----ADQLAPADAALAEAEAKKGRDITLOEANDIINNLIKOPRRVNDNKTAEEA 1354  
DB 1312 SRLTATFASQLHOGARAALTAQSSVQAATVTVMGARTLLADLEGMKLQFPRPKQAAALQ 1371  
QY 1355 LRKTPALNQTITEANEKTRQAQALGSAADATAEAKKAHEABERIASAVOKNATSTKAE 1414  
DB 1372 RKADSVDRLLADTRKTKQKERMGNAPLSSAKKKGREAEVLAKDSAKLALLRER 1431  
QY 1415 ERTFAEVTDLNDEVNNMLKQL-QEAEKELKRDQDADQDMMAGMASQAQAEABINARKA 1473  
DB 1432 KOAHERASLTSQTQATLQQAASQVLALEARQLEAEARVAGLS-----EMEQQIRES 1486  
QY 1474 KNSVTSLSLSIINDLEQLGLDT--VDLNKLNIEGTLNKAKOBM-KVSDLDKRVSDLEN 1530  
DB 1487 RISLEKDIETLSLLARLSLDTHOAPAQALNETQWALERLRLQLQSGSLQRLKLSLEQ 1546  
QY 1531 EAKKQEAAMIDYNRDIBEMKDIRNLEDIRKTLPSGC 1567  
DB 1547 ESQQLQIQCFESDLAEIRADKQNLLEAILHSLPENC 1583

RESULT 12  
US-09-561-709B-3  
; Sequence 3, Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001



; CURRENT APPLICATION NUMBER: US/09/561.709B  
; CURRENT FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-3

Query Match 42.1%; Score 3600; DB 4; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 1.4e-200;  
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;  
Qy 2 AAMDECTDEGRPCORCMPEFNAFNVVATVTCGPPEEYCVQGVGTGYSKSLCDA 61  
Db 20 AGMGACVDGGRPCORCLPVFENAAFGRLAASHTCGSPFDFPHVGAAGAHACORCDA 79  
Qy 62 CQPHLQGAAPLTDDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITVRLKFHT 121  
Db 80 ADPQRHNASYLTDFHSQDEBTWQSPSMAFGVQYPTSVNITLRLGKAYBITVRLKFHT 139  
Qy 122 SRPESFAIKTRDEGDPWIPYQYSGSCENTYKXANRGPRTGDEQOALCTDEFSDISP 181  
Db 140 SRPESFAIKTRADGWPETQYFASCKTYGRPEQOYLRGDEBFAVCTSEFSDISP 199  
Qy 182 LTGNVAPSTLEGRPSAYNFONSPLQEWVTATDIRVTLNRLNTFGDEVENDPKVLKSY 241  
Db 200 LSGNVAFSTLEGRPSAYNFESFGLQEWVTSTELLISLDRNTFGDDIFKDPKVLQSY 259  
Qy 242 YAI5DFVAGRCCKNGHASECKWNEFDKLVNCKHNTYVDCEKCLPFFNDRPWRATAE 301  
Db 260 YAVSDFVAGRCCKNGHASECGPDAVAGLACRCOHNNTGDCERCLPFFQDRPWARGTAE 319  
Qy 302 SASCLPCDNGRSGOECVDFDELRYSTGHGCHCTNCOONTDGAHCERCRCNFRRLGNEA 361  
Db 320 AAHECLPCNCSGRSEECTFDELFRSTGHGRCCHCHDHTAGPHCERCRCQENFHWDRMP 379  
Qy 362 CSSCHSPVGLSTQDSYGRCSCKPGVMGDKDRCPGFHSLTACGRPCSCDPSGSD 421  
Db 380 CQPCDCQAGSLHLQCDDTGTCAKPTVTGKDCRCLPGFHSLSSEGGRCPCNCPAGSLD 439  
Qy 422 ECVETGRCVKONVEGNCRCCKPGFNLESSNPRGCTPCFCFSGHSSVCTNAVGSVYS 481  
Db 440 TCDPRSGRCPCKENVEGNLCRCPGTFLQPHNPAGCSCFCYGHKSKVCASTAQFVHH 499  
Qy 482 ISSTFQIDEDGWRAEQRDGSEASLEWSSERODIAVISDSYFPRYFIAPAKFLGKQVLSY 541  
Db 500 ILSDFHQGAEGWARSVSGSEHSQWSPN---GVLLSPDEBELTAPGKFLGDRPFSYG 555  
Qy 542 QNLSFSFVDRDRDRLSADLVLEGAGLRVSVPLIAQNSYPSSETTVKYVFRHLH---EAT 598  
Db 556 QPLILTFRVPDPSLPVQ-LELEGTGLALS--LRHSLSGFQDARASQGGRAQVPLQET 612  
Qy 599 DYPWRPALTPPEFQKLIANLTSIKIRGTYSERSAG--YLDVITLASARPQPGVPATWVES 656  
Db 613 SEDVAPLPPEFQELLANLTSRLRVSPSPAGPVFLTEVRLTSARGLSPSPASWVEI 672  
Qy 657 CTCPVYGGQPCMCCLSYRRETNLGPYSCVLCACNGHSETCDPTGVCNCRDNTAGP 716  
Db 673 CSCPTGYGTQFCESCAPGYKREMPQGGFYASCVPCTCNQHG-TCDPNTGICVCSHTEGP 731  
Qy 717 HCEKSDGYGDSGTAGTSDQPCPCPGSSCAVVPKTKVVCNCTGTTGKRCCLCDD 776  
Db 732 SCERCLPFYGNPFAQADDQPCPCQCSACTIPESGEVCTHCPGGRCRECVCD 791  
Qy 777 GYFGDPLGRNGPVLICRLCQCSNDIDPNAVGNCRNLGTCECLKICLYNTAGFYCDCKDGF 836  
Db 792 GFPGDPLGLFQHPQCHQCCSGNVDPNAVGNCDPLSGHCLRLCLHNTTGDHCEHCQSGFY 851

Qy 837 GNPLAPNADCKKACNCNPFYGTMTKQSSCNFVTOQCCELPHTVQDQACDPGFVNLQSG 896  
Db 852 GSALAPRPADKCMPCSCHPQGSVSEQMPCDPVTQCSCLPHTVARDSCRCYFGFDFLQPG 911  
Qy 897 QCCERCDCHALGSTNGCCDIITGCECQPGITGQCHCECEVNHGFGEGCKPCDCDCHPEG 956  
Db 912 RGCISCKCHPLGSOEDQCHPKTGTQCTCRPGVTGQACDRCQGLFGSSIKGRCACRCSPLG 971  
Qy 957 SLSLQCKDDGRCECREGFGVGNRCQCEBENYFNRSWPGQCEPCACYRLVKDKVADHRVKL 1016  
Db 972 AASAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCCQPCYALVKEETAKL 1031  
Qy 1017 QELSLIANLGTGBMWTDQAFEDRLKEAREVNDLLREAAQVQKDVQDNLDRLQRVNNT 1076  
Db 1032 TLTEGWLQSGCGSPW---GFLDILLGAPRG--DVYOGHLLPGARAFLEQWMLGEGA 1086  
Qy 1077 LSSQISRLQINRTIETETCNLAQARAHVENTERLIEIASRELEKAKVAAAANVSVTQES 1136  
Db 1087 VKAAREQQLRNKNGARCAQAGSQKCTCTQLADLEAVLESSEEEILHAAAILASLEIPQ-EG 1145  
Qy 1137 TQDPNNMTLLAEBARKLAERHQBADDIVRVAKTANDTSTAYNLLTLTLAGENQTAPEI 1196  
Db 1146 PSQPTKWSHLATEARALARSHRDTATKIATAWRALLASNTSYALLMNL--EGRVALET 1203  
Qy 1197 E-ELNRKYEQAQNTSODLEKQAAARVHEAKRAGDKAVEIYASVAQLSPDSETL----- 1249  
Db 1204 QEDLEDRYQEVQAAQKALRTAVAEVLPEAE-----SVLATVQVQVGDATAPYLALLASP 1256  
Qy 1250 -----ENANNIKMEAEENLEQIIDOKLKYDDELREDMRGKELEVNKLEKTKTQOT--- 1301  
Db 1257 GALPOKSAEIDLGLKAKALEKTV---ASWQHMAE-AARTLOTAAQATLRTQTSPLTWAR 1311  
Qy 1302 -----ADQLLARADAALAAEAAKGRDITLOEANDILNNLKDFDRRVNDNKTAAEEA 1354  
Db 1312 SRLTATFASQLHOGARAALTOASSVQOATVTVMGARTLLADLBSGMLQFFPRKDOAALQ 1371  
Qy 1355 LKIKIPAINQTTTEANETKTRQAQALGSAADAATKAKNAHEABRIASVQKNATSTKAEA 1414  
Db 1372 RKADSVSDRLADTRKTKQAERMLGNAAPLSSAKKKGREAVLAKDSAKLAKALLER 1431  
Qy 1415 ERTFAEVDLDNEVNNMLKOL-OEAERKELKQDDADODMMWAGWASQAQAEAEINARKA 1473  
Db 1432 KOHRRASRLISQOATLQOASQVVLASEARRQELAEAEVGVAGLS-----EMEQQIRES 1486  
Qy 1474 KNSVTSLSIINDLEQLGOLDT--VDLNKLNIEGTLINKAKDEM-KVSDLDKRVSDLEN 1530  
Db 1487 RISLEKDIETLSLLARGLSDTHQAPALNETQWALERLRLOLQSGSPGLSKLSLEQ 1546  
Qy 1531 EAKQCEAAIMDYNRDIEETWKDINLEDIRKTLPSGC 1567  
Db 1547 ESQOELQIQGFESDLAEIRADKQNTZAILHSLPENC 1583

RESULT 13  
US-08-317-450B-13  
; Sequence 13, Application US/08317450B  
; Patent No. 5660982  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Kallunki, Pekka  
; APPLICANT: Pyke, Charles  
; TITLE OF INVENTION: Laminin Chains: Diagnostic and  
; TITLE OF INVENTION: Therapeutic Use  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
; STREET: Ten South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Patent In Release #1.0, Version #1.30
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 94,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-450B-13
Query Match
Best Local Similarity 30.9%; Score 2637; DB 1; Length 1193;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;
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Db 9 CLCFSLLLPAARATSRRE----VDCNGKSRQCIFDELHRTGTNGFRCLNCNDNTDGLH 64
QY 346 CERCRNFRPLGNNEACSSCHSPVGLSTQDSYGRCSCKGVGMDKDRCPQFHSIT 405
Db 65 CERCKNGFYRHRDRCLPCNCKNSKSGARCDNSGRCSCKPVTGARCDRLCPGFHMLT 124
QY 406 EAGC-----RPGCDPSGSDICNVTGRVCKDNVEGFCRCKPFFNLESSNPR 457
Db 125 DAGCTQDRLDLSKDCDDFAGTAGPC--DAGRCVCKPVTGRCRCSGYNLGGNPE 182
QY 458 GCTPCFCFHSSVCTNAVGVSVISSTFQIBEDGWRABQRDGSBASLWSSERODIAVI 517
Db 183 GCTQCFYCHSASCRSSAESYVHKITSTFHQVDGKAVQRNGSPAKLQWSQRHQDFSS 242
QY 518 SDSYFPRYFAPAKFKGVLVSGONLSPSFVDRDRTLSAEDLVLEGARLVSVPLIA 577
Db 243 AQRLDPIVFAKFGUNQVSTGQSLDFYDRGRHPSAHDVLEGAGURITAPLMP 302
QY 578 QGNSYSPSETTVKYVFLHEATDYPWRPALTPFEQKLLNLTSLIKIRGTYSERSAGYLD 637
Db 303 LGKTLPCGLTKTYTFLNHPNSNWSQSLSYFEYRLLNLTLALIRATYGSYTGIDN 362
QY 638 VTLASAPGPGYPATWESCTCPVGGQFCMCLSGYRETPNLGPSPCVLCACNGHS 697
Db 363 VTLISARPVSGAPAPWVEQCICPVGYKGFQCDGASGYKRSARLGFPGTCPCQCG-G 421
QY 698 ETCDPDTGVCNCRDNTAGPHCKSCSDGYGDSGTAGTSSDCPCPCPGSSCAVWPKTKEV 757
Db 422 GACDPTGDCYSGDENPDIEACDPIGFYNDPHDPRS--CKFCPCCHNGFSCSVIPETEV 479
QY 758 VTCNCTGTGTRKCELCDDGYGDPGLGRNGPVLRLCLCOCSNIDPNVAGNCNRLTGCL 817
Db 480 VCNCPGPGVTGARCELCDGYGDPGEHGPVRPCQPCQCNVNDPFSASGNCRLTGCL 539
QY 818 KCIYNTAGFYCDRCXKDFGPNLAPNADKACACNPNYTKWQSSCNPNVPGQCECLPH 877
Db 540 KCIHNTAGYICQCKAGYFGDPLAPNADKACACNPNMGS-----580
QY 878 VTGQDCGACDPGFYNLQSGGCGERCDCALGSTNGQCDIRTGCCQCPGITGHCERCEV 937
Db 581 -----580
QY 938 NHFGFGECKPCDCHPEGSLSLQCKDDGRCRCSFGVGNRCDCQCEENFYNRSWPGQE 997

581 -----EPVG-----CRSDGTCVCKPFGGPNCEH-----GAFS 608
QY 998 CPACYRLVKVADHRVVKLQELSLIANLTGDMVTDOAFEDRLKEAREVMDLLEAQ 1057
Db 609 CPACYNQVKIQMDFQMOQLQRMALISKAQGGGVVFDTELEGRMOQAQALQIURDAQ 668
QY 1058 DVKDQDNLMDRLQRVNNTLSSQISRLQNTIRNTIETGNLAEQARAHVENTERLIEIASR 1117
Db 669 ISEGASRSLGLQAKVRSQENSQSRDLDLKMTVERVALGSQYQNRVTRHLITQMQL 728
QY 1118 ELEKAAVAANVSUTQPESTGDPNNMTLLAEARKLAERKQKQADDIRVAKTANDTSTE 1177
Db 729 SLAESEASLGNNTIPASDHYVGNPFKSLAQEAETRLAESHVESASNMEOQTREDEYSKQ 788
QY 1178 AYNLLRTL-----AGENCFAFEIENLNKRYEQAKNISQDLEKQAKRVEEAKRAGDK 1230
Db 789 ALSVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQH 847
QY 1231 AVEIYASVAQLSPDLSETLE-NEANNIKMAENLEQLIDOKLDYEDLREDMRGKELEVK 1289
Db 848 SLRLDSVPLQGVSDQSFQVEERAKIKQKADSLSSLVTRHMDFKTKQNLGNWKBEAQ 907
QY 1290 NLEKKGTEQOTADOLLARADAALAEAAKGRDRTLQEAANDILNNLKDFDRRVNDNKT 1349
Db 908 QLLQNGSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVSILKNLREFDLQVDRKA 967
QY 1350 AAEALRKIPAINQITTEANETREAAQALGSAADAATEAKNKAHERIASAVQKNATS 1409
Db 968 EAEAMKRLSVISKVSDASDKTQQAERALGSAADAQAKNGAGEALEISSEIEQBIGS 1027
QY 1410 TKAAETFAEVTDLNNEVNNMLKQLQEAELKELKQDDADQDMVMAGMASQAQAEIN 1469
Db 1028 LNLEANTYADGALAMKGLASLSEMEVEGELEKLEFDTNMDAVQMVITEAQKVDTR 1087
QY 1470 ARKAKNSVTSLSIINDLLEQLGQLDVTDLNKLNEIEGTINKAKDEMKVSDLRKVSLE 1529
Db 1088 AKNAGVTIQTDLNTLDGLLHMDPLSVDEGLVLEQLKLSRAKTOIN-SQLRPMMSLE 1146
QY 1530 NEAKQBAALMDYNDRIEEMKDIRNLEDYRKLTPGCFNTPSIEK 1575
Db 1147 ERARQORGHLLHLETSIDGLADYKLNLENIRDLNLPFCYNTQALEQ 1192

RESULT 14
US-08-800-593-13
; Sequence 13, Application US/08800593
; Patent No. 6143505
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,593
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,450
; FILING DATE: 04-OCT-1994

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-593-13

Query Match      30.9%; Score 2637; DB 3; Length 1193;
Best Local Similarity 39.4%; Pred. No. 7.5e+145;
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

QY 286 CLPFNDPWRRAETASASECLPCDNGRSGQECVDFDELVRSYTGHHGCHTNCNDNDTGAH 345
DB 9 CLCFSLLPAAATSRRE-----VDCNGKARQCIFDELHRQTGNGFRCLNCNDNDTGLH 64
QY 346 CERCFNFRFGNEACSSCHSPVSLSTQCSYGRCSCKPGVMGDKDRCPQGFHSLT 405
DB 65 CEKCKNGFYHRERDRCLPCNCSKGLSARCONSGRCSCKPGVTGARCDCLPFGFHLT 124
QY 406 EAGC-----RCSGDPSPSIDENQVETGRVCKDNGVGFNCERCCKPGFNFLESSNPR 457
DB 125 DAGTCQORLDSKCDOPAGIAGPC--DAGRCVCKPAVTGERCDRCRSYTYNLGDNPE 182
QY 458 GCTCFCFGHSVCTNAVGVSYVSISSFQIDEGWRAEQRDGSEASLEWSSRRQDIAMI 517
DB 183 GCTCFCYGHSACSSRAEYSVHKITSTFHQDVGKAVQVRNGSPAKLQWSQRHQDVFS 242
QY 518 SDSFPFYFIPAKFLGKVLVSYQNLSFSFRVDRDRTRLSAEDLVLEGAGLVSVPLIA 577
DB 243 AQRLDPIYFVAPAKFLNGQVSYQSLSFYDVRDGRHFSADHVLLEGAGLKITAPLMP 302
QY 578 QGNSVPGETTVKYVFRLEHATDYWRPALTPFEQKLNNLNTSIKIRGYSERSAGYLD 637
DB 303 LGKTLPCGLTKTYFRLNEHPSNWSQLSYFERYRLRLNLITARATYGEYSTGVIDN 362
QY 638 VTLASAPGPGVATWVESCTCPVGYGQPCMECLSYRRETNLGYPSPCVIACNNGHS 697
DB 363 VTLISAPVSGAPAPWVEQCICPVGYGQFCQDCASGYKDSARLPGFGTCIFCNCQG-G 421
QY 698 ETCDEPTEGVNCRNTAGPHCEKSDGYGSDTAGTSSDQCPGCGSSCAVVPKTKV 757
DB 422 GACDPTDGDVSGDENPDIEADCPIGFYNDPHDPRS--CKPFCPCHNGFSCVPIPETEV 479
QY 758 VCTNCPGTTGKRCLELDDGYGDPPLGRNGFVRLCRLCQCSNDINPDNAVGNCRNLGTGCL 817
DB 480 VCNNGPVGVTGARCELADGADYFGDPFGEHGPVPCQPCQCNNSVNDPSASGNCRLTGRL 539
QY 818 KCIYNTAGFYCDKCDGFFGNPLAPNADKCKACNCPYGTMTKQSSCNPNVTGQCECLPH 877
DB 540 KCIHNATGICYDQCKAGYFGDPLAPNADKCRACNCPMGS-----580
QY 878 VTGDCGACDFGFYFNLSQSGCERCDCCHALGSTNGQCDIRTGQCECQFGITGHCERCEV 937
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DB 581 -----EPVG-----CRSDGTCTCKPGFGFNCHE-----GAFS 608
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DB 609 CPACYNQVKIQMDQPMQQLQRWEALISKAQGGDGVVPDTELEGRMQAEQALQILRDAQ 668
QY 1058 DVKQVDQNLMDRLQVRNNTLSQISRLQNIINTTETGNLABQARAHVENTERLIEASR 1117
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RESULT 15
US-08-317-450B-15
; Sequence 15, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BANNER & ALLEGRETTI, LTD.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,450B
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1111 amino acids
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TYPE: amino acid		Query Match	
; TOPOLOGY: linear		29.5%; Score 2516.5; DB 1; Length 1111;	
; MOLECULE TYPE: protein		Best Local Similarity 39.7%; Pred. No. 6.7e-138;	
US-08-317-450B-15		Matches 486; Conservative 215; Mismatches 385; Indels 137; Gaps 11;	
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Db	9	CLCFSLLLPAARATSRRE-----VDCNNGSRQCIFDRELHRTGTGNGFRCLNCNDNDTGH	64
QY	346	CERCENRFFELGNNEACSSCHSPVGLSTQCDSYGRCSCKPGWGDCKDRCPGFHSLT	405
Db	65	CEKCKNGFYHRERDRCLPCNCSKGLSARCDNSGKCSCKPGVTGARCDRLPGFHMILT	124
QY	406	EAGC-----RPCSDPSGSDENVTGRCVKDNGVEGFCNCRCKPGFENLESSNPR	457
Db	125	DAGCTQDRLDKCDPCDPAIAGPC--DAGRCVCCKPAVTGERCKDRCSRGGYTNLOGNPE	182
QY	458	GCTPCFCFGHSSVCTNAVGYSVYSI8STFOIDEGWRAEQRDGSEASLEWSSERQDIAYI	517
Db	183	GCTQCFCYGHASCRSSAEYSVHKITSTFHQDVGKAVQRNGSPAKLQWSQRHQDVFS	242
QY	518	SDSYFPRPYTAPAKFLQKVLSTGQNLFSFRVDRDRDRLSARDIYLEGALRVSVPLIA	577
Db	243	AQRLDPVYFVAPAKFLNGQVSYGQSLSFDRYDRGRHPSAHDVILEGAGURITAPLMP	302
QY	578	QGRSYPBETTVKVVFRLEHATDVPWRPALPFFEFQKLLNLTSTIKIRGTYSRSAGYLD	637
Db	303	LGKTLPCGLTKYTFRLNEHPSNNWSFOLSYFEYRLLNLTALIRATYGEYSTGYDN	362
QY	638	VTLASRPPGVPATWVETCTCPVYGGQFCENCLSGYRRETNLGYPSPCVLCACNHGS	697
Db	363	VTLISARFVSGAPWPVEQCICPVYKGFQCDQCSAGYKRD SARLPGFGTFCPCNQG-G	421
QY	698	ETCDPETGVCNCRNTAGHCEKSGDGYGDS TAGTSSDCQPCPGSGSCAVVPKTKV	757
Db	422	GACDPDGTGDCYSGDENPDIEADCPITGFYNDPHDPRS--CKPCPCHNGFSCSVIPET	479
QY	758	VCNCPGTGTTGKRCCLDDGYFGDPLGRNGVRVLCRLCQCSNDIDNAVGNCRNLTGEC	817
Db	480	VCNCPGPGVTGARCELCAQGYFGDPPFGEHGFVRPQPCQNSNVDPSPASGNCRLTGR	539
QY	818	KCIYNTAGFYCDKQDQFFGNPLAPADKCKACNCPYCTMKQOQSSCNPNVTGCCECL	877
Db	540	KCIHNTAGIYCDQCKAGYFGDPLAPADKCRACNCPMGS-----	580
QY	878	VTGDCGACDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGITGHCERCE	937
Db	581	-----	580
QY	938	NHFGGPEGCKPCDCHPEGSLSLQCKDDGRCEBREGFVGNRCQCBENFYNRSWPGCQ	997
Db	581	-----EPVG-----CRSDGTVCVKPGFGPNCEH-----GAFS	608
QY	998	CPACVRLVKVADHVRKLOELESILNLGTGDEMVTDOAFEDRLKEAREVMDLLEAQ	1057
Db	609	CPACYNQVKIQMDQFMQOLQMEALISKAQGDGVFDTLEGRMQOAEALQDILRDAQ	668
QY	1058	DVKDVQNLMDRLQVRNLTSSQISRLQNTRTIETGNLAQBARAHVENTERLIEIASR	1117
Db	669	ISEGASRSLGLAKAVASQENSYSRLDLDLMTVERVRALGSQYQNRVDRTHRLITQM	728
QY	1118	ELEKAKVAANVSVTQPESTGDPNNMTLLAEAPKLAERHKOADDIVRVAKTANDTSTE	1177
Db	729	SLAESEASLNTNIPASDHYVGPNGPKSLAQEATRLAESHVESASWNEQLTRETDYSK	788
QY	1178	AYNLLRLT-----AGENQTAPEIEELARKYSQAKNISQDLEKQARVHEEAKGDX	1230
Db	789	ALSLVRKALHBGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIEADRSYQ	847

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Job time : 18.9221 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 40.0948 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-16  
Perfect score: 8544  
Sequence: 1 QAMDECTDEGRFCRCMPE.....EDIRKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
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  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	8544	100.0	1609	14	Sequence 16, Appl
3	8544	100.0	1609	14	Sequence 12, Appl
4	8540	100.0	1609	9	US-10-299-058-12
5	8540	100.0	1609	15	US-09-938-275-11
6	8056	94.3	1607	9	US-10-372-683-36
7	8043	94.1	1605	14	US-09-938-275-10
8	8038	94.1	1572	14	US-10-037-182-18
9	3600	42.1	1587	9	US-10-037-182-20
10	3600	42.1	1587	12	US-09-845-583-10
11	3598	42.1	1575	12	US-10-262-839-210
12	3240	37.9	1557	15	US-10-262-839-212
13	2637	30.9	1193	9	US-10-369-493-6816
14	2637	30.9	1193	14	US-10-756-0718-13
15	2637	30.9	1193	14	US-10-392-113-14
					Sequence 115, Appl

16	2637	30.9	1193	14	US-10-227-738-13
17	2637	30.9	1193	14	US-10-053-662A-31
18	2637	30.9	1193	15	US-10-298-027-330
19	2637	30.9	1193	15	US-10-298-027-1269
20	2637	30.9	1193	15	US-10-603-725-26
21	2637	30.9	1193	16	US-10-188-832-147
22	2630	30.8	1172	15	US-10-603-725-28
23	2629	30.8	1193	15	US-10-603-725-30
24	2622	30.7	1172	15	US-10-603-725-32
25	2612.5	30.6	1190	14	US-10-053-662A-2
26	2516.5	29.5	1111	9	US-09-756-0718-15
27	2516.5	29.5	1111	12	US-10-392-113-15
28	2516.5	29.5	1111	14	US-10-227-738-15
29	2454.5	28.7	1171	15	US-10-603-725-36
30	2454.5	28.7	1192	12	US-10-392-113-12
31	2454.5	28.7	1192	14	US-10-053-662A-32
32	2454.5	28.7	1192	15	US-10-603-725-34
33	1782.5	20.9	3084	9	US-09-938-275-4
34	1782.5	20.9	3084	14	US-10-262-670-2
35	1776	20.8	3070	10	US-09-961-403-7
36	1726	20.2	3075	9	US-09-938-275-5
37	1673	19.6	1765	14	US-10-037-182-8
38	1673	19.6	1786	9	US-09-873-676-113
39	1673	19.6	1786	9	US-09-938-275-6
40	1673	19.6	1786	14	US-10-037-182-6
41	1643	19.2	1786	9	US-09-938-275-7
42	1643	19.2	1786	14	US-10-037-182-10
43	1626.5	19.0	2823	15	US-10-369-493-5220
44	1626.5	19.0	2823	15	US-10-369-493-5221
45	1622.5	19.0	1725	14	US-10-037-182-12

ALIGNMENTS

RESULT 1  
US-10-037-182-16  
; Sequence 16, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggevason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-16

Query Match	100.0%	Score	8544	DB	14	Length	1576
Best Local Similarity	100.0%	Pred. No.	0				
Matches	1576	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	QAMDECTDEGRFCRCMPEFVNAAFNVVVAINTCGTTPPEYCVQGTGVTGKXCHLCD	60				
DB	1	QAMDECTDEGRFCRCMPEFVNAAFNVVVAINTCGTTPPEYCVQGTGVTGKXCHLCD	60				
QY	61	AGQPHLQGAFLFDYNNQADTTWQSTMLAGVQYSSINLTLLHKGAFITTVRLKHF	120				
DB	61	AGQPHLQGAFLFDYNNQADTTWQSTMLAGVQYSSINLTLLHKGAFITTVRLKHF	120				
QY	121	TSRPESFAIKRTREDGPIVQYVSGSCENTYSKANEGFIRTCGDEQALCTDFSDIS	180				

Db 121 TSPPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFRTGGDEQOALCTDFESDIS 180  
QY 181 PLTGGNVAFTLEGRSAFNENSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240  
Db 181 PLTGGNVAFTLEGRSAFNENSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240  
QY 241 YIAISDFAVGGRCKNGHASECMKNEFDFKLVNCKHNTYGVDCCKLFFNDRPWRATA 300  
Db 241 YIAISDFAVGGRCKNGHASECMKNEFDFKLVNCKHNTYGVDCCKLFFNDRPWRATA 300  
QY 301 ESASECLPCDCNCRSDECFDPELYRSTGHGHCNTCODNTDGAHCRCRENFRLGNNE 360  
Db 301 ESASECLPCDCNCRSDECFDPELYRSTGHGHCNTCODNTDGAHCRCRENFRLGNNE 360  
QY 361 ACSSCHSPVGLSTQCDYGRCSCKPGVMGDKDRCPQPGHSLTEACRSCDPSGSI 420  
Db 361 ACSSCHSPVGLSTQCDYGRCSCKPGVMGDKDRCPQPGHSLTEACRSCDPSGSI 420  
QY 421 DECNVETGRVCVKDNVEGNCRCRCPGFNFLESSNPRGCTPCFCFGHSSVCTNAGVSVY 480  
Db 421 DECNVETGRVCVKDNVEGNCRCRCPGFNFLESSNPRGCTPCFCFGHSSVCTNAGVSVY 480  
QY 481 SISSTFQIDEDGWRAQRDGSASLEWSSERQDIAVISDSYFPFYFIAPAKFLQKVLISY 540  
Db 481 SISSTFQIDEDGWRAQRDGSASLEWSSERQDIAVISDSYFPFYFIAPAKFLQKVLISY 540  
QY 541 GQNLSPFSFVDRDRDTLSAEDLVLSAGLRVSVPILIAOGNSVPSETTVKVFRLHEATDY 600  
Db 541 GQNLSPFSFVDRDRDTLSAEDLVLSAGLRVSVPILIAOGNSVPSETTVKVFRLHEATDY 600  
QY 601 PWRPALTPFEFOKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGPGVATWVSTCTCP 660  
Db 601 PWRPALTPFEFOKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGPGVATWVSTCTCP 660  
QY 661 VGYGGQFCMCLSGVRRPFPNLPYSPVLCACNGHSETCDPFGVNCNDRNTAGPCEK 720  
Db 661 VGYGGQFCMCLSGVRRPFPNLPYSPVLCACNGHSETCDPFGVNCNDRNTAGPCEK 720  
QY 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTEVVCNCPGTGTTGKRCCLDDGYFG 780  
Db 721 CSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTEVVCNCPGTGTTGKRCCLDDGYFG 780  
QY 781 DPLGRNGPVLRLCQCSNDIPNAGVNCNLTGECCKCIYNTAGFYCDRCCKGFFGNPL 840  
Db 781 DPLGRNGPVLRLCQCSNDIPNAGVNCNLTGECCKCIYNTAGFYCDRCCKGFFGNPL 840  
QY 841 APNPADKCKACNPNYGTMKQSSCNPNVTGQCECLPHVTGQDGCACDPGFYNLQSGGCE 900  
Db 841 APNPADKCKACNPNYGTMKQSSCNPNVTGQCECLPHVTGQDGCACDPGFYNLQSGGCE 900  
QY 901 RCDCHALGSTNGOCDIRTGQCECPGIGTGCHERCENHFGFEGCKPCDCHPEGSLSL 960  
Db 901 RCDCHALGSTNGOCDIRTGQCECPGIGTGCHERCENHFGFEGCKPCDCHPEGSLSL 960  
QY 961 QCKDGRCEGRCFVGNRCQCEENYFYNRSPWPGQCECPACRYLVKQVADHRVKLQELE 1020  
Db 961 QCKDGRCEGRCFVGNRCQCEENYFYNRSPWPGQCECPACRYLVKQVADHRVKLQELE 1020  
QY 1021 SLIANLGTDEMVTQAPEDRLKEAREVMOLLREAOQVDKVDQNLMDRLQRVNTLSSQ 1080  
Db 1021 SLIANLGTDEMVTQAPEDRLKEAREVMOLLREAOQVDKVDQNLMDRLQRVNTLSSQ 1080  
QY 1081 ISRLQNIINTIETGNLAEPARAHVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1140  
Db 1081 ISRLQNIINTIETGNLAEPARAHVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1140  
QY 1141 NNWTLAEBARKLAERHKEQADDIVRVAKTANDTSTAYNLLRLTLAGENQTAPELBN 1200  
Db 1141 NNWTLAEBARKLAERHKEQADDIVRVAKTANDTSTAYNLLRLTLAGENQTAPELBN 1200  
QY 1201 RYEQAKNTISQLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSTLENEANNIMEA 1260  
Db 1201 RYEQAKNTISQLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSTLENEANNIMEA 1260

QY 1261 ENLEQILDOKLKQVEDLBEDMRGKEVKNLLEKGTQEQQTADOLLARAADAALAEAA 1320  
Db 1261 ENLEQILDOKLKQVEDLBEDMRGKEVKNLLEKGTQEQQTADOLLARAADAALAEAA 1320  
QY 1321 KGGRDTLQEAANDILNNLKDFRRVNDNKTAEEALRKIPAINQITTEANEXTREAOQALG 1380  
Db 1321 KGGRDTLQEAANDILNNLKDFRRVNDNKTAEEALRKIPAINQITTEANEXTREAOQALG 1380  
QY 1381 SAAADATKAKNAHEABRIASAVOKNATSTKABAEERTFAEVTDLDNVNNMLKQLEAEK 1440  
Db 1381 SAAADATKAKNAHEABRIASAVOKNATSTKABAEERTFAEVTDLDNVNNMLKQLEAEK 1440  
QY 1441 ELKRRQDDADQDDMMAGNASQAQAEAEINAKAKSVTSLSIINDLLEQLGQDVTVDLN 1500  
Db 1441 ELKRRQDDADQDDMMAGNASQAQAEAEINAKAKSVTSLSIINDLLEQLGQDVTVDLN 1500  
QY 1501 KLNBEGLTNKAKDBMKVSDLDKRVSDLENEAKKQEAAMDYNDRIEIMKDINLEDIR 1560  
Db 1501 KLNBEGLTNKAKDBMKVSDLDKRVSDLENEAKKQEAAMDYNDRIEIMKDINLEDIR 1560  
QY 1561 KTLPSGCPNTPSIEKP 1576  
Db 1561 KTLPSGCPNTPSIEKP 1576

## RESULT 2

US-10-037-182-14  
; Sequence 14, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-14

Query Match 100.0%; Score 8544; DB 14; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCWPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 60  
Db 34 QAAMDECTDEGGRPQRCWPEFVNAAFNVTVATNTCGTPPEEYCVQTVGTGVTKSCHLCD 93  
QY 61 AGQPHLQGAFLDYNNQADTTWQSOOTWLAGVOYVSSINLTGLGKAFDITYVELKPH 120  
Db 94 AGQPHLQGAFLDYNNQADTTWQSOOTWLAGVOYVSSINLTGLGKAFDITYVELKPH 153  
QY 121 TSPPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFRTGGDEQOALCTDFESDIS 180  
Db 154 TSPPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFRTGGDEQOALCTDFESDIS 213  
QY 181 PLTGGNVAFTLEGRSAFNENSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 240  
Db 214 PLTGGNVAFTLEGRSAFNENSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSY 273  
QY 241 YIAISDFAVGGRCKNGHASECMKNEFDFKLVNCKHNTYGVDCCKLFFNDRPWRATA 300  
Db 274 YIAISDFAVGGRCKNGHASECMKNEFDFKLVNCKHNTYGVDCCKLFFNDRPWRATA 333

QY 301 ESASECLPCDCNCRSGOECYFDPELYRSTGHGHCNTNQDNTDGAHCRCRENFRLGNNE 360  
Db 334 ESASECLPCDCNCRSGOECYFDPELYRSTGHGHCNTNQDNTDGAHCRCRENFRLGNNE 393  
QY 361 ACSSCHCSFVGLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLEAGCRPCSDPSGSI 420  
Db 394 ACSSCHCSFVGLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLEAGCRPCSDPSGSI 453  
QY 421 DECNVETGRCVKDNGVEGNCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNAVGYSY 480  
Db 454 DECNVETGRCVKDNGVEGNCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNAVGYSY 513  
QY 481 SISSTFQIDEDGWRARQDGESEASLEWSSERQDIAVISYPRPIAPAKFLGQVLSY 540  
Db 514 SISSTFQIDEDGWRARQDGESEASLEWSSERQDIAVISYPRPIAPAKFLGQVLSY 573  
QY 541 GQNLSPFRVDRDRTLRSADLVLEAGLRVSPLIAQGNPSYPTTXYVFLHEATDY 600  
Db 574 GQNLSPFRVDRDRTLRSADLVLEAGLRVSPLIAQGNPSYPTTXYVFLHEATDY 633  
QY 601 PWRPALTPPEFQKLANLTSIKIRGTYSERSAGYLDVTLASARPQGVPAWRESCTCP 660  
Db 634 PWRPALTPPEFQKLANLTSIKIRGTYSERSAGYLDVTLASARPQGVPAWRESCTCP 693  
QY 661 VGYGGQFCENCLSGYRETNLGPYSPVLCACNGHSETCDPTGVCNCRDNTAGHCEK 720  
Db 694 VGYGGQFCENCLSGYRETNLGPYSPVLCACNGHSETCDPTGVCNCRDNTAGHCEK 753  
QY 721 CSDGYGDSSTAGSSDCQPCPCPGSSCAVVPKTKVWVCTNCPGTGKRCBELCDDGYFG 780  
Db 754 CSDGYGDSSTAGSSDCQPCPCPGSSCAVVPKTKVWVCTNCPGTGKRCBELCDDGYFG 813  
QY 781 DPLGRNGPVLRLCQSDNIDNAGVNCNRLTGECLKCIYNTAGFVCDRCCKDGRFGNPL 840  
Db 814 DPLGRNGPVLRLCQSDNIDNAGVNCNRLTGECLKCIYNTAGFVCDRCCKDGRFGNPL 873  
QY 841 APNPADKCKACNPNYGTMKQSSCNPNVTQCCECLPHVTGQDCGACDPGFYALQSQGCE 900  
Db 874 APNPADKCKACNPNYGTMKQSSCNPNVTQCCECLPHVTGQDCGACDPGFYALQSQGCE 933  
QY 901 RCDCHALGSTNGQCDITGTCBQPGITGQCHRCVNHFGFPGCEKCDCHPEGLSL 960  
Db 934 RCDCHALGSTNGQCDITGTCBQPGITGQCHRCVNHFGFPGCEKCDCHPEGLSL 993  
QY 961 QCKDDGRCCEGREGVGNRCQCEENFYNRSWFGQCECPACVRLVKDVKADHRVKLQELE 1020  
Db 994 QCKDDGRCCEGREGVGNRCQCEENFYNRSWFGQCECPACVRLVKDVKADHRVKLQELE 1053  
QY 1021 SLIANLTGDEMVTDOAFEDRLKEAREVNDLLREAOVDKVDQNDLMDRLQRYNNTLSQ 1080  
Db 1054 SLIANLTGDEMVTDOAFEDRLKEAREVNDLLREAOVDKVDQNDLMDRLQRYNNTLSQ 1113  
QY 1081 ISRLQNTIRNITBETGNLAEOARAHVENTERLIIASRELEKAKAAVANSVTOPESTGDP 1140  
Db 1114 ISRLQNTIRNITBETGNLAEOARAHVENTERLIIASRELEKAKAAVANSVTOPESTGDP 1173  
QY 1141 NNMTLLAEBARKLAERHKQADDIRVAKTANTSTEAYNLLRTLAGENQTAFFEELN 1200  
Db 1174 NNMTLLAEBARKLAERHKQADDIRVAKTANTSTEAYNLLRTLAGENQTAFFEELN 1233  
QY 1201 RKYEOAKNI SODLEKQARVHEEAKRAGDKAVIYASVAQLSPDSETLENEANNIKMEA 1260  
Db 1234 RKYEOAKNI SODLEKQARVHEEAKRAGDKAVIYASVAQLSPDSETLENEANNIKMEA 1293  
QY 1261 ENLEQLIDQKLYEDLREDMRGKEVKNLLEKGTQEQOTADQLLARADAALKALAEBA 1320  
Db 1294 ENLEQLIDQKLYEDLREDMRGKEVKNLLEKGTQEQOTADQLLARADAALKALAEBA 1353  
QY 1321 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEBALRKIPAINOTITTEANEKTEAOQALG 1380  
Db 1354 KKGRTDLOEANDILNNLKDFDRRVNDNKTAAEBALRKIPAINOTITTEANEKTEAOQALG 1413

QY 1381 SARAADATEAKNKAHEABRIASAVQKNATSTKAABERTFAEVTDLNEVNNMLKQLEAEK 1440  
Db 1414 SARAADATEAKNKAHEABRIASAVQKNATSTKAABERTFAEVTDLNEVNNMLKQLEAEK 1473  
QY 1441 ELKEKQDADQDQMMAGWASQAQAEAFINARKAKNSVTSLLSINDLLEQLGOLDTVDLN 1500  
Db 1474 ELKEKQDADQDQMMAGWASQAQAEAFINARKAKNSVTSLLSINDLLEQLGOLDTVDLN 1533  
QY 1501 KLNIEGTLNKAKDEMKSVDLDRKVSLENEAKQAEAAINDYNRDIEEIMKDIRNLEDIR 1560  
Db 1534 KLNIEGTLNKAKDEMKSVDLDRKVSLENEAKQAEAAINDYNRDIEEIMKDIRNLEDIR 1593  
QY 1561 KTLPSGCFNTPSIEKP 1576  
Db 1594 KTLPSGCFNTPSIEKP 1609  
RESULT 3  
US-10-299-058-12  
; Sequence 12, Application US/10299058  
; Publication No. US20030103975A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, JONATHAN C.R.  
; APPLICANT: GONZALES, MEREDITH  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION  
; FILE REFERENCE: 1720-1-002 CIP  
; CURRENT APPLICATION NUMBER: US/10/299,058  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/706,235  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/163,199  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-299-058-12  
Query Match 100.0%; Score 8544; DB 14; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QAAMDECTDEGRPORCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCD 60  
Db 34 QAAMDECTDEGRPORCMPEFVNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSCHLCD 93  
QY 61 AGOPHLOHGAAPLTDYNNQADTTWQSQOTMLAGVQYPPSSINLTLLHKGAFDITVRLKFH 120  
Db 94 AGOPHLOHGAAPLTDYNNQADTTWQSQOTMLAGVQYPPSSINLTLLHKGAFDITVRLKFH 153  
QY 121 TSRPESFAIKRTREDGPMIPYQYVSGSCENTYKANGFIRTCGDEQQALCTDEFSDIS 180  
Db 154 TSRPESFAIKRTREDGPMIPYQYVSGSCENTYKANGFIRTCGDEQQALCTDEFSDIS 213  
QY 181 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 240  
Db 214 PLTGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSY 273  
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPPFNDRWRRAATA 300  
Db 274 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCCKLPPFNDRWRRAATA 333  
QY 301 ESASECLPCDCNCRSGOECYFDPELYRSTGHGHCNTNQDNTDGAHCRCRENFRLGNNE 360  
Db 334 ESASECLPCDCNCRSGOECYFDPELYRSTGHGHCNTNQDNTDGAHCRCRENFRLGNNE 393  
QY 361 ACSSCHCSFVGLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLEAGCRPCSDPSGSI 420  
Db 394 ACSSCHCSFVGLSTQCDYGRCSCKPGVMGDKDCRCQPGFHSLEAGCRPCSDPSGSI 453  
QY 421 DECNVETGRCVKDNGVEGNCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNAVGYSY 480



Db 454 DECNVETGRVCKNDVEGFCNCRCKGFFNLESNPRGCTFCFCFGHSSVCTNAGVSIV 513  
Qy 481 S1SSTFQIDEDGWAEQRDGESEASLEWSSSRQDIIVISDSYFPYFIAPAKFLGKQVLSY 540  
Db 514 S1SSTFQIDEDGWAEQRDGESEASLEWSSSRQDIIVISDSYFPYFIAPAKFLGKQVLSY 573  
Qy 541 GQNLSPFRVDRDTRLASADLVLEGAGLVSPVPLAAGNSYPSSETTKYVFRLEHATDY 600  
Db 574 GQNLSPFRVDRDTRLASADLVLEGAGLVSPVPLAAGNSYPSSETTKYVFRLEHATDY 633  
Qy 601 PWRPALTPFFQKLLNNLTISIKIRGTYSERSAGYLDVTLASARPQGVPAWVESCTCP 660  
Db 634 PWRPALTPFFQKLLNNLTISIKIRGTYSERSAGYLDVTLASARPQGVPAWVESCTCP 693  
Qy 661 VYGGOFCFENCLSGYRRETNLPYSPVLCACNGHSETCDPETGVCNCRDNTAGHCHCK 720  
Db 694 VYGGOFCFENCLSGYRRETNLPYSPVLCACNGHSETCDPETGVCNCRDNTAGHCHCK 753  
Qy 721 CSBGYYGDSSTAGSSDQCPGCGSSCAVVPKTEWVCTNCTGTGKRCCLDDGYFG 780  
Db 754 CSBGYYGDSSTAGSSDQCPGCGSSCAVVPKTEWVCTNCTGTGKRCCLDDGYFG 813  
Qy 781 DPLGRNGFVRLCRLQCSNDIDNVAAGNCRNLGECCLKIYNTAGVCDRCCKGFFGNPL 840  
Db 814 DPLGRNGFVRLCRLQCSNDIDNVAAGNCRNLGECCLKIYNTAGVCDRCCKGFFGNPL 873  
Qy 841 APNPADCKKACNCPYGTMKQSSCNVPTQCCECLPHVTGQDCGACDPGFYNLQSQGCE 900  
Db 874 APNPADCKKACNCPYGTMKQSSCNVPTQCCECLPHVTGQDCGACDPGFYNLQSQGCE 933  
Qy 901 RCDCHALGSTNGQCDITGQCEQCPGITGQCHRCERVENHFGPQEGCKPCDCHPEGSLSL 960  
Db 934 RCDCHALGSTNGQCDITGQCEQCPGITGQCHRCERVENHFGPQEGCKPCDCHPEGSLSL 993  
Qy 961 QCKDDGRCCEGREGVGNRCQCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLOELE 1020  
Db 994 QCKDDGRCCEGREGVGNRCQCEENYFYNRSWPGCECPACRYLVKDKVADHRVKLOELE 1053  
Qy 1021 SLIANLTGDEWMTQAFEDRLKEAREVMDLIREAQDVKDQVQDNLMRLQRVNNLTSSQ 1080  
Db 1054 SLIANLTGDEWMTQAFEDRLKEAREVMDLIREAQDVKDQVQDNLMRLQRVNNLTSSQ 1113  
Qy 1081 ISRLQNTNRTIETGNLAEQARAHVENTERLIIETASRELEKAVAAANSVTPQESTGDP 1140  
Db 1114 ISRLQNTNRTIETGNLAEQARAHVENTERLIIETASRELEKAVAAANSVTPQESTGDP 1173  
Qy 1141 NNMTLLAEARKLAERHKQADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1200  
Db 1174 NNMTLLAEARKLAERHKQADDIRVAKTANDTSTEAYNLLRLTLAGENQTAFEIEELN 1233  
Qy 1201 RKYEQAKNI SODLEKQARVHEEAKRAGDKAVIYASVAQLSPIDSETLENEANNIKMEA 1260  
Db 1234 RKYEQAKNI SODLEKQARVHEEAKRAGDKAVIYASVAQLSPIDSETLENEANNIKMEA 1293  
Qy 1261 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQEQQTADQLLARADAALAEAEA 1320  
Db 1294 ENLEQLIDQKLKDYEDLREDMRGKELEVKNLLEKGTQEQQTADQLLARADAALAEAEA 1353  
Qy 1321 KKGRTDLOEANDILNLIKDFDRVNDNKTAAEALRKIPAINOTITEANEKTEAQOALG 1380  
Db 1354 KKGRTDLOEANDILNLIKDFDRVNDNKTAAEALRKIPAINOTITEANEKTEAQOALG 1413  
Qy 1381 SAADATEAKNAHEERIASAVOKNATSTKAEABRTFAEVTDLDRVNNMLKQLOEAEK 1440  
Db 1414 SAADATEAKNAHEERIASAVOKNATSTKAEABRTFAEVTDLDRVNNMLKQLOEAEK 1473  
Qy 1441 ELKPKQDDADQDMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN 1500  
Db 1474 ELKPKQDDADQDMWAGMASQAQAEAEINARKAKNSVTSLLSIINDLLEQLGQDVTVDLN 1533  
Qy 1501 KLNIEGTGLNKADEMVKSDLDKRVSDLENEAKQEAAMINDYNRDIBEIMKDIRNLEDIR 1560

Db 1534 KLNIEGTGLNKADEMVKSDLDKRVSDLENEAKQEAAMINDYNRDIBEIMKDIRNLEDIR 1593  
Qy 1561 KTLPSGCENTPSIEKP 1576  
Db 1594 KTLPSGCENTPSIEKP 1609  
RESULT 4  
US-09-938-275-11  
; Sequence 11, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P11047  
; DATABASE ENTRY DATE: 1991-11-01  
US-09-938-275-11  
Query Match 100.0%; Score 8540; DB 9; Length 1609;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Qy 61 AGQHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYVSSINLTLLHKGAPDITTVRLKPH 120  
Db 94 AGQHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYVSSINLTLLHKGAPDITTVRLKPH 153  
Qy 121 TSRPESFAIYKRTREDQFPWIPYQYSGSCENTYSKANRGFIRTGDSQQAALCTDEFSDIS 180  
Db 154 TSRPESFAIYKRTREDQFPWIPYQYSGSCENTYSKANRGFIRTGDSQQAALCTDEFSDIS 213  
Qy 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDITVTLNRLNTFGDEVFNDPKVLKSY 240  
Db 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDITVTLNRLNTFGDEVFNDPKVLKSY 273  
Qy 241 YYAISDPVAVGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPPFFNDRPWRATA 300  
Db 274 YYAISDPVAVGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPPFFNDRPWRATA 333  
Qy 301 ESASECLPCDCNCRSQCIBYFDPPELYRSTGHGCHCTNCDNTDGAHCRCRNFRLGNE 360  
Db 334 ESASECLPCDCNCRSQCIBYFDPPELYRSTGHGCHCTNCDNTDGAHCRCRNFRLGNE 393  
Qy 361 ACSSCHCSFVGSLSLSTQCDYSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRCPCSDPGSI 420  
Db 394 ACSSCHCSFVGSLSLSTQCDYSYGRCSCKPGVMGDKDCRCQPGFHSLTEAGRCPCSDPGSI 453  
Qy 421 DECNVETGRVCKNDVEGFCNCRCKGFFNLESNPRGCTFCFCFGHSSVCTNAGVSIV 480  
Db 454 DECNVETGRVCKNDVEGFCNCRCKGFFNLESNPRGCTFCFCFGHSSVCTNAGVSIV 513  
Qy 481 S1SSTFQIDEDGWAEQRDGESEASLEWSSSRQDIIVISDSYFPYFIAPAKFLGKQVLSY 540  
Db 514 S1SSTFQIDEDGWAEQRDGESEASLEWSSSRQDIIVISDSYFPYFIAPAKFLGKQVLSY 573  
Qy 541 GQNLSPFRVDRDTRLASADLVLEGAGLVSPVPLAAGNSYPSSETTKYVFRLEHATDY 600  
Db 574 GQNLSPFRVDRDTRLASADLVLEGAGLVSPVPLAAGNSYPSSETTKYVFRLEHATDY 633

GENERAL INFORMATION:  
APPLICANT: GERRITSEN, MARY E.  
APPLICANT: PEALE JR., FRANKLIN V.  
APPLICANT: WU THOMAS D.  
TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
FILE REFERENCE: P1928R1P1  
CURRENT APPLICATION NUMBER: US/10/372,683  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: US 10/271,690  
PRIOR FILING DATE: 2002-10-16  
PRIOR APPLICATION NUMBER: US 60/344,534  
PRIOR FILING DATE: 2001-10-18  
NUMBER OF SEQ ID NOS: 49  
SEQ ID NO 36  
LENGTH: 1609  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-372-683-36

Query Match 100.0%; Score 8540; DB 15; Length 1609;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QAAAMDECTDEGRPCRCMPFVNAAFNVVATVATTCGTPPEEYCVQGTGVTGKSKLCLD 60  
DB 34 QAAAMDECTDEGRPCRCMPFVNAAFNVVATVATTCGTPPEEYCVQGTGVTGKSKLCLD 93  
QY 61 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYQSSINLTLHLKAFDITVYRLKFK 120  
DB 94 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYQSSINLTLHLKAFDITVYRLKFK 153  
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DB 154 TSRESFAIYKTRTREDGFWPIYQYVSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 213  
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DB 214 PLTGONVAFSTLEGRPSAYNFDNSFVLQEWWTATDIRVTNLRNLTFGDEVNDPKVLKSY 273  
QY 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFNDRPWRATA 300  
DB 274 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCKHNTYGVDCCKLPFNDRPWRATA 333  
QY 301 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRCRNFRLGNE 360  
DB 334 ESASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCQDNTDGAHCRCRCRNFRLGNE 393  
QY 361 ACSSCHCSFVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPCSDPSGSI 420  
DB 394 ACSSCHCSFVGSLSLSTQCDYSYGRCSCKPGVMGDKCDRCQPGFHSLSLTAAGRCPCSDPSGSI 453  
QY 421 DECNVETGRVCVKDNVGFNCRCCKPGFFNLESNPRGCTPCFCFHSVCTNAVGYSVY 480  
DB 454 DECNVETGRVCVKDNVGFNCRCCKPGFFNLESNPRGCTPCFCFHSVCTNAVGYSVY 513  
QY 481 SISSTFQIDEDGWRARQDSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 540  
DB 514 SISSTFQIDEDGWRARQDSEASLEWSSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 573  
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DB 634 PWRPALTPFEFQKLNLLNTLSIKIRGTYSERSAGVLDVTLASAPGPGVATWYESCTCP 693  
QY 661 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720  
DB 694 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753  
QY 721 CSDGYGDSGTAGTSDCQPCPCPGSSCAVVPKTKVYVCTNCTGTGTTGKRCCLCDGCGYFG 780

QY 601 PWRPALTPFEFQKLNLLNTLSIKIRGTYSERSAGVLDVTLASAPGPGVATWYESCTCP 660  
DB 634 PWRPALTPFEFQKLNLLNTLSIKIRGTYSERSAGVLDVTLASAPGPGVATWYESCTCP 693  
QY 661 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720  
DB 694 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753  
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DB 814 DPLGRNGPVRLLRCLQCSNIDNPVNGVNCNRLTGECLKICYNTAGFYCDRCXGDFGNPL 873  
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DB 874 APNPADKCAKACNPNYGTWKQSSCNPNVTGCECLPHVTGQDCGACDPGFYNLQSGQCE 933  
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DB 934 RCDCHALGSTNGQCDIRTGCEQCPGTTGQHCRCCEVNHFGFPECKPCDCHPEGSLSL 993  
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DB 994 QCKDDGRCRCRBEFVGNRCDOCEBENTFYNRSWFGQCECPACVRLVKDKVADHRVKLOELE 1053  
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DB 1054 SLIANLTGDEMTDQAFEDRLKEAREVMDLLREAQDVKDQNDLMDRLQRVNTLSQ 1113  
QY 1081 ISRLQNRINTIETGNLAQARAHVENTERLIIASRELEKAKVAAANVSVTQPESTGDP 1140  
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DB 1474 ELKRXKODDQDMMAGMASQAAQAEIINARKAKNSVTLSLSIINDLLQLQGLDVTDLN 1533  
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Db 814 DPLGRNGPVLCRLCCSDNIDNNAVGNCLTGECLKCIYNTAGFYCDRCCKDGFNGPL 873
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Db 1594 KTLPSGCFNTPSIEKP 1609
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## RESULT 6

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US-09-938-275-10
; Sequence 10, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1607
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02468
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-10
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Query Match 94.3%; Score 8056; DB 9; Length 1607;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 1469; Conservative 59; Mismatches 48; Indels 0; Gaps 0;

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Db 32 RAAMDECADEGRPQRCMPFVNAFNVTVVATNTCGTPPEEYCVQIGVTVTKSCHLCD 91
Qy 61 ACOPHLOHGAELTDYNNQADTTWQSOTMLAGVQYSSINLTLLHAKAPDITTVRLKFH 120
Db 92 ACQQLHGAELTDYNNQADTTWQSOTMLAGVQYSSINLTLLHAKAPDITTVRLKFH 151
Qy 121 TSPESFAIYKTRTREDGPWIPVQYYSGCENTYSKANRGFIRTCGDEQQAALCTDFE 180
Db 152 TSPESFAIYKTRTREDGPWIPVQYYSGCENTYSKANRGFIRTCGDEQQAALCTDFE 211
Qy 181 PLTGGNVAFSTLEGPSPAYNFONSPVLOEWVATDITRVTLNRLNTFGDEVNDRK 240
Db 212 PLTGGNVAFSTLEGPSPAYNFONSPVLOEWVATDITRVTLNRLNTFGDEVNDRK 271
Qy 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCBKCLPFFNDRP 300
Db 272 YYAISDFAVGRCCKNGHASECMKNEFDKLVNCNKNTYGVDCBKCLPFFNDRP 331
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Qy 421 DECNVETGRVCVKONVGFNCERCKPGFNLESNPRGCTPCFCGHSSVCTTNAV 480
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Db 632 PWRPALTPPEFQKLNNLTSIKIRGTYSERSAGYLDVTLASARPFGVPATVWES 691
Qy 661 VYGGGFCFCEMLCSGVRRETNLGPYSPCLVLCANGHSETCDPETGVCNCRDNTAG 720
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Qy 721 CSDGYGDS TAGTSSDCOPCFPGSSCAVVPKTEVCTNCTGTGKRCCLDDGYFG 780
Db 752 CSDGYGDS TAGTSSDCOPCFPGSSCAVVPKTEVCTNCTGTGKRCCLDDGYFG 811
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Qy 841 APNPADKCAKACNPNYGTWKQSSCNPNVTGQCECLPHVTGDCGACDGFYNLQ 900
Db 872 APNPADKCAKACNPNYGTWKQSSCNPNVTGQCECLPHVTGDCGACDGFYNLQ 931
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901 RCDHALGSTNGQCDIRTCQCEQPGITQOHCERCERNVHFGPGCKPCDCHPBGSL 960  
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1561 KTLPSGCFNTPSIEKP 1576  
1592 KTLPSGCFNTPSIEKP 1607

RESULT 7  
US-10-037-182-18  
; Sequence 18, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-18

Query Match 94.18; Score 8043; DB 14; Length 1605;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;  
QY 1 QAAMDECTDEGRPQRCMPPEFVNAAFNVVATNTCGTPEEYCVQGTGVTKSKCHLCD 60  
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DB 92 AQOHLQHGAAFLTDYNNQADTTWQSQTMLAGVOYESSINLTLHLKAPDITTVRLKEH 151  
QY 121 TSRESFAIYKRTEDGFWPIYQYSGSCENTYSKANRGFIRTCGDEQQALCTDEFSDIS 180  
DB 152 TSRESFAIYKRTEDGFWPIYQYSGSCENTYSKANRGFIRTCGDEQQALCTDEFSDIS 211  
QY 181 PLTGNAVAFSTLEGRPSAYNPDNSVLOEWWTATDIRVTLNRLNTFGDEVNDPKVLSY 240  
DB 212 PLTGNAVAFSTLEGRPSAYNPDNSVLOEWWTATDIRVTLNRLNTFGDEVNDPKVLSY 271  
QY 241 YVAISDFAVGRCCKNGHASECMNEFDKLVCKNCNHTYGVDCBKLPFFNDRWRBATA 300  
DB 272 YVAISDFAVGRCCKNGHASECMNEFDKLVCKNCNHTYGVDCBKLPFFNDRWRBATA 331  
QY 301 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNTE 360  
DB 332 ESASECLPCDCNCRSQECYFDPPELYRSTGHGCHCTNCQDNTDGAHCRCRENFRLGNTE 391  
QY 361 ACSSCHSPVCSLSITQDCDSYGRCSCKPGVMGDKDCRCQPGFHSILTEAGRCPCSDPGSSI 420  
DB 392 ACSSCHSPVCSLSITQDCDSYGRCSCKPGVMGDKDCRCQPGFHSILTEAGRCPCSDPGSSI 451  
QY 421 DECNVETGRVCXKNVGEFNCRCCKPGFFNLESSNPRGCTPCFCFHSSVCTNAGVSIVY 480  
DB 452 DECNVETGRVCXKNVGEFNCRCCKPGFFNLESSNPRGCTPCFCFHSSVCTNAGVSIVY 511  
QY 481 SISSTFOIDEGWRAEQDSEASLEWSSSEODTAVISDSYFPEYFIAPAKFLQKQVLSY 540  
DB 512 DISSTFOIDEGWRAEQDSEASLEWSSSEODTAVISDSYFPEYFIAPAKFLQKQVLSY 571  
QY 541 GQNTSFSFRVDRRTLSAEDLVLEGAGLRVSVPLIAQGNYSPESETTVKYVFRLEHATDY 600  
DB 572 GQNTSFSFRVDRRTLSAEDLVLEGAGLRVSVPLIAQGNYSPESETTVKYVFRLEHATDY 631  
QY 601 PWRPALTPFEQKLNLLTSIKIRGTYSERAGVLDVLTASARPPGVPATWVESCTCP 660  
DB 632 PWRPALTPFEQKLNLLTSIKIRGTYSERAGVLDVLTASARPPGVPATWVESCTCP 691  
QY 661 VYGGQFCFCEMCLSGYRRTPNLGYPVPCVLCACNGHSETCDPETGVNCNCRDNTAGPHCEK 720  
DB 692 VYGGQFCFCEMCLSGYRRTPNLGYPVPCVLCACNGHSETCDPETGVNCNCRDNTAGPHCEK 751  
QY 721 CSDGYGDSSTAGTSDCQPCPCGGSSCAVVPKTKVWVCTNCPGTGTTGKRCCELCDGDFG 780  
DB 752 CSDGYGDSSTAGTSDCQPCPCGGSSCAVVPKTKVWVCTNCPGTGTTGKRCCELCDGDFG 811  
QY 781 DPLGNGPVRLCRLCQCSNDIDPNAVGNCRNLGTBCLKCIYNTAGFYCDRCDFGFFGNPL 840  
DB 812 DPLGNGPVRLCRLCQCSNDIDPNAVGNCRNLGTBCLKCIYNTAGFYCDRCDFGFFGNPL 871  
QY 841 APNPADKCKACACN-YGTVQOQSSCNVPTGQCCPLHVTGQDGCACDPCGFYNLQSGQCE 900  
DB 872 APNPADKCKACACN-YGTVQOQSSCNVPTGQCCPLHVTGQDGCACDPCGFYNLQSGQCE 930  
QY 901 RCDHALGSTNGQCDIRTCQCEQPGITQOHCERCERNVHFGPGCKPCDCHPBGSL 960  
DB 932 RCDHALGSTNGQCDIRTCQCEQPGITQOHCERCERNVHFGPGCKPCDCHPBGSL 990  
QY 961 QCKDDGRCCEGFGVNRCDQCEENFYNRSPGCECPACVRLVKDKVADHRVKLQBLE 1020  
DB 992 QCKDDGRCCEGFGVNRCDQCEENFYNRSPGCECPACVRLVKDKVADHRVKLQBLE 1050

QY 1021 SLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAOVDKVDONLMDRLQVNNLTSSQ 1080  
Db 1051 SLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAOVDKVDONLMDRLQVNNLTSSQ 1110  
QY 1081 ISRLQNIIRNTIETGNI LAQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDP 1140  
Db 1111 ISRLQNIIRNTIETGNI LAQARARSVESTEQIEIASRELEKAKM-AANVSITQPESTGEP 1169  
QY 1141 NMWTLAEEARKLAERHKEADDDIVRVAKTANDSTTEAYNLLRLTLAGENQTAPEIEELN 1200  
Db 1170 NMWTLAEEARKLAERHKEADDDIVRVAKTANETSABAYNLLRLTLAGENQTAPEIEELN 1229  
QY 1201 RKYEQAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSETLNEANNIKMEA 1260  
Db 1230 RKYEQAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSALEANEKIKKEA 1289  
QY 1261 ENLQOLIDOKLKYEDLREDNRGELEVNKLEKGTQOOTADOLLARADAALAEAAA 1320  
Db 1290 ADDRLIDOKLKYEDLREDNRGELEVNKLEKGTQOOTADOLLARADAALAEAAA 1349  
QY 1321 KKGRTDLOEANDILNLLKDFORVNDNKTAEEALRIPAINQITTEANEKTRAEAOALG 1380  
Db 1350 KKGRTDLOEANDILNLLKDFORVNDNKTAEEALRIPAINRTEANEKTRAEAOALG 1409  
QY 1381 SAADATEAKNAHEAERIASAVOKNATSTIAEAERTPAEVTDLDNVNNMLQLOBAEK 1440  
Db 1410 NAAADATEAKNAHEAERIASAVOKNATSTIAEAERTPAEVTDLDNVNNMLQLOBAEK 1469  
QY 1441 ELKRQDDADQMMAGVASOAAQAEALNARKAKNSVTSLLSIINDLLEOLGOLDTVDLN 1500  
Db 1470 ELKRQDDADQMMAGVASOAAQAEALNARKAKNSVTSLLSIINDLLEOLGOLDTVDLN 1529  
QY 1501 KLINEGTNKAQDMKVSDDLDRKVSLENBAKQEAAMINDYNRDIIEIMKDIINLEDIR 1560  
Db 1530 KLINEGTNKAQDMKVSDDLDRKVSLENBAKQEAAMINDYNRDIIEIMKDIINLEDIR 1589  
QY 1561 KTLPSGCGENTPSIEKP 1576  
Db 1590 KTLPSGCGENTPSIEKP 1605

RESULT 8

US-10-037-182-20  
; Sequence 20, Application US/10037182  
; Publication No. US2003004899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thybøll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-20

Query Match 94.1%; Score 8038; DB 14; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
QY 3 AMDECTDEGRPQRCPMPFVNAAFNVTVVNTTCGTPPEEYCVGTGVTGKSHLCLDAG 62  
Db 1 ANDECADEGRPQRCPMPFVNAAFNVTVVNTTCGTPPEEYCVGTGVTGKSHLCLDAG 60

QY 63 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITVYRLKPHTS 122  
Db 61 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITVYRLKPHTS 120  
QY 123 RPESFAIYKRTREDGFWPIYQYSGSCENTYSKANRGFIRTCGDEQOALCTDESDISPL 182  
Db 121 RPESFAIYKRTREDGFWPIYQYSGSCENTYSKANRGFIRTCGDEQOALCTDESDISPL 180  
QY 183 TCGNVAFSTLEGRPSAYNFNDSPVLQEWVTATDIRVTNLNRLNTFGDEVFNPKVLKSYYY 242  
Db 181 TCGNVAFSTLEGRPSAYNFNDSPVLQEWVTATDIRVTNLNRLNTFGDEVFNPKVLKSYYY 240  
QY 243 AISDFAVGRCKCNHASECMKNBEPKLVCMCKNTYGVDCCKLPFFNDRPWRATAES 302  
Db 241 AISDFAVGRCKCNHASECMKNBEPKLVCMCKNTYGVDCCKLPFFNDRPWRATAES 300  
QY 303 ASECLPCDCNCGRSQCYFDPPELYRSTGHGHCNTCODNTDGAHCRCRENFRILGNNEAC 362  
Db 301 ASECLPCDCNCGRSQCYFDPPELYRSTGHGHCNTCODNTDGAHCRCRENFRILGNNEAC 360  
QY 363 SSCCHSPVGSJSTQCDSTYGRCSCKPGVMGDKDRQCPGFHSLTTEAGRCPCSDPSGSDE 422  
Db 361 SSCCHSPVGSJSTQCDSTYGRCSCKPGVMGDKDRQCPGFHSLTTEAGRCPCSDPSGSDE 420  
QY 423 CNVETGRVCCKDNVGEVNCERCCKPGFNLSSNPRGCTPCFCFGHSSVYCTNAVGVSYYSI 482  
Db 421 CNVETGRVCCKDNVGEVNCERCCKPGFNLSSNPRGCTPCFCFGHSSVYCTNAVGVSYYSI 480  
QY 483 SSTFOIDEDGMRAEQRDSEASLEWSRQDIATVSDSYFFRYFTIAPAKFKQKVLVSQ 542  
Db 481 SSTFOIDEDGMRAEQRDSEASLEWSRQDIATVSDSYFFRYFTIAPAKFKQKVLVSQ 540  
QY 543 NLSFSDRDRRTRLSAEDLVLEAGLRSVPLIAQNSYSETTVKVFLHEATDIPW 602  
Db 541 NLSFSDRDRRTRLSAEDLVLEAGLRSVPLIAQNSYSETTVKVFLHEATDIPW 600  
QY 603 RPALTFEFPKLLNLTISIKINGTYSERSAGYLDVTLASARPGSGVATVWESCTCPVG 662  
Db 601 RPALTFEFPKLLNLTISIKINGTYSERSAGYLDVTLASARPGSGVATVWESCTCPVG 660  
QY 663 YGQPCCEMCLSGYRRETPNLGYSVCLCAHNSHETCDPBTGVNCNDNTAGHCEKCS 722  
Db 661 YGQPCCEMCLSGYRRETPNLGYSVCLCAHNSHETCDPBTGVNCNDNTAGHCEKCS 720  
QY 723 DGYVGDSTAGTSSDCQPCPGSSCAVVPKTKVYVCTNCTPTGTGKRCCELDDGYFGDP 782  
Db 721 DGYVGDSTAGTSSDCQPCPGSSCAVVPKTKVYVCTNCTPTGTGKRCCELDDGYFGDP 780  
QY 783 LGRNGEVRCLRCQCSNDIDPNAVGNRLTGECLKCIYNTAGFYCDRCCKGFCGNPLAP 842  
Db 781 LGRNGEVRCLRCQCSNDIDPNAVGNRLTGECLKCIYNTAGFYCDRCCKGFCGNPLAP 840  
QY 843 NPADKCKACNCPYGTMKQSSCNPTVQCECLPHVTGQDCGACDPGFYNLQSGGCERC 902  
Db 841 NPADKCKACNCPYGTMKQSSCNPTVQCECLPHVTGQDCGACDPGFYNLQSGGCERC 899  
QY 903 DCHALGSTNGQCDIRTGQCECOPGITGHCRCVNNHFGFPGEGCKPCDCHPEGSLSQC 962  
Db 900 DCHALGSTNGQCDIRTGQCECOPGITGHCRCVNNHFGFPGEGCKPCDCHPEGSLSQC 959  
QY 963 KDDGRCCEGFGVNRCDCEENYFVNRSWPCCPCACRYLVKDKVADHRVKLQLESL 1022  
Db 960 KDDGRCCEGFGVNRCDCEENYFVNRSWPCCPCACRYLVKDKVADHRVKLQLESL 1019  
QY 1023 IANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOVDKVDONLMDRLQVNNLTSSQIS 1082  
Db 1020 IANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOVDKVDONLMDRLQVNNLTSSQIS 1079  
QY 1083 RLQNIINTIETGNI LAQARAHVENTERLIEIASRELEKAKVAAANVSITQPESTGDPNN 1142  
Db 1080 RLQNIINTIETGNI LAQARARSVESTEQIEIASRELEKAKM-AANVSITQPESTGEPNN 1138  
QY 1143 MTLAEBARKLAERHKEADDDIVRVAKTANDSTTEAYNLLRLTLAGENQTAPEIEELNRK 1202

Db 1139 MTLAEEARRLAERHQBADDIVRAKTAETSAEYNNLLRTLAGENQTLAELEENRK 1198  
Qy 1203 YEAKNIISQLEKQARVHEEAKRAGDKAVIYASVAQLSPDLSETTLENNANIMBAEN 1262  
Db 1199 YEAKNIISQLEKQARVHEEAKRAGDKAVIYASVAQLTPVDSALENEANKIKKEAAD 1258  
Qy 1263 LEOLIDOKLKYEDREDMRGKELEVNKLEKGTQEQOTDOLLARADAARALAEAAK 1322  
Db 1259 LDRLIDOKLKYEDREDMRGKELEVNKLEKGTQEQOTDOLLARADAARALAEAAK 1318  
Qy 1323 GRDTIQEANDILNNLKDFRRVNDNKNKTAEEALRKIPAINOTITTEANEKTRAEQAALGSA 1382  
Db 1319 GRSTIQEANDILNNLKDFRRVNDNKNKTAEEALRRIPAINRTIAEANEKTRAEQAALGNA 1378  
Qy 1383 ADATAEAKNAHEERIASAVOKNATSKAEAEFTFAEVTDLDRVNNMLQLOAEKEL 1442  
Db 1379 AADATEAKNAHEERIASAAOKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANEL 1438  
Qy 1443 KEKQDADODMMWAGWASQAQAEABINARKAKNSVTSLSLIINDLEQLGOLDTVDLNLK 1502  
Db 1439 KEKQDADODMMWAGWASQAQAEABINARKAKNSVSSLSQLNNLLDQLGOLDTVDLNLK 1498  
Qy 1503 NEIEGTLNKAKDMKVSDDLDRKVSLENEAKQEAAMINDYNRDIBEIMKDRNLEDIRKT 1562  
Db 1499 NEIEGTLNKAKDMKASDLDRKVSLESEAKQEAAMINDYNRDIAEIIKIDHNELEIKKT 1558  
Qy 1563 LPSGCFNTPSIEKP 1576  
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 9  
US-09-845-583-10  
; Sequence 10, Application US/09845583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champliand, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-10

Query Match 42.1%; Score 3600; DB 9; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 4.9e-196;  
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

Qy 2 AAMDECTDEGGPQRCMPFVNAFVNVVANTCGTTPPEYCVGTGTGVTKSCHLCA 61  
Db 20 AGWACYDAGRPQRCPLPVFENAAFGRLAQASHTCGSPPEDFCPHVGAAGAGAHQRCDA 79  
Qy 62 GQPHLOHGAFTLDYNNQADTTWQSQTMLAGVOYPPSSINLTLLHKGAFDITYVRLKFT 121  
Db 80 ADPQRHNAASYLTDHFSQDESTWQSPSNAFGVQPTSVNITLRLGKAYEITYVRLKFT 139  
Qy 122 SRPESFAIKYRTREDGPNWTPYQYSGSCENTYSKANRGFIRTGGEQALCTDFSDISP 181  
Db 140 SRPESFAIKYRGRADGPWEPYQYFASCKYGRPEGVLRPEGEVAFCTSEFSDISP 199  
Qy 182 LTGQNVAFSTLEGRPSAYNFDSPLVQEWVTATDTRVTLNRLNTGDEVDNPKVLSKY 241

Db 200 LSGNVAFSTLEGRPSAYNFESPLQEWVTSTELLISLDRNLNTFGDDIFKDPKVLQSYV 259  
Qy 242 YALSDFAVGRCKCNCHASHCEKMNFEKLVKCNKXNTYGVDCCKCLPFPPNDRPWBATAE 301  
Db 260 YAVSDFSVGRCKCNCHASHCECOPDVAGQLACQHNNTTGTDCERCLFFQDPRWAKGTAE 319  
Qy 302 SASCELPDCNCRSQRCYFDPPELYRSTGHGHGHTNCQDNTDGAHCERCRENFRFLGNFEA 361  
Db 320 AAHECLPCNCSGSEBCTFDRELFRSTGHGGRCHCRDHTAGPHCBCEQENFVMDPRMP 379  
Qy 362 CSSCHSPVGSLSQCDSDSYGRCSCKPGVMGDKDCRCQPGFHSLTAGCPCSCDPSGSD 421  
Db 380 CQPCDCQASGLHLOCDTGTCAKPTVTGWCKDRCLPGFHSLSGEGCPCPCNPGASLD 439  
Qy 422 ECVNVEGRCKVCKDNVGFNCERCKPGFNFLESNPRGCTPCFCFHHSSVCTNNAVGSVYS 481  
Db 440 TCDPRSGRCECKENVEGNLDCRCRPTFNLPQHPNAGCSCSCYCHSKVCASATAQVQVHH 499  
Qy 482 ISSTFQIDEDGWRABORDGSEASLEWSSERQDIAVISDSYFPFYFTAPAKFLKQVLSVG 541  
Db 500 ILSDPHQGAEMWARSVGGSEHSPQSPN----GVLLSPDEBEELTAPGKFLGQDRFSYG 555  
Qy 542 QNLSFSPRDRRTRLSAEDLVLEGAGLAVSVPLIAQGNISYSETTVKYVFLH---EAT 598  
Db 556 QPILITFRVPPGSPLPVQ--LRLEGTGLALS--LRHSSLSGPODARASQGGRAQVPLQET 612  
Qy 599 DYPWRPALTPFEQKLIANNLTISIKIRTYSEBSAG--YLDVDTLASARPGVPAWVES 656  
Db 613 SEDVAPLPPFHTORLLANLTSLRLVSPGSPAGPVFLTEVLTSARPGLSPASWVEI 672  
Qy 657 CTCPEVGYGOFCEMCLSGYRETPNLGPYSPVLCACNGHSETCDPBTGVCNCRDNTAGP 716  
Db 673 CSCPTGYTGFCSCAPGYKREMPQGGPYASCVFCTCNOHG--TCDDNTGLVCVSHHTGP 731  
Qy 717 HCEKCSGYYGDSGTAGTSSDCPCPCGGSSCAVWPKTKEVWCTNGCTGTGTKRCLCDD 776  
Db 732 SCERCLPGFYGNPFAGADDCCPCPCGQSACTTIPESGEVWCTHCPGQGRRCVCCDD 791  
Qy 777 GYFGDELGRNGPVRLCRLCQCSNIDPNVGNCRNLTGELCKIYNTAGFYCDKXGDF 836  
Db 792 GFTGDLPLGLFGHPQCHQCQCSGNVDNAGVNCPLSLGHLRCLHNTTGDHCEHCEGFY 851  
Qy 837 GNPLAPNPADKCKACNPNVGTWKQSSCNPNVTGQCECLPHVTGQDCGACDPCFYNLQSG 896  
Db 852 GSALAPADKCMPCSCHPGSGVSEQWPCDPTVGTQSCCLPHVTARDCSRCPYGFDFLQPG 911  
Qy 897 QGCERCDCHALGSTNGQCDIRTCQCCQCPGITGCHCEVCEVNHFGFPGCKPCDCHPEG 956  
Db 912 RGCRCCKCHPLGSQEDQCHPKTQCTCRPGVTQACDRQCLGFFGSSIKGCRACRCSPLG 971  
Qy 957 SLSLOCKDGRCEGREGVGNRCQCEENYFYNRSWPGQCECPACVRLVKDVADHRVKL 1016  
Db 972 AASAQCHYNGTCVCRFGEGYKCDRCHYNFFLTADGTHCQCCPSYALVKEETAKLKARL 1031  
Qy 1017 QELESJIANLGTGDEMVTDOAFEDRLKEABREVMDDLREAQDVKYVDQNLMDRLQRVNT 1076  
Db 1032 TLTEGMWQSDCGSPW--GFLDILLGEAPRG--DVYQGHLLLPAGAREAFLEQMGLGA 1086  
Qy 1077 LSSQISRLQINRTIETGNLAEOARAHVENTERLIEIASRELEKAKAAVAAVSVTQPS 1136  
Db 1087 VKAAREQLQNKARGARCAQAGSOKTCTQLADLEAVLESSEEEILHAAAILASLEIQ-EG 1145  
Qy 1137 TGPNNMTLAEARKLAERHKEADDIVRAKTAETDSTEAYNLLIRTLIAGENQTAFAI 1196  
Db 1146 PSQTKWHLAIEARALARSHRDTATKIATAWRALLASNTSYALLWNLL--EGRVALET 1203  
Qy 1197 E-ELNKYEOAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDLSETL----- 1249  
Db 1204 QRLDREYQEVQAAKALRTAVAEVLPEAB-----SVLATVQVQADTAPYALLASP 1256  
Qy 1250 -----ENNAENIWEAENLEPOLIDQKLKYEDDLREDMRKELEVNKLEKGTQEQOT--- 1301  
Db 1257 GALPQKSRADLGLKAKALEKTV-----ASQWQHMAE-AAETLQTAQAATILRQTEPLTMA 1311

QY 1302 -----ADQLARADAAKALAEBAKKGRTDLOEANDIINLUKDFORRVNDNKTAEEA 1354  
DQ 1312 SRLTATFASQLHGARAALTOASSVQAATVTVMGARTLLADLEGMLQFPRPKDOAALQ 1371  
QY 1355 LRKIPALNOTITEANETREAOQALGSAADATEAKNKAHEABRIASAVOKNATSTKAEA 1414  
DQ 1372 RKADSVDRLLADTRKTKQHERWLGNAFLUSSAKKKKGREAEVLAKDSAKLAKALLRER 1431  
QY 1415 ERTFAEVTDLNENVMMLKQI-QBAEKELKPKODDQDDMMAGMASQAQAEABINARKA 1473  
DQ 1432 KQARRASRLTSQTATLOASQOVLASEARRQBLEAEARVGAGLS-----EMEQQIRES 1486  
QY 1474 KNSVTSLLSIINDLEOLGOLDT---VDLNKLNTEEGTLNKADEM-KVSDLDKRVSDLEN 1530  
DQ 1487 RISKEIETLSEALAGSLDTHQAQAQALNETQWALERLRLOLQSGPSGLQRLKLSLEQ 1546  
QY 1531 EAKQEAAMIDYNDRIEIMKDIRNLEDIRKTLPSGC 1567  
DQ 1547 ESQOEIQLQGFESDLAEIRADKQNLBAILHSLPENC 1583  
RESULT 10  
US-10-262-839-210  
Sequence 210, Application US/10262839  
Publication No. US20040038877A1  
GENERAL INFORMATION:  
APPLICANT: Alsobrook, John,  
APPLICANT: Anderson, David W.,  
APPLICANT: Boldog, Ferenc,  
APPLICANT: Burgess, Catherine,  
APPLICANT: Catterton, Elina,  
APPLICANT: Edinger, Shlomit,  
APPLICANT: Ellerman, Karen,  
APPLICANT: Gerlach, Valerie,  
APPLICANT: Gorman, Linda,  
APPLICANT: Guo, Xiaojia,  
APPLICANT: Ji, Weizhen,  
APPLICANT: Kekuda, Ramesh,  
APPLICANT: Leach, Martin,  
APPLICANT: Li, Li,  
APPLICANT: Miller, Charles,  
APPLICANT: Patturajan, Meera,  
APPLICANT: Reiger, Daniel,  
APPLICANT: Rothenberg, Mark,  
APPLICANT: Shimkets, Richard,  
APPLICANT: Smithson, Glenda,  
APPLICANT: Spytek, Kimberly,  
APPLICANT: Taupier, Raymond, jr.,  
APPLICANT: Vernet, Corine,  
APPLICANT: Voss, Edward,  
APPLICANT: Zerhusen, Brian,  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-462A  
CURRENT APPLICATION NUMBER: US/10/262,839  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/326,483  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/327,917  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/328,029  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/328,056  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/381,101  
PRIOR FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 60/371,972  
PRIOR FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: 60/327,342  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 60/328,044  
PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,849  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/374,738  
PRIOR FILING DATE: 2002-04-23  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 367  
SOFTWARE: CuraseqList version 0.1  
SEQ ID NO 210  
LENGTH: 1587  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-262-839-210

Query Match 42.1%; Score 3600; DB 12; Length 1587;

Best Local Similarity 43.5%; Pred. No. 4.9e-196;  
Matches 695; Conservative 263; Mismatches 575; Indels 64; Gaps 20;

QY 2 AAMDECTDEGRPQRCMPFVNAAFNVTVAINTCGTPPEBYCVQGTGVTGKSHCLDA 61  
DQ 20 AGMGACYDAGRPQCLPVENAFAFGLAQASHTCGSPEDFCPHVGAAGAHQRCDA 79  
QY 62 GOPHLOHGAFLTDYNNQADTTWQSQTLAGVYPPSSINTLHLGKAFDITVYRLKFT 121  
DQ 80 ADPQRHNASYLTDPHSQDESTMQSPMAFGVQPTSVNITLRLGKAYEITVYRLKFT 139  
QY 122 SRPESFAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQOALCTDEFSDISP 181  
DQ 140 SRPESFAIYKRSRADGPWEYQYFSASCKTYGRPEGOYLAPGEDERVAFCSTSEFSDISP 199  
QY 182 LTGNNVASTLEGRPSAYNFNSPVLQEWVTATDIRVTNLRLNTEGDFVNDPKVLKSY 241  
DQ 200 LSGGNVAFSTLEGRPSAYNFNSPVLQEWVTSTELLISLRLNTEGDFVNDPKVLKSY 259  
QY 242 YAIISDFAVGGRCCKNGHASEQWNEFDKLVNCKNHTYGVDCCKLPFFNDRPWRRTAE 301  
DQ 260 YAVSDFSVGGRCCKNGHASEQWNEFDKLVNCKNHTYGVDCCKLPFFNDRPWRRTAE 319  
QY 302 SASSELPDCCNGRSECFDFDELFRSTGHGCHTNCQNDTGACRCERENFFRLGNEA 361  
DQ 320 AAHECLPCNCSGRSECFDFDELFRSTGHGCHTNCQNDTGACRCERENFFRLGNEA 379  
QY 362 CSSCHCSPVGLSTOCDYSGRCCKPVGMDKDRCPGFHSLTEAGRCPCDPSGSD 421  
DQ 380 CQPCDQASAGSLHLCDDTGTGACKPTVTKWCDRLPGFHSLSSEGGRCPCDPSGSD 439  
QY 422 ECVETGRCKVKNVEGNCRCRKPFPNLESSNPRGTCPCFCGHSSVCTNNAVYSYVS 481  
DQ 440 TCDPRSGRCPCCKENVEGNCRCRKPFPNLESSNPRGTCPCFCGHSSVCTNNAVYSYVS 499  
QY 482 ISSFTQIDBDGWRARQDRGSEASLEWSSERQDIAVISDSYPPRYFIAPAKFLGKQLSYG 541  
DQ 500 ILSDPHQAGNHWARSVGSSEHSPQWSPN---GVLLSPEDEBELTAFGKLGDRQPSY 555  
QY 542 QNLSTSFVRDRDRLSLAEADLVLEGAGLURSVPLIAQNSYSPSETTVKYVFLH---EAT 598  
DQ 556 QPLILTFRVPDGSPLPVQ-LRLEGTGLALS--LHSSLSGPDARASQGRRAQVFLQET 612  
QY 599 DYPWRPALTPPEFQKLLANLTSIKIRGTVSERSAG--YLDVDTLASARPFGVPATVYES 656  
DQ 613 SEDVAPPLPPFHFQRLANLISLRVSPGSPAGVPFLTEVRLTSARPGLSPASWVEI 672  
QY 657 CTCVPVYGQFCMCLSGYRRETPNLGPYSPCVLCACNGHSETCDPFGVNCNDRNTAGP 716  
DQ 673 CSCPTGYTGQFCESCAPGYKREMPQGGPYASCPVCTCNQHG-TCDPNTGICVCSHTEGP 731  
QY 717 HCEKSDGVYGDSTAGTSSDCQPCPGSSCAVVPKTEVVCTNCPGTGTGKRCLEDD 776  
DQ 732 SCERCLPGFYGNPFAGQADDQPCPCQSQSACTTIPESGEVVVCTHCPQGRRRREVCD 791  
QY 777 GYFGDPLGRNGPVLRLCRLCQCSDNIDPNAVGNCLNLTGECCLKICVNTAGFYCDRCQDFF 836  
DQ 792 GFFGDFLGLFGHPQCHQCQSGNVDPNAVGNCDPLSGHCLRLCLNHTTGDHCEHQEGFY 851



837	QY	GNPLAPNADKCKACNCPYGTWKMQSSCHNPVTGQCCLPHVTGQDCGADCPFYNNLQSG	896
852	Db	GSALAPRADKCMFCSCHPQCSSEQMPCDFVTGQCCLPHVTARDCSRYPGFDFDLPQG	911
897	QY	QGERCDCHALGSTNGQCDIIRTGQCEQOPGTTGQHCERCCEVNVHFGFPEGCKPCDCHPEG	956
912	Db	RGCRSCCKHPLGSGEDDCHPKTGGCTCRPGVTGQACDRCOLGFFGSSIKGCRACRCSPLG	971
957	QY	SLSLQCKDGRCEBREGFVGNRCDQCBENTFYNNKSWFGQCECPACTYPLVKDKVADHRVKL	1016
972	Db	AASAQCHYNGTCVCRPGFEGYKCDRCRCHYNFFLTADGTHCQCPSCPSYALVKEETAJLKARL	1031
1017	QY	QELLESILANLTGDMVYTQAFEDRLKEAREVMDDLREAOVDKVDQNLMDLRQVRNNT	1076
1032	Db	TLTECHMLQSGSDCSPW---GPLDILLGEAPRG--DVYQGHLLPGAREAFLEQMGMLEGA	1086
1077	QY	LSSQISRLQONRNTIETGNLAEQARAHVENTERLIIIASRELEKAKVAANVSVTOPES	1136
1087	Db	VKAAREQOLNRKGARCAQAGSQKTCQLADLEAVLESSEETILHAAAILASIEPO--EG	1145
1137	QY	TGDPNNMTLLAEARKLAERHKQBADDIVRVAKTANDTSTEAYNLLRLTLAGENOTAFEI	1196
1146	Db	PSQTKWSHLAIETABALARSHRDTATKIAATAPWALLASNTSVALLWNLL--EGRVALET	1203
1197	QY	E-ELNRKYEQAKNISQDLEKQARVHEEKRAQDAVEIIVASVAQLSPLDSETL-----	1249
1204	Db	QRDLEDYQEQYQAKALRTAVAEVLPEAE-----SVLATVQVGADTAPYLLALLASP	1256
1250	QY	-----ENEANNIKMEAEENLEQIDOKLKYDEDLREDMRGKLEVEKNLLEKGYKEBOQT---	1301
1257	Db	GALPQKSRADLGLKAKALEKTV---ASQWQHMAE--AARTLQTAQAATLROTEPLTWAR	1311
1302	QY	-----ADQLLARADAALAEBAKKGDRDTQOEANDIILNLLKDFDRRVNDNKTAEEA	1354
1312	Db	SLRTATFASQLHQARAAALTOASSSVQAAVTYVNGARTLLADLEGMKLOFPFRKDAQALQ	1371
1355	QY	LRKIPALNOTITEANETREAOQALGSAADADATEAKNKAHEABRIASAVOKNATSTKAEA	1414
1372	Db	RKADSVSDRLADTRKTKTQAERMLGNAAPLSSSAKKKGREAEVLAKDSAKLAKALLRER	1431
1415	QY	ERTFAEVTDLNEVNNMLKOL--QBAEKELKRQDDADQDMMQMAGMASQAQAEAINARKA	1473
1432	Db	KQAHRRASRLTSTQATLQOASQOVLASEARRQBLEEAERVGAGLS-----EMEQQITRES	1486
1474	QY	KNSVTSLLSTINDLLEQOLDGT--VDLNKLNIETGTLNKAQDEM-KVSDLDNRKVSLEN	1530
1487	Db	RI SLEKDIETILSELLARGLSDTHQAPQAALNETQWALERIRLQLOSGFSGSLQKLSLLEQ	1546
1531	QY	EAKKQEAAMIDYNRDIEEIMKDIRNLEDIKRTLPSGC	1567
1547	Db	ESQCEHQIOGFSRDLAEIRADKONLEAILHSPENC	1583

RESULT 11

US-10-262-839-212  
; Sequence 212, Application US/10262839

Publication No. US20040038877A1  
GENERAL INFORMATION:

Db 380 CQPCDCQSSAGSLHLCDDTGTCAKPTVTGKCDRLCPGFHSLSBGGCRPCTCNPAAGSLD 439  
QY 422 ECVETGRCVCKONVEGNCERCKGFFNLSSNPRGCTPCFCFSGSVCTNAGVSYYS 481  
Db 440 TCDPRSGRCPCKEVNEGNCDCRCRGTFLQLPHNPAAGSCFCYSHSKVCASTAQFQVHH 499  
QY 482 ISFTFOIDBGRABORDGSEASLBWSSERQDIAVISDFYPIAPAKFLGQVLSYG 541  
Db 500 ILSDFHQAGAGWARSVSGSEHSPQWSPN- ---GVLLSPDEBEELTAPGKFLGQRFSGY 555  
QY 542 QNLSPSFRVDRDRTRLSADLVLGAGLRVSPVLLAQNVSPESETVYKVFRLH- ---EAT 598  
Db 556 QPILITFRVPPGDSPLVQ- LREGTGLALS- LKHSLSPQDARASQGGRAVQPIQET 612  
QY 599 DYPWRPALPFPFQKLLNLLTSIKIRGYVSERAG- YLDDVTLASAPGPGVPATWVES 656  
Db 613 SEDVAPPLPFPFQKLLNLLTSIKIRGYVSERAG- YLDDVTLASAPGPGVPATWVES 672  
QY 657 CTCFVGYGQFCCEMCLSGYRRRTPLNPGVSPVLCACNGHSETCDPETGVNCNRDNTAGP 716  
Db 673 CSCPTGYTGQFCECAPGYKREMPQGGPYASCVPCTCNQHG- TCDPNTGICVCSHHTGP 731  
QY 717 HBEKSDGYGDSGTAGTSDCQPCPCGGSSCAVVKTKVVCNCTPTGTGKRCCLCDD 776  
Db 732 SCERCLPGFYGNPFAGQADDCQPCPCGQSACTTIPESGEVVTCHCPQGRGRCEVCD 791  
QY 777 GYFGDPLGNGVPLRCLCQCSNDNDPNAVGNCRNLTCCLKCTYNTAGFVCDCKDGF 836  
Db 792 GFPGDPLGLFGHPQCHQCQCSNVDPNAGNCDPLSGHCLRLHNTTGHCHCQGGFY 851  
QY 837 GNPAPNADKCAKNCNPGYTMKQSSCNVPTGQCECLPHVTGQDCGACDPFYNLQSG 896  
Db 852 GSALAPRPADKCMPCSCHFQSGVSPQFPCVPTGQCSCLPHVTARDGSRGYPGFFDLQPG 911  
QY 897 QGCECDDCHALGSTNGQCDIRTGQCECOPGITGQHCERCEVNHFGFPGEGCKPCDCHPEG 956  
Db 912 RGRSCSKCHPLGSDQDCHPTGTGCTCRPTGVTGACDRCQLGFGSGSIKCRACRCSPLG 971  
QY 957 SLSLQCKDDRCCEGREGVGNRCDOCEENFYNRSWPCQCEPCACYLKVKDVAHRVKL 1016  
Db 972 AASAQCHYNGTVCVRPGFEGYKDCRCHYNFFLTADGTHCQCPSCYALVKEETAKL 1031  
QY 1017 QLESLSIANLGTGDEMVTDOAFEDRLKEAREVMDLLREADQVDQNDMLRLQVNT 1076  
Db 1032 TLTEGWLQSGDCGSPW- ---GPLDILLGAPRG- DVYQGHLLPGAREAPLEQWMLGEGA 1086  
QY 1077 LSSQISRLQNTRIETENGLAEQARAHVENTERLIEIASRELEKAKVAAANVSVTQPS 1136  
Db 1087 VKAAREQLQRLNKGARCAQAGSQCTQOLADLEAVLESSEEEILHAAAILASLEIPQ-EG 1145  
QY 1137 TGDPPNMTLLAABEARLKHQADDIRVAKTANDTSTEAYNLLRLTLAGNOTAFEI 1196  
Db 1146 PSQPTKWSHLATEARALAPSHRDATKTAATWALLASNTSYALLNLLI- EGRVALET 1203  
QY 1197 E-ELNRKYEQAQNTSODLEKQARVHEAKAGDKAVEIVASVAQSLSPDSETL- --- 1249  
Db 1204 ORLDREYQEVQAAQKALRTAVAEVLPEAE- ---SVLATVOQVADTAPYLLALASP 1256  
QY 1250 - ---ENANNIKMAENLEQILDKLQDYEDLREDMRGKEVNLNLEKTEQQTADQ 1304  
Db 1257 GALPKSRAEDLGLKAKALETV- ---ASWQHMAE- AARTLQTAQATLQTEPT- -K 1309  
QY 1305 LLARADAKALAEBAKKGRTUQLEANDILNLLKDFRRVNDNKTAAEALRKIPAINOT 1364  
Db 1310 LHQEARAALTQASGSVQATVTYNGARTLLADLEGMKLQFRRPKQQAALQKADSVDRL 1369  
QY 1365 ITEAREKTRQAALGSAADATBAKNAKHAERIASAVQKNATSTKAEAEERTFAEVTDL 1424  
Db 1370 LADTEKTKQAERMLGNAAPLSSSAKKKGRAEVLAKDSAKLAKALLREKQAHRAEASRL 1429  
QY 1425 DNEVNNMLKQL- QEAKEKELKQDQDADQDMMAGASQAQAEATINARKANONVTSLLSI 1483

Db 1430 TSQTQATLQASQOQVLASEARRQBLEAEARVAGLS- ---EMEQIRESRISLEKDIET 1484  
QY 1484 INDLEQLGOLDT- ---VDLKLNEIEGTINKAKDEM- KVSOLDKRVKVDLENEAKKQBAAIM 1540  
Db 1485 LSELLARLGSJLTHQAPAAALNETQWALERLQLGSPGLQRLKLSLEQESQOQLOIQ 1544  
QY 1541 DYNRDIEIMKDIRNLEDIRKTLPSGC 1567  
Db 1545 GPESDLABIRADKQNLKAILHSLPENC 1571  
RESULT 12  
US-10-369-493-6816  
; Sequence 6816, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xiaohong  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6816  
; LENGTH: 1557  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6816

Query Match 37.9%; Score 3240; DB 15; Length 1557;  
Best Local Similarity 33.0%; Pred. No. 1.4e-175; Indels 166; Gaps 32;  
Matches 636; Conservative 289; Mismatches 541;  
QY 7 CTDEGGR- PQRMPPEFVNAAFNVTVATNTGTP- PEEYCVQGTGVTGKSCHLCDAGQP 64  
Db 25 CYDRATQPRQRCVDFVNAAFNLEQVNTTCGTGKRTKFCVQSGHTGQSVCTCDDRHE 84  
QY 65 HLQGAFLDYNNQADTTWQSTQMLAGVQVSSNLTLHLKKAFTDITVRLKHTSRP 124  
Db 85 GFSHPAKYLTDFVGNNTWQSDTHQEQGYFTTNLTLLVLRKSDITVRLKHTSRP 144  
QY 125 ESPAIYKRTREDGPWIPYQYISGSCENTYSKANRGFIRTGDEQQAALCTDFSDISPLTG 184  
Db 145 ESFTIYKKTHTDSEWEPWQYSGSCATYGLSDRAPI- LPGAENATQCTKEFSDISPTG 203  
QY 185 GNVAFTLEGRPSAYNFDNSPVLQEWVTATDITVTLNRLNTFGDEVNDPKVLSYYAI 244  
Db 204 GNIAFTLEGRPSAHAFEBEVEVLQKWTASAIRLSLRNNTFGDEVNDPKVLSYYAI 263  
QY 245 SDPAVGRCRCNGHAGSCMKNEF- ---DKLVNCKNHTYGVDCCKLPFFNDPRMRRATA 300  
Db 264 SDPAVGRCRCNGHAGSCVSGSSVDGENLRVCRCEHNTQCADNCECLPFYNDPRMRSCTS 323  
QY 301 ESASECLPCDCNGRSQSCYFDPBLYSTGHGHTCNCQNTDGAHCERCERENFFRLGNNE 360  
Db 324 VEANEICACNSQLSNRCYFDQQLPFEETHGGHCHDCQNTQGVHCEQCIANHWRRPGEN 383  
QY 361 ACSCCHSPGVSLSTQCDSDYGRCSCKPGVNGKCDRCQPGFHSLTEAGRCPCSDPSGI 420  
Db 384 YCVACGCGEGLSTQCDNBEKQCKPGVTRGFRCDQCLDGFDFSTNGCKNGCCTGSSL 443  
QY 421 D- ---ECNVETGRVCNDVEGFCERCKPGFFNLESNPRGCTPCFCFCHSSVCTNAVGY 477  
Db 444 NNQPRCDSSSGSCSKLVNREGQCKKGYFDLSTENQFGCTPCFCFCHSSICNTADGY 503  
QY 478 SVYISISTFOIDBGRABORDGSEASLBWSSERQDIAVISDFYPIAPAKFLGQV 537



Db 243 AQLDPPVYFVAPAKFLGNQVSYGQSLSPDYRVDGRHPSAHDVILEGAGLITAPLMP 302  
Qy 578 QGNSYPSSETTVKYVFRLEHATDYPWRPALTPFEQKLLNNLTISIIRGTYSERSAGYLD 637  
Db 303 LGKTLFCGLTKYTFRLNEHPSNNWSPQLSYFEYRLLRLNLTAIRATYGEYSTGYIDN 362  
Qy 638 VTLASAPGPGVPATWVESCTCPVYGQGFCEMCLSGYRRETPNLGYPSPCVLCAACNGHS 697  
Db 363 VTLISARPSGAPAPWVEQICPVYKGGQFCQDCASGYKRDGRLPGFTCPCNQCG-G 421  
Qy 698 ETCDPBTGVCNCRDNTAGPHECKSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKYE 757  
Db 422 GACDPDTGDCYSDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCVPIPEEV 479  
Qy 758 VCTNCPGTGKRCCLDDGYPGLGRNGPVLRLCCLQCSNDIDNPNAVCNRLTGECL 817  
Db 480 VCNCPGPGTGARCELADGYPGDPGEPVPRQPCQCNVDPSPASGNCRLTGRL 539  
Qy 818 KCIYNTAGFYCDRCQDGFNGPLAPNADKCKACNCPYGTMMQKQSSCNVPTGQCECLPH 877  
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCKACNCPMGS----- 580  
Qy 878 VTGQDCGACDPGFYNTLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEV 937  
Db 581 ----- 580  
Qy 938 NHFGFEGCGKPCDCHPEGSLSLQCKDGRCECRGFGVGNRCDOCEENFYFNRSPGQCE 997  
Db 581 -----BPVG-----CRSDGTCTCKFGFGPNCHE-----GAPS 608  
Qy 998 CPACYRLVKDKVADHRVKLQELSLIANLGTGDEMVTQAPEDRLKEAREVMDLLREAQ 1057  
Db 609 CPACYNQVTKMQDQFMQQLQMEALISKAQGGGVPVDTLEGRMQQAEALQDLIRDAQ 668  
Qy 1058 DVKDQDQNLMDLRLQVNNLTLSQISLONIRNTIETGNLAEQAPAHVENTERLIEIASR 1117  
Db 669 ISGASRSGLQAKVRSGENSYQSLDLQMTVERVALGSOQNRVDRTHRLITOMQL 728  
Qy 1118 ELEKAKVAANVSUPTGDPNNMTLAEAPARKLABEHKQEAADDIVRAKTANDTSTE 1177  
Db 729 SLAESASLGNNTIPASDHYVGNPGFKSLAQEAATRLAESHVESASNMQLTRETEDYSKQ 788  
Qy 1178 AVNLLRLTI-----AGENQTAFEIEELNRKYEQAKNISODLEKQAAVHEERAKRAGDK 1230  
Db 789 ALSVRLKALHEGVSGSGSPDGAV-VQGLVEKLEKLSLAQLTREATQAEIADRISQH 847  
Qy 1231 AVEIYASVQLPLDSEITL-NEANNIKMEANLEQLIDQKLKDYEDLEDMRGKELEVK 1289  
Db 848 SLRLDSVSPLOGSVDSQSPQVEAKRIKQKADSLSSLVTRHMDPEFKTKNGLGNWKEAQ 907  
Qy 1290 NLLKKGKTEQOTADQLARADAKALAEAAKKGRTDLOEANDIILNLIKDFDRVNDKT 1349  
Db 908 QLLONGKSGREKSDQLSLANLAKSRAGALSWMGNATFYVESILKNLRFEDLQVDRKA 967  
Qy 1350 ABEALRKIPAINQITTEANETREAAQALGSAADATEAKYKAHEAFRIASAVQKNATS 1409  
Db 968 EABEAMKRLSYISQKVSASDSTQQAERALGSAADAAQRAKNAGAGEALEISSETEQIGS 1027  
Qy 1410 TKAEABRTFAEVTDLNENVMMLKQAEKELKRDADODMMWAGMASQAQAEAIN 1469  
Db 1028 LNEANVTADGALAMEKGLASKSENRVEGELEKELEFDTNMDAVQMVITEAKQVDR 1087  
Qy 1470 ARKAKNSVTLISIINDLEQQLDTPVLDLNKINEIEGTLNKAKDEMVKSLDRKVSdle 1529  
Db 1088 AKNAGVTIQDTLNTLDGLHLMDQPLSVDEGLVLEQLKRAKTQIN-SQLRPMSELE 1146  
Qy 1530 NEAKKCEAALMDYNDRIEIMKDINLEDIRTKLPSCGFNTPSTEK 1575  
Db 1147 ERARQORGHLEHLETSIDGILADVKNLENIRDNLPFGCYNTQALEQ 1192

RESULT 14  
US-10-392-113-14

; Sequence 14, Application US/10392113  
; Publication No. US2003022493A1  
; GENERAL INFORMATION:  
; APPLICANT: Deleu, Laurent  
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION  
; FILE REFERENCE: 21108.0005U3  
; CURRENT APPLICATION NUMBER: US/10/392,113  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: 60/365,078  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: PCT/US01/32127  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/239,705  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Descriptive of Artificial Sequence:/Note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-392-113-14

Query Match 30.9%; Score 2637; DB 12; Length 1193;  
Best Local Similarity 39.4%; Pred. No. 2,1e-141;  
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

Qy 286 CLPFFNDPWRARVAESAECPLDCNCRSQECYDFDELRYSTGCHGHCCTNCQDNDGAH 345  
Db 9 CLCFSLLLPAARATSRRE----VDCNGKSRQCIFDELRHQINGFRCLNCNDNDGIIH 64  
Qy 346 CERCRENFRLLONNEACSSCHSCSPVGSLSLSTQDSYGRCSCKPGVMGDKCDRCOPGHSLT 405  
Db 65 CEKCKNGFYRHRERDRCLPCNCSKSLARCSNCSGRCSCKPGVTGARCDCRCLPGFHMLT 124  
Qy 406 EAGC-----RPSCDPSGIDECNVETGRCVCKCNVEGFCRCRCCKPGFFNLESNPR 457  
Db 125 DAGCTQDQRLDLSKDCDDPAGIAGPC--DAGRCVCKPAVTVGERCDRCRSGYVNLDSNPE 182  
Qy 458 GCTPCFCGHSVCTNAVGVSYVISSTFQIDEDGWABORDGSEASLEWSSERQIAVI 517  
Db 183 GCTQCFYCHSASCRSAEYSVHKITSTPHQDVGKAVQNRSGSPAKLQWSQRHQDFSS 242  
Qy 518 SDSYPRFYIAPAKFLGKQVLSYQNLSPFRVDRDRTRLSAEDLVLEGAGLRVSVPLIA 577  
Db 243 AQLDPPVYFVAPAKFLGNQVSYGQSLSPDYRVDGRHPSAHDVILEGAGLITAPLMP 302  
Qy 578 QGNSYPSSETTVKYVFRLEHATDYPWRPALTPFEQKLLNNLTISIIRGTYSERSAGYLD 637  
Db 303 LGKTLFCGLTKYTFRLNEHPSNNWSPQLSYFEYRLLRLNLTAIRATYGEYSTGYIDN 362  
Qy 638 VTLASAPGPGVPATWVESCTCPVYGQGFCEMCLSGYRRETPNLGYPSPCVLCAACNGHS 697  
Db 363 VTLISARPSGAPAPWVEQICPVYKGGQFCQDCASGYKRDGRLPGFTCPCNQCG-G 421  
Qy 698 ETCDPBTGVCNCRDNTAGPHECKSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKYE 757  
Db 422 GACDPDTGDCYSDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCVPIPEEV 479  
Qy 758 VCTNCPGTGKRCCLDDGYPGLGRNGPVLRLCCLQCSNDIDNPNAVCNRLTGECL 817  
Db 480 VCNCPGPGTGARCELADGYPGDPGEPVPRQPCQCNVDPSPASGNCRLTGRL 539  
Qy 818 KCIYNTAGFYCDRCQDGFNGPLAPNADKCKACNCPYGTMMQKQSSCNVPTGQCECLPH 877  
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCKACNCPMGS----- 580  
Qy 878 VTGQDCGACDPGFYNTLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGITGOHCERCEV 937

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Db 581 ----- 580
QY 938 NHFGFEGECKPCDCHPEGSLSLQCKDGRCEGFGVGNRCDQCBENFYNRSWPGQOE 997
Db 581 -----EPVG-----CRSDGTCTVCKPGFGGPNCEH-----GAPS 608
QY 998 CPACYELVKDQVADHRVKLOELESILANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMELISKAQGGGVVDPDTELEGRMQQAQALQDILRDAQ 668
QY 1058 DVKDQDQNLMDRLQRYNNLTSSQISRLQNTIETGNCNLAQRAHVNTERLIEIASR 1117
Db 669 ISEGASRSLGLQAKVRSQENSYSQSRLLDLMKMTVERVRALGSGYQNRVDRTHRLITQML 728
QY 1118 ELEKAKVAANVSVPQESTGDPNNMTLLAEARKLAERHKEADDIVRVAKTANDTSTE 1177
Db 729 SLAESASLGNWTNIPASDHYVGVNGFKSLAQEATRLAESHVESASNMQLTRETEDYSKQ 788
QY 1178 AYNLLRLTL-----AGENOTAFEBIEELNRKVEQAKNISODLEKQARVHEAKAGDK 1230
Db 789 ALSVRKALHEGVSGSGSPDGAU-VQGLVEKLEKTSIAQQLTREATQAEIADRSYOH 847
QY 1231 AVBIYASVAQLSPLDSETLE-NEANNIKMEAEENLEQIDQKLKDYEDLREDMRGKELEVK 1289
Db 848 SLRLDSVSLQGVSPQSQVEAEKIKQKADSLSLTVTRHMDFKRTQKNLGNWKEEAQ 907
QY 1290 NLEKKTQOOTADQLARADAALAEAAKAGRTTLOEANDILNLLKDFDRVNDNKT 1349
Db 908 QLLQNGKSGREKSDQLLSRANLAKSAQEAALSGNATFYEVESILKULREFDLOVDNRKA 967
QY 1350 AAEALRKTPAINQTTTEANEKTRAQALGSAADATEAKNKAHEARIASAVOKNATS 1409
Db 968 EAEAMKRLSYISKVSDASDKTQOARERALGSAADAQAKAGAGALEISSEIQEIGS 1027
QY 1410 TKAEARTFAVTDLNEVNMUKLOEAEKELKRKQDDADQMMVAGMASAAQEAEBIN 1469
Db 1028 LNLAEANTADGALAMEKGLASLASENREVEGELERKELEFDTNMDAVQMVITEAQKVDTR 1087
QY 1470 ARKAKSVTSLGIINDLEQLQDVLNKLNEIEGTNLKAKDEKMSVLDLDRKVSLE 1529
Db 1088 AKNAGVTIQTINTLQGLHMDPLSVBEGVLVLEQKLSRAKQIN-SQLRPMWSELE 1146
QY 1530 NEAKQEAAMVNDRIEIMKDRLNEDIRKTLPSGCPNTPSIEK 1575
Db 1147 ERARQQRGHLHLETSIDGLADVKLENIRDLNLPFGCYNTQALEQ 1192

RESULT 15
US-10-171-311-115
; Sequence 115, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIORITY APPLICATION NUMBER: US 60/298,159
; PRIORITY FILING DATE: 2001-06-13
; PRIORITY APPLICATION NUMBER: US 60/298,155
; PRIORITY FILING DATE: 2001-06-13
; PRIORITY APPLICATION NUMBER: US 60/335,936
; PRIORITY FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-115

Query Match 30.9%; Score 2637; DB 14; Length 1193;
Best Local Similarity 39.4%; Pred. No. 2.1e-141;
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;

QY 286 CLPFNDPWRERATAESASECLPCDCNCRSGOECEVDEPDELVRSTGCHGHCNCDNDTGAH 345
Db 9 CLCFSLLLPARATSRRE-----VDCNKGSRQCLFDELHRQITONGFRCLNCNDNDTDGIH 64
QY 346 CERENFFRILGNNEACSSCHSPVSGSLSTQCDUSYGRCSCKPGVMGDKCDRCOPGFHSLT 405
Db 65 CEKCKNGFYRHRERDRCLPCNCSKSGLSARCDNSGRCSCKPGVTGARCDCCLPGFHLMT 124
QY 406 BAGC-----RCSCDPSGSDENVTGRCVCKDNVTEGFCNRCCKPFFNLESNPR 457
Db 125 DAGTQOQRLLDSKCDPCPAGIAGPC--DAGRCVCKPAVTGERCCDRCSGYNYLNDGNGPE 182
QY 458 GCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAMI 517
Db 183 GCTQCFYGHSSASCRSSAEYSVHKITSTFHQDVGWKAVQNRGSPAKLQWSQRHQDVFS 242
QY 518 SDSFPFYFTAPAKFLKQVLSYQNTLSFSFRVDRDRTRLSAEDLVLEGAGLAVSVPLIA 577
Db 243 AQRLDPYFYVAPAKFLGNQVSYGSLFDYRVDGRGRHPSAHADVILLEGAGLRITAPLMP 302
QY 578 QGNSVPGSETTVKYVFRLEHATDYPWRPALTPFFQKLLNLTSTIKIRGTYSERSAGYLD 637
Db 303 LGKTLPCGLTKTYTFRLEHPSNNWSPLSYFEYRLLRLNLTLRATYGEYSTGYIDN 362
QY 638 VTLASAPPGVATWVESCTCPVYGGQFCMCLSYRRRETNLGSPYSCVLCACNGHS 697
Db 363 VTLISAPFVSGAPAPWYEQICIPVYKGQFCQACSGYKDSARLGFPGTICPCNCGQ-G 421
QY 698 ETCDPETGVNCRDNTAGHCEKCSGYYGDSSTAGTSSDQCPQCPGSGSSCAVVPKTKEV 757
Db 422 GACDPDGDYSGDENPDIECADCPIGFYNDPHDPRS--CKPCFCHNGFSCSYMPETEYV 479
QY 758 VTCNCPGTGTRKRCCLDDGDFGDPIDGRNGPVLRLCQCSNDIDPNAVCNRLTGECL 817
Db 480 VCNNCFPGVTGARCCLCAGDFGDFPFGHGFVAPFCQPCNNNVDPFSAGNCDRLTGRCL 539
QY 818 KCIYNTAGVCDRCCKGFGNPLAPNADKCAKCNPNYGTMKQSSCNVPTQCECLPH 877
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCPMGS----- 580
QY 878 VTGDQACADPGFYNLQSGQGCERCDCHALGSTNGQCDITGTQCECQPGITGHCERCEV 937
Db 581 ----- 580
QY 938 NHFGFEGECKPCDCHPEGSLSLQCKDGRCEGFGVGNRCDQCBENFYNRSWPGQOE 997
Db 581 -----EPVG-----CRSDGTCTVCKPGFGGPNCEH-----GAPS 608
QY 998 CPACYRLVKQVADHRVKLOELESILANLGTGDEMVTDOAFEDRLKEAREVMDLLREAQ 1057
Db 609 CPACYNQVKIQMDQFMQQLQRMELISKAQGGGVVDPDTELEGRMQQAQALQDILRDAQ 668
QY 1058 DVKDQDQNLMDRLQRYNNLTSSQISRLQNTIETGNCNLAQRAHVNTERLIEIASR 1117
Db 669 ISEGASRSLGLQAKVRSQENSYSQSRLLDLMKMTVERVRALGSGYQNRVDRTHRLITQML 728
QY 1118 ELEKAKVAANVSVPQESTGDPNNMTLLAEARKLAERHKEADDIVRVAKTANDTSTE 1177
Db 729 SLAESASLGNWTNIPASDHYVGVNGFKSLAQEATRLAESHVESASNMQLTRETEDYSKQ 788
QY 1178 AYNLLRLTL-----AGENOTAFEBIEELNRKVEQAKNISODLEKQARVHEAKAGDK 1230
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Search completed: May 18, 2004, 15:42:59  
Job time : 47.0948 secs

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.504 Seconds

(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-16

Perfect score: 8544

Sequence: 1 QANDECDGGRPCRMPE.....EDIKTLPSGCFNTPSIEKP 1576

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8540	100.0	1609	1 MMHUB2	laminin gamma-1 ch
2	8056	94.3	1607	1 MMHUB2	laminin gamma-1 ch
3	3433	40.2	1639	1 MMHUB2	laminin gamma-1 ch
4	3240	37.9	1557	2 T28811	hypothetical prote
5	2637	30.9	1193	2 A44018	laminin B2t chain
6	2454.5	28.7	1192	2 S69000	laminin gamma 2 ch
7	1782.5	20.9	3084	1 MMHUB2	laminin alpha-1 ch
8	1774.5	20.8	3106	1 S53868	laminin alpha-1 ch
9	1726	20.2	3075	2 S14458	laminin alpha-1 ch
10	1673	19.6	1786	1 MMHUB1	laminin beta-1 cha
11	1669.5	19.5	1790	1 MMHUB1	laminin beta-1 cha
12	1643	19.2	1786	1 MMHUB1	laminin beta-1 cha
13	1626.5	19.0	2823	2 T23064	hypothetical prote
14	1626.5	19.0	2823	2 P87908	protein T22A3.8 li
15	1626.5	19.0	3102	2 T43291	laminin alpha cha
16	1606.5	18.8	1808	2 T15099	hypothetical prote
17	1595.5	18.7	1791	1 MMHUB1	laminin beta-2 cha
18	1578	18.5	1798	2 S53869	laminin beta-2 cha
19	1486.5	17.4	3712	2 S18253	laminin alpha-1 ch
20	1479.5	17.3	1797	2 A55677	laminin beta-2 cha
21	1394	16.3	3672	2 T23433	hypothetical prote
22	1394	16.3	3704	2 T37316	probable laminin a
23	1327.5	15.5	3635	2 T10053	laminin alpha 5 ch
24	1164.5	13.6	606	2 A54665	netrin-1 precursor
25	1061.5	12.4	581	2 B54665	netrin-2 precursor
26	986.5	11.5	612	2 JH0799	laminin-related pr
27	923	10.8	1170	2 A53612	laminin B1k chain
28	884.5	10.4	1168	2 I56585	kalinin B1 - mouse
29	880	10.3	4391	2 A38096	perlecan precursor

30	867.5	10.2	3707	2 S18252	heparan sulfate pr
31	630	7.4	1751	1 MMHUB2	laminin alpha-2 ch
32	609	7.1	1180	2 F88369	protein unc-52 [im
33	609	7.1	2295	2 C88369	protein unc-52 [im
34	588	6.9	3375	2 T19821	hypothetical prote
35	588	6.9	1620	2 T27283	hypothetical prote
36	574.5	6.7	1111	2 T26972	hypothetical prote
37	572.5	6.7	1816	1 S68960	laminin alpha-4 ch
38	549	6.4	1574	2 T13954	MEGF6 protein - ra
39	510	6.0	1713	2 A55347	adhesive ligand ep
40	485	5.7	303	2 B45067	laminin B1 chain
41	480.5	5.6	2524	2 A35844	notch protein - Af
42	479	5.6	400	2 T46388	hypothetical prote
43	452.5	5.3	2703	1 A24420	notch protein - fr
44	451	5.3	2437	2 S42612	transmembrane prot
45	450.5	5.3	2318	2 S45306	notch 3 protein -

ALIGNMENTS

RESULT 1

MMHUB2  
laminin gamma-1 chain precursor - human  
N:Alternate names: laminin chain B2  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999  
C:Accession: S13548; A28158; S13549; B34961; S14664; S23567  
R:Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.  
J. Biol. Chem. 265, 221-228, 1991  
A:Title: Structure of the human laminin B2 chain gene reveals extensive divergence from  
A:Reference number: S13548; MUID:91093128; PMID:1965895  
A:Accession: S13548  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1609 <KAL>  
A:Cross-references: CB:W5217; NID:9186937  
A:Note: the nucleotide sequence was submitted to GenBank, February 1991  
R:Kallunki, T.; Kallunki, T.; Tryggvason, K.  
J. Biol. Chem. 263, 6751-6758, 1988  
A:Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the  
A:Reference number: A28158; MUID:88198245; PMID:3360804  
A:Accession: A28158  
A:Molecule type: mRNA  
A:Residues: 1-211, 'I', 213-1609 <PIK>  
A:Cross-references: EMBL:J03202; NID:9186916; PIDN:AAA59488.1; PID:9307107  
R:Kallunki, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; Hei  
Cytogenet. Cell Genet. 48, 137-141, 1988  
A:Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to  
A:Reference number: S13549; MUID:89169663; PMID:3234037  
A:Accession: S13549  
A:Molecule type: mRNA  
A:Residues: 1393-1609 <FUK>  
A:Cross-references: EMBL:J027654; NID:9186923; PIDN:AAA59489.1; PID:9186924  
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
Lab. Invest. 60, 772-782, 1989  
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A:Reference number: A34961; MUID:89280632; PMID:2733383  
A:Accession: B34961  
A:Molecule type: mRNA  
A:Residues: 868-1551, 'N', 1553-1609 <OLS>  
R:Santos, C.L.S.; Sabbaga, J.; Brentani, R.  
DNA Seq. 1, 275-277, 1991  
A:Title: Differences in human laminin B2 sequences.  
A:Reference number: S14664; MUID:92216129; PMID:1806043  
A:Accession: S14664  
A:Molecule type: mRNA  
A:Residues: 1282-1609 <SAN>  
A:Cross-references: EMBL:X13939; NID:934237; PIDN:CAA32122.1; PID:934238  
R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkariainen, T.; Tryggvason, K. K.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P  
A:Title: Genes for the human laminin B1 and B2 chains.  
A:Reference number: S23566



A:Accession: S23567  
A:Molecule type: DNA  
A:Residues: 801-1491, 'R', 1483-1609 <VU>  
A:Note: mRNA was also sequenced  
C:Genetics:  
A:Gene: GDB:LMAC1; LAMB2  
A:Cross-references: GDB:120136; OMIM:150290  
A:Map position: 1q31-1q31  
A:Introns: 140/1, 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;  
3; 1525/1  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:34-1609/Product: laminin gamma-1 chain #status predicted <MAT>  
F:34-285/Domain: VI <DOM6>  
F:286-504/Domain: V <DOM5>  
F:286-339/Domain: laminin-type EGF-like homology <LE01>  
F:342-395/Domain: laminin-type EGF-like homology <LE02>  
F:398-442/Domain: laminin-type EGF-like homology <LE03>  
F:445-492/Domain: laminin-type EGF-like homology <LE04>  
F:495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:505-689/Domain: laminin-type EGF-like homology  
F:690-1034/Domain: III <DOM3>  
F:690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F:724-770/Domain: laminin-type EGF-like homology <LE07>  
F:773-825/Domain: laminin-type EGF-like homology <LE08>  
F:828-881/Domain: laminin-type EGF-like homology <LE09>  
F:884-932/Domain: laminin-type EGF-like homology <LE10>  
F:935-980/Domain: laminin-type EGF-like homology <LE11>  
F:983-1028/Domain: laminin-type EGF-like homology <LE12>  
F:1035-1609/Domain: II/I <DOM1>  
F:1035-1609/Region: heptad repeats  
F:40-50/Disulfide bonds: #status predicted  
F:60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carboxy  
F:1031,1034,1600/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 8540; DB 1; Length 1609;  
Best Local Similarity 99.9%; Pred. No. 6.8e-307;  
Matches 1575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QAAMDECTDEGGRPQRCMPFVNAFNVVATNTGTPPEEYCVGTGTVTKSCHLCD 60  
DB 34 QAAMDECTDEGGRPQRCMPFVNAFNVVATNTGTPPEEYCVGTGTVTKSCHLCD 93  
QY 61 AGQPHLOHGAFLDYNNQADTTWQSQTMLAGVQVPSSINLTLHLGKAFDIYVRLKPH 120  
DB 94 AGQPHLOHGAFLDYNNQADTTWQSQTMLAGVQVPSSINLTLHLGKAFDIYVRLKPH 153  
QY 121 TSRESEFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDIS 180  
DB 154 TSRESEFAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDIS 213  
QY 181 PLTGNNVAFSLGGRPQRCMPFVNAFNVVATNTGTPPEEYCVGTGTVTKSCHLCD 240  
DB 214 PLTGNNVAFSLGGRPQRCMPFVNAFNVVATNTGTPPEEYCVGTGTVTKSCHLCD 273  
QY 241 YYAISDFAVGRCKNGHASECMKNFEDKLVCNCKNTYGVDCCKLPFFNDRPWRATA 300  
DB 274 YYAISDFAVGRCKNGHASECMKNFEDKLVCNCKNTYGVDCCKLPFFNDRPWRATA 333  
QY 301 ESASECLPCDCNGRSQECYFPPELYRSTGHGHCNTNQDNTDGAHCRCHRENFRLGNE 360  
DB 334 ESASECLPCDCNGRSQECYFPPELYRSTGHGHCNTNQDNTDGAHCRCHRENFRLGNE 393  
QY 361 ACSSCHSPVSLSTQCDSDYGRCKPQVGMGDKCDRCQPGFHSLSITEAGCPSCDPSGSI 420  
DB 394 ACSSCHSPVSLSTQCDSDYGRCKPQVGMGDKCDRCQPGFHSLSITEAGCPSCDPSGSI 453  
QY 421 DECNVETGRVCYKONVEGFNCERCKPGFFNLSSNPRGCTPCFCFGHSSVCTNAVGSYV 480

DB 454 DECNVETGRVCYKONVEGFNCERCKPGFFNLSSNPRGCTPCFCFGHSSVCTNAVGSYV 513  
QY 481 SISSTFOIDEDGWRABORDGSEASLEWSSERQDIIVSDSYFFPRYFIAPAKFLGKQVLSY 540  
DB 514 SISSTFOIDEDGWRABORDGSEASLEWSSERQDIIVSDSYFFPRYFIAPAKFLGKQVLSY 573  
QY 541 QONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSSYSETTVKKVFRLEHATDY 600  
DB 574 QONLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQGNSSYSETTVKKVFRLEHATDY 633  
QY 601 PWRALPFFEROKLNNLTSLKRGTYSEBSAGVLDVTLASARPGPGVATWVSESTCP 660  
DB 634 PWRALPFFEROKLNNLTSLKRGTYSEBSAGVLDVTLASARPGPGVATWVSESTCP 693  
QY 661 VYGGQCEMCLSGYRRETNLPGSPVLCACNGHSETCDPPTGVNCNRDNTAGPCHCK 720  
DB 694 VYGGQCEMCLSGYRRETNLPGSPVLCACNGHSETCDPPTGVNCNRDNTAGPCHCK 753  
QY 721 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVVCNCPGTGKCELCDDGVFG 780  
DB 754 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVVCNCPGTGKCELCDDGVFG 813  
QY 781 DPLGRNGPVRCLRCQCSNDIDPNAVGNCRNLTGCECLKIYNTAGFYCDRCCKGFFGNPL 840  
DB 814 DPLGRNGPVRCLRCQCSNDIDPNAVGNCRNLTGCECLKIYNTAGFYCDRCCKGFFGNPL 873  
QY 841 APNPADKCKACNCPYTMKQSSCNVPTGQCECLPHVTGDCACDPGFVNLGSGGCE 900  
DB 874 APNPADKCKACNCPYTMKQSSCNVPTGQCECLPHVTGDCACDPGFVNLGSGGCE 933  
QY 901 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFEGEGKPCDCHPEGSLSL 960  
DB 934 RCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFGFEGEGKPCDCHPEGSLSL 993  
QY 961 QCKDDGRCEGFGVNRCDCEYFNRSWPCQCPACRYLVKQVADHRVKLE 1020  
DB 994 QCKDDGRCEGFGVNRCDCEYFNRSWPCQCPACRYLVKQVADHRVKLE 1053  
QY 1021 SLIANLGTGDEWVTDQAFEDRLKAEVMDLLREAOVDKVDQVQNLMDRLQVNTLSQQ 1080  
DB 1054 SLIANLGTGDEWVTDQAFEDRLKAEVMDLLREAOVDKVDQVQNLMDRLQVNTLSQQ 1113  
QY 1081 ISRLQINRTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSUTQPESTGDP 1140  
DB 1114 ISRLQINRTIETGNLAQARAHVENTERLIEIASRELEKAKVAAANVSUTQPESTGDP 1173  
QY 1141 NNMTLLAEARKLAERHKEADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIBELN 1200  
DB 1174 NNMTLLAEARKLAERHKEADIVRVAKTANDTSTAYNLLRTLAGENQTAPEIBELN 1233  
QY 1201 RKYEQAKNISQDLEKQARVHEEAKRAGDKAVIYASVAQLSPLOSSETLEANEANNIKMEA 1260  
DB 1234 RKYEQAKNISQDLEKQARVHEEAKRAGDKAVIYASVAQLSPLOSSETLEANEANNIKMEA 1293  
QY 1261 ENLEQIDOKLKVDEDLREDMRGKEVNLLEKGTKEQQTADQLLARADAKALAEBA 1320  
DB 1294 ENLEQIDOKLKVDEDLREDMRGKEVNLLEKGTKEQQTADQLLARADAKALAEBA 1353  
QY 1321 KKGRTDLEANDILNNLXDFDPRVNDNKTAAEALRKIPAINQITTEANEKTRAQQAALG 1380  
DB 1354 KKGRTDLEANDILNNLXDFDPRVNDNKTAAEALRKIPAINQITTEANEKTRAQQAALG 1413  
QY 1381 SAAADATSAKKAHAEERIASAVQKNATSTKAEAEERTPAEVTDLDNVNNMLKQLEAEK 1440  
DB 1414 SAAADATSAKKAHAEERIASAVQKNATSTKAEAEERTPAEVTDLDNVNNMLKQLEAEK 1473  
QY 1441 ELKRRQDDADQMMWAGMASQAQAEINARKAKNSVTSLSIINDLLEQLGOLDTVDLN 1500  
DB 1474 ELKRRQDDADQMMWAGMASQAQAEINARKAKNSVTSLSIINDLLEQLGOLDTVDLN 1533  
QY 1501 KLNIEGTINKAKEMKVSIDLKRVSDLENEAKQBAAIMYNDIRDIEMKDIRNLEDIR 1560  
DB 1534 KLNIEGTINKAKEMKVSIDLKRVSDLENEAKQBAAIMYNDIRDIEMKDIRNLEDIR 1593

QY 1561 KTLPSGCFNTPSIEKP 1576  
 DB 1594 KTLPSGCFNTPSIEKP 1609

## RESULT 2

MMMSB2

laminin gamma-1 chain precursor - mouse

N:Alternate names: laminin chain-B2

C:Species: Mus musculus (house mouse)

C&gt;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C:Accession: A28469; A27729; A28082; S02680; S05337; S07037; A02870; S13544; S14552

R:Sasaki, M.; Yamada, Y.

J. Biol. Chem. 262, 17111-17117, 1987

A&gt;Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.

A:Reference number: A28469; MUID:88059118; PMID:3680290

A:Accession: A28469

A:Molecule type: mRNA

A:Residues: 1-1607 &lt;AS&gt;

A:Cross-references: EMBL:J03484; NID:G198694; PIDN:AAA39405.1; PID:G293688

R:Durkin, M.E.; Bartos, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.

Biochemistry 27, 5198-5204, 1988

A&gt;Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.

A:Reference number: A27729; MUID:89000737; PMID:3167041

A:Accession: A27729

A:Molecule type: mRNA

A:Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'

A:Cross-references: EMBL:J02930; NID:G198702; PIDN:AAA39408.1; PID:G293691

A&gt;Note: the authors translated the codon TAT for residue 544 as Asp and GCG for residue

R:Ogawa, K.; Burchelo, P.D.; Sasaki, M.; Yamada, Y.

J. Biol. Chem. 263, 8384-8389, 1988

A&gt;Title: The laminin B2 chain promoter contains unique repeat sequences and is active in

A:Reference number: A28082; MUID:88228071; PMID:2836421

A:Accession: A28082

A:Molecule type: DNA

A:Residues: 1-215, 'A', 217-239 &lt;OGA&gt;

A:Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G954184

R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A&gt;Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A:Reference number: S02678; MUID:88336259; PMID:2458101

A:Accession: S02680

A:Molecule type: protein

A:Residues: 227-238 &lt;FU&gt;

R:Hartl, L.; Oberbaumer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A&gt;Title: The N terminus of laminin A chain is homologous to the B chains.

A:Reference number: S00624; MUID:88225080; PMID:3267223

A:Accession: S05327

A:Molecule type: protein

A:Residues: 227-338, 387-393, 'F', 395-405, 881-912, 1022-1034 &lt;HAR&gt;

R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A&gt;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A:Reference number: S01790; MUID:89030693; PMID:3181157

A:Accession: S02037

A:Molecule type: protein

A:Residues: 1362-1377, 'X', 1379-1392, 'X', 1394-1406 &lt;DEU&gt;

R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A&gt;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A:Reference number: A02870; MUID:85051302; PMID:6209134

A:Accession: A02870

A:Molecule type: mRNA

A:Residues: 1391-1474, 'K', 1476-1575, 'N', 1577-1607 &lt;BAR&gt;

A:Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:G817975

R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Balzoppo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A&gt;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A:Reference number: S13543; MUID:85257455; PMID:3848400

A:Accession: S13544

A:Molecule type: protein

A:Residues: 1506-1523, 'X', 1525 <PAU>  
 R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, Lab. Invest. 60, 772-782, 1989  
 A>Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
 A:Reference number: A34961; MUID:89280632; PMID:2733383  
 A:Accession: S14552  
 A:Molecule type: protein  
 A:Residues: 881-912; 1022-1034; 1364-1377; 1379-1392; 1394-1409; 1506-1525; 1593-1606 <OLS>  
 C:Genetics:  
 A:Gene: Lamb-2  
 A:Map position: 1  
 A:Introns: 138/1; 239/3  
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C:Function:  
 A:Description: interact with cells and with other basement membrane proteins to promote  
 C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:34-1607/Product: laminin gamma-1 chain #status predicted <MAT>  
 F:34-283/Domain: VI <DOM6>  
 F:284-502/Domain: laminin-type EGF-like homology #status atypical <LE01>  
 F:284-337/Domain: laminin-type EGF-like homology <LE02>  
 F:340-393/Domain: laminin-type EGF-like homology <LE03>  
 F:396-440/Domain: laminin-type EGF-like homology <LE04>  
 F:443-490/Domain: laminin-type EGF-like homology <LE05>  
 F:493-502/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:503-687/Domain: IV <DOM4>  
 F:688-1032/Domain: III <DOM3>  
 F:688-719/Domain: laminin-type EGF-like homology #status atypical <LE06>  
 F:728-768/Domain: laminin-type EGF-like homology <LE07>  
 F:771-823/Domain: laminin-type EGF-like homology <LE08>  
 F:826-879/Domain: laminin-type EGF-like homology <LE09>  
 F:882-930/Domain: laminin-type EGF-like homology <LE10>  
 F:933-978/Domain: laminin-type EGF-like homology <LE11>  
 F:981-1026/Domain: laminin-type EGF-like homology <LE12>  
 F:1033-1607/Domain: II/I <DOM2>  
 F:1033-1607/Region: heptad repeats  
 F:1033-48/Disulfide bonds: #status Predicted  
 F:58,132,574,648,1020,1105,1159,1173,1203,1221,1239,1437/Binding site: carbohydrate (Asn  
 F:1029,1032/Disulfide bonds: interchain #status Predicted  
 F:1378,1393/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:1598/Disulfide bonds: interchain (to chain B1) #status experimental

Query Match 94.3%; Score 8056; DB 1; Length 1607;  
 Best Local Similarity 93.2%; Pred. No. 4.3e-289;  
 Matches 1469; Conservative 59; Mismatches 48; Indels 0; Gaps 0;  
 QY 1 QAAMDECTDEGRPCRCMPFVNAFNVTVVATNTCTGPPEEYCVQTVGTGKTSCHLCD 60  
 DB 32 RAAMDECADEGRPCRCMPFVNAFNVTVVATNTCTGPPEEYCVQTVGTGKTSCHLCD 91  
 QY 61 AQPHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITVRLKPH 120  
 DB 92 AQQHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLGKAFDITVRLKPH 151  
 QY 121 TSRPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 180  
 DB 152 TSRPESFALYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDEFSDIS 211  
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 DB 212 PLTGGNVAFSTLEGRPSAYNFDSNVLQEWWTATDIRVTNLRLNTFGDEVNDFPKVLSY 271  
 QY 241 YYAISDFAVGRCCKNCGHASECMKNFEDKLVNCKNTYGVDCCKCLPFPPNDRPWRATA 300  
 DB 272 YYAISDFAVGRCCKNCGHASECMKNFEDKLVNCKNTYGVDCCKCLPFPPNDRPWRATA 331  
 QY 301 ESASECLPCDNCGRSQCYDPPELYRSTGHGHCNTQDNTDGAHCRERCENFFRLGNNE 360  
 DB 332 ESASECLPCDNCGRSQCYDPPELYRSTGHGHCNTQDNTDGAHCRERCENFFRLGNTE 391  
 QY 361 ACSSCHSPVGSJSTQCDSYGRCSCKPKVGMGDKCDRCQCPGFHSLTEAGCRPCSDPSGSI 420

392 ACSPCHCSPVGLSTQCDSDYGRCKCPGVGMDKCDRCQCPGFHSLTEAGCPSCDLRGST 451  
421 DECNVETGRVCCKDNVGFNCERCKPGFNFLESNPRGCTPCFCFGHSSVCTNAVGSYVY 480  
452 DECNVETGRVCCKDNVGFNCERCKPGFNFLESNPKGCTPCFCFGHSSVCTNAVGSYVY 511  
481 SISSTFOIDEGWRAEQRDGEASELEWSSERODIATVSDSYFFRYFTIAPAKFKQLVLSY 540  
512 DISSTFOIDEGWREQRDGEASELEWSSRQDIATVSDSYFFRYFTIAPVKFLGNQVLSY 571  
541 GQNLSPFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQGNYSPESTVKVYFRLHEATDY 600  
572 GQNLSPFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQGNYSPESTVKIYFRLHEATDY 631  
601 PWRPALTPPEQKLLNLTSTIKIRGTYSERSAGYLDVDTLASARPPGPGVPATVVESTCP 660  
632 PWRPALSPFEQKLLNLTSTIKIRGTYSERTAGYLDVDTLQASARPPGPGVPATVVESTCP 691  
661 VGYGQCEMCLSGVRETNLPGVSPVLCAACNGHSETCDPEGVNCRCNDTAGPCEK 720  
692 VGYGQCFCECLPGYRRRTPSLGYPSPVCLTCNGHSETCDPEGVNCRCNDTAGPCEK 751  
721 CSDGYGDSGTAGTSSDCPCPCPGSSCAVVPKTKVVCVTCNCPGTGTTGKRCCLCDDGYFG 780  
752 CSDGYGDSGTILGTSSDCPCPCPGSSCAIYVPTKKEVVCTHCPGTGTAGKRCCLCDDGYFG 811  
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812 DPLGNGVRLCRPCQCNNDIDPNAVGNCRNLTGCECLKIYNTAGFYCDRCCKGFFGNPL 871  
841 APNPADKCKACNCPYGMKQSSCNPVYTGQCECLPHVTGDCGACDPFGYNLQSGGCE 900  
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932 RCDCHALGSTNGQCDIRTGQCECQPGITGQCHCEVNHFGFEGCKPCDCHHEGSLSL 991  
961 QCKDGRCEBGFVGNRCDOCEENFYNRSWPGQCEPCYRLVQKVDKVDHVKLOELE 1020  
992 QCKDGRCEBGFVGNRCDOCEENFYNRSWPGQCEPCYRLVQKVDKVDHVKLOELE 1051  
1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMOLLREAQVKVDQONLMDRLQRVNNTLSQ 1080  
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1081 ISRLQNIIRNTIETGILAEARSRVSTEQIETIASRELEKAKAAANVSITQESTGEP 1140  
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1141 NNMTLLAEERKLAERHKEADDIYRVAKTANDTSTAYNLLRLTAGENOTAFIEBELN 1200  
1172 NNMTLLAEERKLAERHKEADDIYRVAKTANDTSTAYNLLRLTAGENOTAFIEBELN 1231  
1201 RYVEQAKNISQLEKQAAVHEEAKRAGKAVEIYASVAQLSPDSEPLENEANNIKMEA 1260  
1232 RYVEQAKNISQLEKQAAVHEEAKRAGKAVEIYASVAQLTPVDSEALEANNIKMEA 1291  
1261 ENLEQLIDQKLYEDLREDMEKGEVKNLLEKGTQEQOTADQLLAPADAALAEBA 1320  
1292 ADLDRLLIDQKLYEDLREDMEKGEVKNLLEKGTQEQOTADQLLAPADAALAEBA 1351  
1321 KXGRDTLQANDILNNLKDFDRVNDNKTAAEALRKYPAINOTTITEANEXTREAAQALG 1380  
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1381 SAAADATEAKNAHEARERIASAVQKNATSTKAAERTTFAEVTDLNNEVNNMLKQLEABK 1440  
1412 NAAADATEAKNAHEARERIASAVQKNATSTKAAERTTGEVTDLDNEVNNMLKQLEAE 1471  
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1472 ELKPKQDDADQDDMMAGMASQAQAQAEINARKAKNSVTSLSIINDLLEQLGOLDTVDLN 1531

QY 1501 KUNEIEGTINAKADBMKVSDLDKRVKVDLENEAKQEAAMINDYNDIEBIMKIDINLEDIR 1560  
DB 1532 KUNEIEGTINAKADBMKASDLDRKVSLESEARKQEAAMINDYNDIEBIMKIDINLEDIK 1591  
QY 1561 KTLPSGCFNTPSIEKP 1576  
DB 1592 KTLPSGCFNTPSIEKP 1607  
RESULT 3  
MMFFB2  
laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: laminin chain B2  
C:Species: Drosophila melanogaster  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000  
C:Accession: A31483; A33737; S01733; A40502  
R:Chi, H.C.; Hui, C.F.  
J. Biol. Chem. 264, 1543-1550, 1989  
A:Title: Primary structure of the Drosophila laminin B2 chain and comparison with human,  
R:Chi, H.C.; Hui, C.F.  
A:Reference number: A31483; MUID:89109164; PMID:2912972  
A:Accession: A31483  
A:Molecule type: mRNA  
A:Residues: 1-1639 <CHI>  
A:Cross-references: EMBL:N25063; NID:g157803; PIDN:AAA28664.1; PID:g157804  
R:Montell, D.J.; Goodman, C.S.  
J. Cell Biol. 109, 2441-2453, 1989  
A:Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits  
A:Reference number: A33737; MUID:90037237; PMID:2808533  
A:Accession: A33737  
A:Molecule type: mRNA  
A:Residues: 1-39, 'T', 'L', '893-1106', 'T', '1108-1459', 'H', '1462-1581', 'G', '1583-1639' <MON  
A:Note: 831-Tyr was also found  
R:Chi, H.C.; Hui, C.F.  
Nucleic Acids Res. 16, 7205-7206, 1988  
A:Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.  
A:Reference number: S01733; MUID:88303364; PMID:3405777  
A:Accession: S01733  
A:Molecule type: mRNA  
A:Residues: 344-1639 <CH2>  
A:Cross-references: EMBL:X07806; NID:g8179; PIDN:CAA30665.1; PID:g1335618  
A:Note: the authors translated the codon GGC for residue 409 as the  
R:Chi, H.C.; Junninga, D.; Wang, S.Y.; Hui, C.F.  
DNA Cell Biol. 10, 451-466, 1991  
A:Title: Structure of the Drosophila gene for the laminin B2 chain.  
A:Reference number: A40502; MUID:91299161; PMID:1840513  
A:Accession: A40502  
A:Molecule type: DNA  
A:Residues: 1-891, 'L', '893-1639' <CH3>  
A:Cross-references: GB:M58417; NID:g157805; PIDN:AAA28665.1; PID:g157806  
C:Genetics:  
A:Gene: lamB2  
A:Cross-references: FlyBase:FBgn0002528  
A:Map position: 3L 67C  
A:Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Keywords: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-33/Domain: signal sequence #status predicted <Sig>  
F:34-1639/Product: laminin gamma-1 chain #status predicted <Mat>  
F:34-297/Domain: VI <DOM6>  
F:298-528/Domain: V <DOM5>  
F:299-356/Domain: laminin-type EGF-like homology <LE01>  
F:359-411/Domain: laminin-type EGF-like homology <LE02>  
F:414-458/Domain: laminin-type EGF-like homology <LE03>  
F:461-511/Domain: laminin-type EGF-like homology <LE04>  
F:514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:529-705/Domain: IV <DOM4>  
F:706-1057/Domain: III <DOM3>  
F:710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F:744-790/Domain: laminin-type EGF-like homology <LE07>

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 8.96059 Seconds  
(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-16

Perfect score: 8544

Sequence: 1 QAAMDECTDEGGRPCRMPE.....EDIRKTLPSGCFNTPSTIEKP 1576

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8540	100.0	1609	1 LMGI HUMAN	P11047 homo sapien
2	8056	94.3	1607	1 LMGI MOUSE	P02468 mus musculus
3	3600	42.1	1587	1 LMGI HUMAN	Q9V6N6 homo sapien
4	3482.5	40.8	1581	1 LMGI MOUSE	Q9V0B6 mus musculus
5	3440	40.3	1639	1 LMGI DROME	P15215 drosophila
6	3222	37.7	1535	1 LMGI CAEEL	Q18823 caenorhabdi
7	2637	30.9	1193	1 LMGI HUMAN	Q13753 homo sapien
8	2529	29.6	1191	1 LMGI MOUSE	Q61092 mus musculus
9	1782.5	20.9	3084	1 LMGI HUMAN	P19137 mus musculus
10	1776	20.8	3110	1 LMGI HUMAN	P24043 homo sapien
11	1774.5	20.8	3106	1 LMGI HUMAN	Q60675 mus musculus
12	1726	20.2	3075	1 LMGI HUMAN	P25391 homo sapien
13	1673	19.6	1786	1 LMGI HUMAN	P07942 homo sapien
14	1669.5	19.5	1790	1 LMGI DROME	P11046 drosophila
15	1643	19.2	1786	1 LMGI HUMAN	P02469 mus musculus
16	1595.5	18.7	1801	1 LMGI HUMAN	P15800 rattus norv
17	1572	18.4	1798	1 LMGI HUMAN	P55268 homo sapien
18	1554	18.2	1799	1 LMGI HUMAN	Q61292 mus musculus
19	1486.5	17.4	3712	1 LMGI DROME	Q00174 drosophila
20	1394	16.3	3672	1 LMGI CAEEL	Q21313 caenorhabdi
21	1359	15.9	3718	1 LMGI HUMAN	Q61001 mus musculus
22	1296.5	15.2	3695	1 LMGI HUMAN	O15230 homo sapien
23	1164.5	13.6	606	1 NET1 MOUSE	Q09022 gallus gall
24	1157	13.5	604	1 NET1 HUMAN	O09118 mus musculus
25	1156	13.5	604	1 NET1 HUMAN	Q95631 homo sapien
26	1141.5	13.4	333	1 LMGI HUMAN	Q61789 mus musculus
27	1061.5	12.4	581	1 NET2 CHICK	Q90923 gallus gall
28	986.5	11.5	612	1 LMGI CAEEL	P34710 caenorhabdi
29	930	10.9	1172	1 LMGI HUMAN	Q13751 homo sapien
30	887	10.4	727	1 LMGI DROME	Q24567 drosophila
31	883.5	10.3	1168	1 LMGI HUMAN	Q61087 mus musculus
32	880	10.3	4391	1 PGEM HUMAN	P98160 homo sapien
33	867.5	10.2	3707	1 PGEM MOUSE	Q05793 mus musculus

#### ALIGNMENTS

##### RESULT 1

LMGI\_HUMAN STANDARD; PRT; 1609 AA.

AC P11047;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Laminin gamma-1 chain precursor (Laminin B2 Chain).

GN LAMC1 OR LAMB2.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=91093128; PubMed=1985895;

RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;

RT "Structure of the human laminin B2 chain gene reveals extensive

RT divergence from the laminin B1 chain gene.";

RL J. Biol. Chem. 266:221-228(1991).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=89198245; PubMed=3360804;

RA Kallunki T., Kallunki T., Tryggvason K.;

RT "Human laminin B2 chain. Comparison of the complete amino acid

RT sequence with the B1 chain reveals variability in sequence homology

RT between different structural domains.";

RL J. Biol. Chem. 263:6751-6758(1988).

RN [3]

RP SEQUENCE OF 1393-1609 FROM N.A.

RA MEDLINE=89198663; PubMed=3234037;

RA Fukushima Y., Pikkarainen T., Kallunki T., Eddy R.L., Byers M.G.,

RA Haley L.L., Henry W.M., Tryggvason K., Shows T.B.;

RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of

RT the gene to chromosome region 1q25-->q31.";

RL Cytogenet. Cell Genet. 48:137-141(1988).

RN [4]

RP SEQUENCE OF 1282-1609 FROM N.A.

RA TISSUE=Endothelial cells;

RA MEDLINE=92216129; PubMed=1806043;

RA Santos C.L.S., Sabbaga J., Brentani R.;

RT "Differences in human laminin B2 sequences.";

RL DNA Seq. 1:275-277(1991).

RN [5]

RP CARBOHYDRATE-LINKAGE SITE ASN-650.

RA MEDLINE=22660472; PubMed=12754519;

RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;

RT "Identification and quantification of N-linked glycoproteins using

RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";

RL Nat. Biotechnol. 21:660-666(2003).

CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin

CC is thought to mediate the attachment, migration and organization

CC of cells into tissues during embryonic development by interacting

CC with other extracellular matrix components.

CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three

CC different polypeptide chains (alpha, beta, gamma), which are bound

Q24568 drosophila  
Q8r4g0 mus musculus  
Q06561 caenorhabdi  
Q96cw9 homo sapien  
Q16363 homo sapien  
P97927 mus musculus  
Q8r4f1 mus musculus  
Q16787 homo sapien  
Q01635 gallus gall  
P21783 xenopus lae  
P07207 drosophila  
P46530 brachydanio

to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The gamma-1 chain is a subunit of laminin-1 (BHS laminin), laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin), laminin-6 (K-laminin) and laminin-7 (KS-laminin).

-1- SUBCELLULAR LOCATION: Extracellular.

-1- TISSUE SPECIFICITY: Found in the basement membranes (major component).

-1- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.

-1- DOMAIN: Domains VI and IV are globular.

-1- SIMILARITY: Contains 1 laminin N-terminal domain.

-1- SIMILARITY: Contains 1 laminin EGF-like domains.

-1- SIMILARITY: Contains 1 laminin IV domain.

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DR EMBL; M55210; AAA59492.1; JOINED.

DR EMBL; M55217; AAA59492.1; JOINED.

DR EMBL; M55201; AAA59492.1; JOINED.

DR EMBL; M55211; AAA59492.1; JOINED.

DR EMBL; M55212; AAA59492.1; JOINED.

DR EMBL; M55213; AAA59492.1; JOINED.

DR EMBL; M55214; AAA59492.1; JOINED.

DR EMBL; M55215; AAA59492.1; JOINED.

DR EMBL; M55216; AAA59492.1; JOINED.

DR EMBL; M55192; AAA59492.1; JOINED.

DR EMBL; M55193; AAA59492.1; JOINED.

DR EMBL; M55194; AAA59492.1; JOINED.

DR EMBL; M55195; AAA59492.1; JOINED.

DR EMBL; M55196; AAA59492.1; JOINED.

DR EMBL; M55197; AAA59492.1; JOINED.

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DR EMBL; M55200; AAA59492.1; JOINED.

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DR EMBL; M55203; AAA59492.1; JOINED.

DR EMBL; M55204; AAA59492.1; JOINED.

DR EMBL; M55205; AAA59492.1; JOINED.

DR EMBL; M55206; AAA59492.1; JOINED.

DR EMBL; M55207; AAA59492.1; JOINED.

DR EMBL; M55208; AAA59492.1; JOINED.

DR EMBL; M55209; AAA59492.1; JOINED.

DR EMBL; J02202; AAA59488.1; -.

DR EMBL; M27654; AAA59489.1; -.

DR EMBL; X13939; CAA32122.1; -.

DR HSP; P02468; 1TLE.

DR PIR; S13548; MMHUB2.

DR HSP; HGNC:6492; LAMC1.

DR MIM; 150290; -.

DR GO; GO:0005604; C:basement membrane; TAS.

DR GO; GO:0007492; P:endoderm development; TAS.

DR GO; GO:0006461; P:protein complex assembly; TAS.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR008212; Lam N2.

DR InterPro; IPR000034; Laminin B.

DR InterPro; IPR002049; Laminin\_EGF.

DR InterPro; IPR008211; LamNT.

DR Pfam; PF00052; laminin\_B; 1.

DR Pfam; PF00053; laminin\_EGF; 9.

DR Pfam; PF00055; laminin\_Nterm; 1.

DR PRINTS; PR00011; EGF\_LAMININ.

DR ProDom; PD002082; Lam N2; 1.

DR SMART; SM00180; EGF\_Lam; 8.

DR SMART; SM00281; LamB; 1.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF\_1; 8.

PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01248; LAMININ\_TYPE EGF; 11.

KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.

FT SIGNAL 1 33

FT CHAIN 34 1609 LAMININ GAMMA-1 CHAIN.

FT DOMAIN 34 285 LAMININ N-TERMINAL (DOMAIN VI).

FT DOMAIN 286 341 LAMININ EGF-LIKE 1.

FT DOMAIN 342 397 LAMININ EGF-LIKE 2.

FT DOMAIN 398 444 LAMININ EGF-LIKE 3.

FT DOMAIN 445 494 LAMININ EGF-LIKE 4.

FT DOMAIN 495 504 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT DOMAIN 505 689 LAMININ DOMAIN IV.

FT DOMAIN 690 723 LAMININ EGF-LIKE 5 (C-TERMINAL).

FT DOMAIN 724 772 LAMININ EGF-LIKE 6.

FT DOMAIN 773 827 LAMININ EGF-LIKE 7.

FT DOMAIN 828 883 LAMININ EGF-LIKE 8.

FT DOMAIN 884 934 LAMININ EGF-LIKE 9.

FT DOMAIN 935 982 LAMININ EGF-LIKE 10.

FT DOMAIN 983 1030 LAMININ EGF-LIKE 11.

FT DOMAIN 1030 1609 DOMAIN II AND I.

FT DOMAIN 1038 1609 COILED COIL (POTENTIAL).

FT DISULFID 286 305 BY SIMILARITY.

FT DISULFID 307 316 BY SIMILARITY.

FT DISULFID 319 339 BY SIMILARITY.

FT DISULFID 342 351 BY SIMILARITY.

FT DISULFID 344 367 BY SIMILARITY.

FT DISULFID 370 379 BY SIMILARITY.

FT DISULFID 382 395 BY SIMILARITY.

FT DISULFID 398 410 BY SIMILARITY.

FT DISULFID 400 416 BY SIMILARITY.

FT DISULFID 418 427 BY SIMILARITY.

FT DISULFID 430 442 BY SIMILARITY.

FT DISULFID 445 456 BY SIMILARITY.

FT DISULFID 447 463 BY SIMILARITY.

FT DISULFID 465 474 BY SIMILARITY.

FT DISULFID 477 492 BY SIMILARITY.

FT DISULFID 724 733 BY SIMILARITY.

FT DISULFID 726 740 BY SIMILARITY.

FT DISULFID 742 751 BY SIMILARITY.

FT DISULFID 754 770 BY SIMILARITY.

FT DISULFID 773 781 BY SIMILARITY.

FT DISULFID 775 792 BY SIMILARITY.

FT DISULFID 795 804 BY SIMILARITY.

FT DISULFID 807 825 BY SIMILARITY.

FT DISULFID 828 842 BY SIMILARITY.

FT DISULFID 830 849 BY SIMILARITY.

FT DISULFID 852 861 BY SIMILARITY.

FT DISULFID 864 881 BY SIMILARITY.

FT DISULFID 884 898 BY SIMILARITY.

FT DISULFID 886 905 BY SIMILARITY.

FT DISULFID 907 916 BY SIMILARITY.

FT DISULFID 919 932 BY SIMILARITY.

FT DISULFID 935 947 BY SIMILARITY.

FT DISULFID 937 954 BY SIMILARITY.

FT DISULFID 956 965 BY SIMILARITY.

FT DISULFID 968 980 BY SIMILARITY.

FT DISULFID 983 995 BY SIMILARITY.

FT DISULFID 985 1001 BY SIMILARITY.

FT DISULFID 1003 1012 BY SIMILARITY.

FT DISULFID 1015 1028 BY SIMILARITY.

FT DISULFID 1031 1031 INTERCHAIN (PROBABLE).

FT DISULFID 1034 1034 INTERCHAIN (PROBABLE).

FT DISULFID 1600 1600 INTERCHAIN (PROBABLE).

FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1107 1107 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1151 1151 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1175 1175 N-LINKED (GLCNAC. . .) (POTENTIAL).

Qy	1021	SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAGDVKDQVNDLMDRLQVNNLTSSQ	1080
Db	1054	SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREAGDVKDQVNDLMDRLQVNNLTSSQ	1113
Qy	1081	ISRLQIRNTIETGNLAEOARAHVENTERLIIASRELEKAKVAAANVSVTQPESTGDP	1140
Db	1114	ISRLQIRNTIETGNLAEOARAHVENTERLIIASRELEKAKVAAANVSVTQPESTGDP	1173
Qy	1141	NNMTLLAEARKLAERHKEQADDIVRAKTANDTSTAYNNLLRTLAGENQTAPEIEELN	1200
Db	1174	NNMTLLAEARKLAERHKEQADDIVRAKTANDTSTAYNNLLRTLAGENQTAPEIEELN	1233
Qy	1201	RKVEQAKNVSQDLEKQAAARVHEEAKAGDKAVEIYASVAQLSPDSETTLENEANNIKMEA	1260
Db	1234	RKVEQAKNVSQDLEKQAAARVHEEAKAGDKAVEIYASVAQLSPDSETTLENEANNIKMEA	1293
Qy	1261	ENLEQLIDQKLYEDLREDMRGKELSVKLLKGTQEQOTADOLLARADAALAEAEA	1320
Db	1294	ENLEQLIDQKLYEDLREDMRGKELSVKLLKGTQEQOTADOLLARADAALAEAEA	1353
Qy	1321	KKGRDITLQEAANDILNNLKDFDRVNDKNTAAEALRKIPAINOTITEANEKTRAEQAALG	1380
Db	1354	KKGRDITLQEAANDILNNLKDFDRVNDKNTAAEALRKIPAINOTITEANEKTRAEQAALG	1413
Qy	1381	SAADATEAKNKAHEARERIASAVQKNTATSKAFAERTFAEVTDLNEVNNMLKQLEAEK	1440
Db	1414	SAADATEAKNKAHEARERIASAVQKNTATSKAFAERTFAEVTDLNEVNNMLKQLEAEK	1473
Qy	1441	ELKRDQDADQDMMAGMASQAQAEIINARKAKNSVTSLSIINDLLLEQLGQDVTDLN	1500
Db	1474	ELKRDQDADQDMMAGMASQAQAEIINARKAKNSVTSLSIINDLLLEQLGQDVTDLN	1533
Qy	1501	KLANEIEGTLNKAKDMKVSDLRKVSLENEAKKQAAIMDYNRDIEEIMKDIRNLEDIR	1560
Db	1534	KLANEIEGTLNKAKDMKVSDLRKVSLENEAKKQAAIMDYNRDIEEIMKDIRNLEDIR	1593
Qy	1561	KTLPSCGCFNTPSIEKP	1576
Db	1594	KTLPSCGCFNTPSIEKP	1609

RESULT 2

LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU	LMG1 MOU
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Qy	1	QAAMDECTDEGRPORCMPEFVNAAFNVTVVATNCGTPPEYCVQGTGVTWSCHLCD	60
Db	34	QAAMDECTDEGRPORCMPEFVNAAFNVTVVATNCGTPPEYCVQGTGVTWSCHLCD	93
Qy	61	ACQPHLQHGAAFLTDYNNQADTTWQSTMLAGVYPPSSINLTGLHKAFTDITYVRLKFX	120
Db	94	ACQPHLQHGAAFLTDYNNQADTTWQSTMLAGVYPPSSINLTGLHKAFTDITYVRLKFX	153
Qy	121	TSRPESFALKYKTRDEGPWIPYQYSGSCENTYSKANEGFRTGDEQALCTDFBSDFS	180
Db	154	TSRPESFALKYKTRDEGPWIPYQYSGSCENTYSKANEGFRTGDEQALCTDFBSDFS	213
Qy	181	PLTGGNVAFSTLEGRPSAYNFONSPLQEWMTATDIRVTLNRLNTFGDEVNDPKVLSY	240
Db	214	PLTGGNVAFSTLEGRPSAYNFONSPLQEWMTATDIRVTLNRLNTFGDEVNDPKVLSY	273
Qy	241	YVAISDFAVGRCCKNGHASECKNEFDKLVNCKXHTYGVDCCEKLPFPNDRPWRATA	300
Db	274	YVAISDFAVGRCCKNGHASECKNEFDKLVNCKXHTYGVDCCEKLPFPNDRPWRATA	333
Qy	301	ESASECLPCDCNCRSGQECYDFDELXSTGHGHCCTNCQDNTDGAHCERCENFRLGNNE	360
Db	334	ESASECLPCDCNCRSGQECYDFDELXSTGHGHCCTNCQDNTDGAHCERCENFRLGNNE	393
Qy	361	ACSSCHCSVGLSTQDSYGRCSCKPGVMGKCDRCQPGHSLTEAGRCSCDPSGSI	420
Db	394	ACSSCHCSVGLSTQDSYGRCSCKPGVMGKCDRCQPGHSLTEAGRCSCDPSGSI	453
Qy	421	DECNVETGRVCCKDNVEGNCRCRCPGFNLSNPRGCTPCFCFGHSVCTNAGVSVY	480
Db	454	DECNVETGRVCCKDNVEGNCRCRCPGFNLSNPRGCTPCFCFGHSVCTNAGVSVY	513
Qy	481	SISSTFQIDEDGWRAEQRDGSASLEWSEERODIAVISDSYPPRYFIAPAKFLGQVLSY	540
Db	514	SISSTFQIDEDGWRAEQRDGSASLEWSEERODIAVISDSYPPRYFIAPAKFLGQVLSY	573
Qy	541	GNLSPSPVDRDRDLRLSADCVLGEAGLRVSVPLIAQNSVPSBTTVKYVRLHEADTY	600
Db	574	GNLSPSPVDRDRDLRLSADCVLGEAGLRVSVPLIAQNSVPSBTTVKYVRLHEADTY	633
Qy	601	PWRPALTPPEFQKLLNLTISKIRTYSERSAGYLDVTLASARPGVPATWVESCTCP	660
Db	634	PWRPALTPPEFQKLLNLTISKIRTYSERSAGYLDVTLASARPGVPATWVESCTCP	693
Qy	661	VGYGQFCWMLSGYRRETPNLGYPSPVLCACNGHSETCDPETGVNCRDNTAGPHCEK	720
Db	694	VGYGQFCWMLSGYRRETPNLGYPSPVLCACNGHSETCDPETGVNCRDNTAGPHCEK	753
Qy	721	CSDGYGDSYTAGTSDDQPCPCPGSSCAVVPKTEVVTCTNCPGTGKRCCLDDGYFG	780
Db	754	CSDGYGDSYTAGTSDDQPCPCPGSSCAVVPKTEVVTCTNCPGTGKRCCLDDGYFG	813
Qy	781	DPLGRNGPVLRLCCLCCSDNDIPNAGVNCNLTGECCLCIYNTAGFYCDRCCKDFGNPL	840
Db	814	DPLGRNGPVLRLCCLCCSDNDIPNAGVNCNLTGECCLCIYNTAGFYCDRCCKDFGNPL	873
Qy	841	APNPADKCAKNCNPGYTMKQSSNPVTGQCECLPHVTGQDCGACDFGYNLQSGQCE	900
Db	874	APNPADKCAKNCNPGYTMKQSSNPVTGQCECLPHVTGQDCGACDFGYNLQSGQCE	933
Qy	901	RCDCHALSTNGQCDIRITGQCECQPGITGOHCERCEVNHFGFPGCKPCDCHPGLSL	960
Db	934	RCDCHALSTNGQCDIRITGQCECQPGITGOHCERCEVNHFGFPGCKPCDCHPGLSL	993
Qy	961	QCKDDGRCECRGFGVNRCDQCEENYFYNRSPGQCECPACVRLVKDVADHRVKLOBLE	1020
Db	994	QCKDDGRCECRGFGVNRCDQCEENYFYNRSPGQCECPACVRLVKDVADHRVKLOBLE	1053

Query Match	100.0%;	Score	8540;	DB 1;	Length	1609;	
Best Local Similarity	99.9%;	Pred. No.	2.9e-308;				
Matches 1575; Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;

QY	1	QAAWDECTDEGGRPORCMPEFNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSHCLD	60
DB	34	QAAWDECTDEGGRPORCMPEFNAAFNVTVVATNTCGTPPEEYCVQGTGVTKSHCLD	93
QY	61	AGOPHLQGAAPLTDYNNQADTTWQSOFTMLAGVQYPSSINLTLLHLGKAFDITVRLKPH	120
DB	94	AGOPHLQGAAPLTDYNNQADTTWQSOFTMLAGVQYPSSINLTLLHLGKAFDITVRLKPH	153
QY	121	TSRPSFAIYKRTREDGPMWIPYQYSGSCENTYSKANRGFTIRTCGDEQQALCTDFFSDIS	180
DB	154	TSRPSFAIYKRTREDGPMWIPYQYSGSCENTYSKANRGFTIRTCGDEQQALCTDFFSDIS	213
QY	181	PLTGCNVAFTLEGRPSAYFNDSNVLQGEWTATDIRVTLLNRLNTFGDEVFNDPKVLKSY	240
DB	214	PLTGCNVAFTLEGRPSAYFNDSNVLQGEWTATDIRVTLLNRLNTFGDEVFNDPKVLKSY	273
QY	241	YVAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCBKCLPPFNDRPWRATA	300
DB	274	YVAISDFAVGRCCKNGHASECMKNEFDKLVNCKHNTYGVDCBKCLPPFNDRPWRATA	333
QY	301	ESASCLPCDNGRSOECYFPPELYRSTGHGHCCTNODNTDGAHCRCRCRENTFRLGNNE	360
DB	334	ESASCLPCDNGRSOECYFPPELYRSTGHGHCCTNODNTDGAHCRCRCRENTFRLGNNE	393
QY	361	ACSSCHSPVSGSLSTQCDYSGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPSCDPSGSI	420
DB	394	ACSSCHSPVSGSLSTQCDYSGRCSCKPGVMGDKDRQCPGFHSLTEAGRCPSCDPSGSI	453
QY	421	DECNVETGRVCCKNVGFCNCRCKPGFNLESSNPRGCTPCFCFGHSSVCTNAGVGSYV	480
DB	454	DECNVETGRVCCKNVGFCNCRCKPGFNLESSNPRGCTPCFCFGHSSVCTNAGVGSYV	513
QY	481	SISSTFQIDEDGWRAEQDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	540
DB	514	SISSTFQIDEDGWRAEQDSEASLEWSSERQDIAVISDSYFPRYFIAPAKFLGKQVLSY	573
QY	541	GQNLSEFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKVFRLHEATDY	600
DB	574	GQNLSEFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKVFRLHEATDY	633
QY	601	PWRPALTFPEFQKLNLLNLTISKIRGYSERSAGVLDVTLASAPRPGVPATWVESCTCP	660
DB	634	PWRPALTFPEFQKLNLLNLTISKIRGYSERSAGVLDVTLASAPRPGVPATWVESCTCP	693
QY	661	VYGGQPCMEMCLSGYRRRTPNLGPYSPCVLCACNGHSETCDPDTGVNCRDNTAGPHCEK	720
DB	694	VYGGQPCMEMCLSGYRRRTPNLGPYSPCVLCACNGHSETCDPDTGVNCRDNTAGPHCEK	753
QY	721	CSDGYGGSTAGTSSDCOPCPGSGSSCAVVPKTKVVVCTNCPGTGTTGKRCCLCDDGYFG	780
DB	754	CSDGYGGSTAGTSSDCOPCPGSGSSCAVVPKTKVVVCTNCPGTGTTGKRCCLCDDGYFG	813
QY	781	DPLGRNGPVRLCRLCQCSNDIDPNAGVNCNRLTGECLKICYNTAGFYCDRCXGFFGNPL	840
DB	814	DPLGRNGPVRLCRLCQCSNDIDPNAGVNCNRLTGECLKICYNTAGFYCDRCXGFFGNPL	873
QY	841	APNPADKACACNCPYGMKQSSCNPNVTGQCECLPHVTGQDCCACDPGFNVLQSGQCE	900
DB	874	APNPADKACACNCPYGMKQSSCNPNVTGQCECLPHVTGQDCCACDPGFNVLQSGQCE	933
QY	901	RCDCHALGSTNGQCDIRTGQCECQFGITGQHCHERCEVNHFGFEGPEGCKPCDCHPEGSLSL	960
DB	934	RCDCHALGSTNGQCDIRTGQCECQFGITGQHCHERCEVNHFGFEGPEGCKPCDCHPEGSLSL	993
QY	961	QCKDDGRCECREGFGVNRCDQCEENYFNRSWPCQCECPACRYLVKDQVADHVKLQELE	1020
DB	994	QCKDDGRCECREGFGVNRCDQCEENYFNRSWPCQCECPACRYLVKDQVADHVKLQELE	1053

QY	1021	SLIANLGTGDEMVTDOAFEDLKEAREVMDLLBREAOQVXDVDQNLMDRLQRVNNLTSSQ	1080
DB	1054	SLIANLGTGDEMVTDOAFEDLKEAREVMDLLBREAOQVXDVDQNLMDRLQRVNNLTSSQ	1113
QY	1081	ISRLQNIINTIEETGNLAEQARAHVENTERLIEITASRELEKAKVAAANVSVTQPESTGDP	1140
DB	1114	ISRLQNIINTIEETGNLAEQARAHVENTERLIEITASRELEKAKVAAANVSVTQPESTGDP	1173
QY	1141	NNWTLLEABEARLAEHRHQEADDIVRVAKTANDTSTAYNLLLTLAGENQTAPEIEELN	1200
DB	1174	NNWTLLEABEARLAEHRHQEADDIVRVAKTANDTSTAYNLLLTLAGENQTAPEIEELN	1233
QY	1201	RKYEQAQKINSODLEKQAAARVHEBAKRGADKAVEIYASVAQLSPLDSETLENNANNIWEA	1260
DB	1234	RKYEQAQKINSODLEKQAAARVHEBAKRGADKAVEIYASVAQLSPLDSETLENNANNIWEA	1293
QY	1261	ENLEQILDQKLKDYEDLREDMRGKELEVKNLLEKXGTEQQTADQLLARADAALAEAEA	1320
DB	1294	ENLEQILDQKLKDYEDLREDMRGKELEVKNLLEKXGTEQQTADQLLARADAALAEAEA	1353
QY	1321	KGGRDTLQEAANDILNNLKDFRRVNDNKTAAEEALRKIPAINQITITEANEKTRTAAQALG	1380
DB	1354	KGGRDTLQEAANDILNNLKDFRRVNDNKTAAEEALRKIPAINQITITEANEKTRTAAQALG	1413
QY	1381	SAAADATKAKKAHEAERIASAVQKNATSTKAAEAERTFAEVTDLDDNVNNMLKQLEAEK	1440
DB	1414	SAAADATKAKKAHEAERIASAVQKNATSTKAAEAERTFAEVTDLDDNVNNMLKQLEAEK	1473
QY	1441	ELKRRQDDADQDMMVAGMASQAQAEIINARKAKNSVTSLLSIINDLLEQLGQDITVDLN	1500
DB	1474	ELKRRQDDADQDMMVAGMASQAQAEIINARKAKNSVTSLLSIINDLLEQLGQDITVDLN	1533
QY	1501	KLNEIEGTILNKAQKDEMYKVDLDRKVSLENEAKQEAAMIDYNRDIIEIMKDRLNLEDIR	1560
DB	1534	KLNEIEGTILNKAQKDEMYKVDLDRKVSLENEAKQEAAMIDYNRDIIEIMKDRLNLEDIR	1593
QY	1561	KTLPSGCFNTPTSEIKP	1576
DB	1594	KTLPSGCFNTPTSEIKP	1609

RESULT 2	
LMGI_MOUSE	
ID	LMGI_MOUSE
AC	P02468; PRT; 1607 AA.
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Laminin gamma-1 chain precursor (laminin B2 chain).
GN	LAMC1 OR LAMB-1 OR LAMB-2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88059118; PubMed=3680290;
RA	Sasaki M., Yamada Y.;
RT	"The laminin B2 chain has a multidomain structure homologous to the
RT	B1 chain.";
RL	J. Biol. Chem. 262:17111-17117(1987).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89000737; PubMed=3167041;
RA	Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;
RT	"Primary structure of the mouse laminin B2 chain and comparison with
RT	laminin B1.";
RL	Biochemistry 27:5198-5204 (1988).
RN	[3]
RP	SEQUENCE OF 1-239 FROM N.A.
RX	MEDLINE=89228071; PubMed=2836421;
RA	Ogawa K., Buzbelo P.D., Sasaki M., Yamada Y.;
RT	"The laminin B2 chain promoter contains unique repeat sequences and

is active in transient transfection.";  
J. Biol. Chem. 263:8384-8389(1988).  
[4]  
SEQUENCE OF 1391-1607 FROM N.A.  
MEDLINE=85051302; PubMed=6205134;  
Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
"Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
coiled-coil alpha-helix.";  
EMBO J. 3:2355-2362(1984).  
[5]  
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.  
MEDLINE=96196434; PubMed=8648630;  
Stetefeld J., Mayer U., Timpl R., Huber R.;  
"Crystal structure of three consecutive laminin-type epidermal growth  
factor-like (LE) modules of laminin gamma1 chain harboring the  
nidogen binding site.";  
J. Mol. Biol. 257:644-657(1996).  
[6]  
STRUCTURE BY NMR OF 824-881.  
MEDLINE=96196435; PubMed=8648631;  
Baumgaertner R., Cziisch M., Mayer U., Poeschl E., Huber R.,  
Timpl R., Holak T.A.;  
"Structure of the nidogen binding LE module of the laminin gamma1  
chain in solution.";  
J. Mol. Biol. 257:658-668(1996).  
-|- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
-|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end. The gamma-1 chain is a subunit of laminin-1 (BHS laminin),  
laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),  
laminin-6 (K-laminin) and laminin-7 (KS-laminin).  
-|- SUBCELLULAR LOCATION: Extracellular.  
-|- TISSUE SPECIFICITY: Found in the basement membranes (major  
component).  
-|- DOMAIN: The alpha-helical domains I and II are thought to interact  
with other laminin chains to form a coiled coil structure.  
-|- DOMAIN: Domains VI and IV are globular.  
-|- SIMILARITY: Contains 1 laminin N-terminal domain.  
-|- SIMILARITY: Contains 11 laminin EGF-like domains.  
-|- SIMILARITY: Contains 1 laminin IV domain.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; X05211; CAA28838.1; -;  
EMBL; J03484; AAA39405.1; -;  
EMBL; J02930; AAA39408.1; -;  
EMBL; J03749; AAA39409.1; -;  
PDB; A28469; MMSB2.  
PDB; 1KLO; 20-AUG-97.  
PDB; 1TLE; 12-FEB-97.  
MGD; MGI:99914; Lamcl.  
GO; GO:0005604; C:basement membrane; IDA.  
InterPro; IPR006209; EGF-like.  
InterPro; IPR008212; Lam\_N2.  
InterPro; IPR000034; Laminin\_B.  
InterPro; IPR002049; Laminin\_EGF.  
InterPro; IPR008211; LamNT.  
Pfam; PF00052; laminin\_B\_1.  
Pfam; PF00053; laminin\_EGF\_9.  
Pfam; PF00055; laminin\_Nterm; 1.  
PRINTS; PR00011; EGF\_LAMININ.  
ProDom; PD002082; Lam\_N2; 1.

DR SMART; SM00180; EGF\_Lam; 8.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 10.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.  
FT SIGNAL 1 33  
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.  
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.  
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.  
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.  
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.  
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 503 687 LAMININ DOMAIN IV.  
FT DOMAIN 688 721 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 722 770 LAMININ EGF-LIKE 6.  
FT DOMAIN 771 825 LAMININ EGF-LIKE 7.  
FT DOMAIN 826 881 LAMININ EGF-LIKE 8 (NIDOGEN-BINDING).  
FT DOMAIN 882 932 LAMININ EGF-LIKE 9.  
FT DOMAIN 933 980 LAMININ EGF-LIKE 10.  
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.  
FT DOMAIN 1029 1607 DOMAIN II AND I.  
FT DOMAIN 1034 1594 COILED COIL (POTENTIAL).  
FT DISULFID 340 349 BY SIMILARITY.  
FT DISULFID 342 365 BY SIMILARITY.  
FT DISULFID 368 377 BY SIMILARITY.  
FT DISULFID 380 393 BY SIMILARITY.  
FT DISULFID 396 408 BY SIMILARITY.  
FT DISULFID 398 414 BY SIMILARITY.  
FT DISULFID 416 425 BY SIMILARITY.  
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FT DISULFID 445 461 BY SIMILARITY.  
FT DISULFID 463 472 BY SIMILARITY.  
FT DISULFID 475 490 BY SIMILARITY.  
FT DISULFID 722 731 BY SIMILARITY.  
FT DISULFID 734 738 BY SIMILARITY.  
FT DISULFID 740 749 BY SIMILARITY.  
FT DISULFID 752 768 BY SIMILARITY.  
FT DISULFID 771 779 BY SIMILARITY.  
FT DISULFID 773 790 BY SIMILARITY.  
FT DISULFID 793 802 BY SIMILARITY.  
FT DISULFID 805 823 BY SIMILARITY.  
FT DISULFID 826 840 BY SIMILARITY.  
FT DISULFID 828 847 BY SIMILARITY.  
FT DISULFID 850 859 BY SIMILARITY.  
FT DISULFID 862 879 BY SIMILARITY.  
FT DISULFID 882 896 BY SIMILARITY.  
FT DISULFID 884 903 BY SIMILARITY.  
FT DISULFID 905 914 BY SIMILARITY.  
FT DISULFID 917 930 BY SIMILARITY.  
FT DISULFID 933 945 BY SIMILARITY.  
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FT DISULFID 954 963 BY SIMILARITY.  
FT DISULFID 966 978 BY SIMILARITY.  
FT DISULFID 981 993 BY SIMILARITY.  
FT DISULFID 983 999 BY SIMILARITY.  
FT DISULFID 1001 1010 BY SIMILARITY.  
FT DISULFID 1013 1026 BY SIMILARITY.  
FT DISULFID 1029 1029 INTERCHAIN (PROBABLE).  
FT DISULFID 1032 1032 INTERCHAIN (PROBABLE).  
FT DISULFID 1598 1598 INTERCHAIN (WITH BETA-1 CHAIN).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1105 1105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1159 1159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).



FT	CARBOHYD	1203	1203	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	1221	1221	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	1239	1239	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	1378	1378	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	1437	1437	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
FT	CONFLICT	216	216	G -> A (IN REF. 3).	
FT	CONFLICT	260	260	E -> D (IN REF. 2).	
FT	CONFLICT	337	337	S -> C (IN REF. 2).	
FT	CONFLICT	447	448	LR -> PS (IN REF. 2).	
FT	CONFLICT	544	544	D -> Y (IN REF. 2).	
FT	CONFLICT	662	662	T -> S (IN REF. 2).	
FT	CONFLICT	886	886	MISSING (IN REF. 2).	
FT	CONFLICT	1158	1158	MISSING (IN REF. 2).	
FT	CONFLICT	1434	1434	V -> A (IN REF. 2).	
FT	CONFLICT	1475	1475	R -> K (IN REF. 4).	
FT	CONFLICT	1576	1576	D -> N (IN REF. 4).	
FT	TURN	775	776		
FT	STRAND	779	781		
FT	STRAND	788	790		
FT	TURN	795	796		
FT	STRAND	797	798		
FT	TURN	800	801		
FT	STRAND	804	805		
Query Match					94.3%; Score 8056; DB 1; Length 1607;
Best Local Similarity					93.2%; Pred. No. 2, 1e-290;
Matches 1469; Conservative					59; Mismatches 48; Indels 0; Gaps 0;
Qy	1	QAADECTDEGRPQRCMEFVNAFNTVATNCTGTPPEBYCVQGTGVTGKSHCLD	60		
Db	32	RAAMDECADEGGRPQRCMEFVNAFNTVATNCTGTPPEBYCVQGTGVTGKSHCLD	91		
Qy	61	AGOPHLOHGAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLLHKAFTDITYVRLKFX	120		
Db	92	AGQOHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLLHKAFTDITYVRLKFX	151		
Qy	121	TSRPESFAYKRTREDGPMIPQYYSGCCENTYSKANRGFIRTTGGDEQALCTDFESDIS	180		
Db	152	TSRPESFAYKRTREDGPMIPQYYSGCCENTYSKANRGFIRTTGGDEQALCTDFESDIS	211		
Qy	181	PLTGGNVAESTLEGRESAYNFNSPVLQEWVATDITRVTLNLTNFGDVFNDPKVLKSY	240		
Db	212	PLTGGNVAESTLEGRESAYNFNSPVLQEWVATDITRVTLNLTNFGDVFNDPKVLKSY	271		
Qy	241	YVAISDFAVGGRCKNGHASECMKNEFDKLVNCKENTYGVDCCKLPFPNDRPWRATA	300		
Db	272	YVAISDFAVGGRCKNGHASECMKNEFDKLVNCKENTYGVDCCKLPFPNDRPWRATA	331		
Qy	301	ESASECLPCDCNGRSQECYFDPBLYRSTGGHCHTNCQNTDGAHCERENFFRLGNNE	360		
Db	332	ESASECLPCDCNGRSQECYFDPBLYRSTGGHCHTNCQNTDGAHCERENFFRLGNTE	391		
Qy	361	ACSSCHCSPVGSISTQCDYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDPPSGSI	420		
Db	392	ACSPCHCSPVGSISTQCDYGRCSCKPGVMGDKDCRCQPGFHSLTEAGCRPCSCDLRGST	451		
Qy	421	DECNVTGRCVKNDYEGNRCERCKPGFNLFSSNPRGCTPCFCFGHSSVCTNAVGVSYV	480		
Db	452	DECNVTGRCVKNDYEGNRCERCKPGFNLFSSNPKGCTPCFCFGHSSVCTNAVGVSYV	511		
Qy	481	STISSTFQIDEGWRABORDGSEASLEWSSERODIAVISDYPFRYFIAPAKFLGKQVLSY	540		
Db	512	DISSTFQIDEGWRABORDGSEASLEWSSDRQDIAVISDYPFRYFIAPAKFLGKQVLSY	571		
Qy	541	GQNLSPSFVRDRDRTLSAEDLVLEGAGLRVSPLIAQGNPSYPSSETTVKYVFLRHEATDY	600		
Db	572	GQNLSPSFVRDRDRTLSAEDLVLEGAGLRVSPLIAQGNPSYPSSETTVKYVFLRHEATDY	631		
Qy	601	PMRPALTPEFQKLLNNLTSIKIRGYTSERSAGYLDVTLASARPGVPAFWVSSCTCP	660		
Db	632	PMRPALUSPFQKLLNNLTSIKIRGYTSERTAGYLDVTLQSRAPGVPFAIWVSSCTCP	691		

Qy	561	VYGGGFCFEMCLSGYRRETNLGPVPCVLACNGHSETCDPETGVCNCRDNTAGPHCEK	720		
Db	592	VYGGGFCFETCLPGYRRETPSLGPYPCVLCNCHSETCDPETGVCDCEDNTAGPHCEK	751		
Qy	721	CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVNVCTNCTGTGTGKCELCDDGYFG	780		
Db	752	CSDGYGDSSTLGTSSDCQPCPCPGSSCAVVPKTKVNVCTNCTGTGTGKCELCDDGYFG	811		
Qy	781	DFLGRNGFVLCRLCCQSDNIDPNAVCNCLTGECLKCIYNTAGVCDRCCKDGFNGPL	840		
Db	812	DFLGSNGFVLCRLCCQSDNIDPNAVCNCLTGECLKCIYNTAGVCDRCCKDGFNGPL	871		
Qy	841	APNPADCKACNPNYGTMTKQSSCNPVTCQCECLPHVTQDQCGACDPGPNYLSQSGGCE	900		
Db	872	APNPADCKACNPNYGTMTKQSSCNPVTCQCECLPHVTQDQCGACDPGPNYLSQSGGCE	931		
Qy	901	RDCCHALGSTNGQCDINTGQCECOPGITGQHCERCEVNHFGFPGEGCKPCDCHEPSLSL	960		
Db	932	RDCCHALGSTNGQCDINTGQCECOPGITGQHCERCEVNHFGFPGEGCKPCDCHEPSLSL	991		
Qy	961	QCKDDGCECREGFGVGNRCQCEENFYNRSWPGCCPCACRYLVKDQVADHRVQLQELE	1020		
Db	992	QCKDDGCECREGFGVGNRCQCEENFYNRSWPGCCPCACRYLVKDQVADHRVQLQELE	1051		
Qy	1021	SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAGDVQDVQDNLMDLRQVNNLTSSQ	1080		
Db	1052	SLIANLGTGDEMVTDOAFEDRLKEAREVMDLLREAGDVQDVQDNLMDLRQVNNLTSSQ	1111		
Qy	1081	ISRLQNTNTEETGNLAQARAHVENTERLIIASRELEKAKVAAANVSITOPSTGDP	1140		
Db	1112	ISRLQNTNTEETGNLAQARAHVENTERLIIASRELEKAKVAAANVSITOPSTGDP	1171		
Qy	1141	NNMTLLAEARKLAERHKQADDIRVAKTANTDTSTAYNLLRLTLAGENQTAPEIEELN	1200		
Db	1172	NNMTLLAEARKLAERHKQADDIRVAKTANTDTSTAYNLLRLTLAGENQTAPEIEELN	1231		
Qy	1201	RKYEQAKNISQDLKQARVHEEAKRAGDKAVIYASVAQLSPIDSETLENEANNIKMEA	1260		
Db	1232	RKYEQAKNISQDLKQARVHEEAKRAGDKAVIYASVAQLSPIDSETLENEANNIKMEA	1291		
Qy	1261	ENLEQLIDQKLQYEDLREDMRGKEVKNLLKSGKTEQOQTADQLLARADAAKALAEAA	1320		
Db	1292	ADLRLIDQKLQYEDLREDMRGKEVKNLLKSGKTEQOQTADQLLARADAAKALAEAA	1351		
Qy	1321	KKGRDITLQEBANDILNNLKDFDRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG	1380		
Db	1352	KKGRDITLQEBANDILNNLKDFDRRVNDNKTAAEALRKIPAINQITTEANEKTRQAQALG	1411		
Qy	1381	SAAADATKAKNAHEAERIASAVQKNATSTKAAEARTFAEVTDLNENNNMLKQLEAEK	1440		
Db	1412	NAAADATKAKNAHEAERIASAVQKNATSTKAAEARTFAEVTDLNENNNMLKQLEAEK	1471		
Qy	1441	ELKQKQDADQDMMAGWASQAQAEAINARKAKNSVTSLSLSTINDLLEQLGOLDTVDLN	1500		
Db	1472	ELKQKQDADQDMMAGWASQAQAEAINARKAKNSVTSLSLSTINDLLEQLGOLDTVDLN	1531		
Qy	1501	KLNEIEGTAKAKDEMKSVDLDRKVSLENEAKQAEAIMDYNRDEIEIMKDRNLEDIR	1560		
Db	1532	KLNEIEGTAKAKDEMKSVDLDRKVSLENEAKQAEAIMDYNRDEIEIMKDRNLEDIR	1591		
Qy	1561	KTLPSGCGFNTPSIEKP	1576		
Db	1592	KTLPTGCGFNTPSIEKP	1607		
RESULT 3					
LMG3 HUMAN					
ID	LMG3_HUMAN	STANDARD;	PRT;	1587	AA.
AC	Q9Y6N6;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Laminin gamma-3 chain precursor (Laminin 12 gamma 3).				

GN LAMC3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=99242614; PubMed=10225960;  
RX Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,  
RA Burgeson R.E., Champlaud M.F.;  
RA "Characterization and expression of the laminin gamma3 chain: a novel,  
RT non-basement membrane-associated, laminin chain.";  
RL J. Cell Biol. 145:605-618(1999).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The gamma-3 chain is a subunit of laminin-12.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and  
CC the reproductive tracts.  
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact  
CC with other laminin chains to form a coiled coil structure.  
CC -!- DOMAIN: Domain IV is globular.  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 1 laminin IV domain.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL: AF041835; AAD36991.1; -  
CC HSSP: P02468; ITLE.  
CC Genew: HGNC:6494; LAMC3.  
CC MIM: 604349; C:extracellular matrix; TAS.  
CC GO: GO:0005578; C:extracellular matrix; TAS.  
CC GO: GO:0016020; C:membrane; TAS.  
CC GO: GO:0005198; F:structural molecule activity; TAS.  
CC InterPro: IPR006209; EGF like.  
CC InterPro: IPR008212; Lam N2.  
CC InterPro: IPR000034; Laminin B.  
CC InterPro: IPR002049; Laminin\_EGF.  
CC InterPro: IPR008211; LamNT.  
CC Pfam: PF00052; laminin\_B; 1.  
CC Pfam: PF00053; laminin\_EGF; 9.  
CC Pfam: PF00055; laminin Nterm; 1.  
CC ProDom: PD002082; Lam N2; 1.  
CC SMART: SM00180; EGF\_Lam; 9.  
CC SMART: SM00136; LamNT; 1.  
CC PROSITE: PS00022; EGF\_1; 7.  
CC PROSITE: PS01186; EGF\_2; 2.  
CC PROSITE: PS01248; LAMININ TYPE EGF; 10.  
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 1587  
FT DOMAIN 20 270 LAMININ GAMMA-3 CHAIN.  
FT DOMAIN 271 326 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 327 382 LAMININ EGF-LIKE 1.  
FT DOMAIN 383 429 LAMININ EGF-LIKE 2.  
FT DOMAIN 430 479 LAMININ EGF-LIKE 3.  
FT DOMAIN 480 489 LAMININ EGF-LIKE 4.  
FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	937	937	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	1587 AA; 172051 MW; 3CB6E09B5F203319 CRC64;		
Query Match 42.1%; Score 3600; DB 1; Length 1587;				
Best Local Similarity 43.5%; Pred No. 5.4e-126; Indels 64; Gaps 20;				
Matches 695; Conservative 263; Mismatches 575;				
QY	2	AAMDECTDEGRPCORCMPEFVNAAFVTVVATNTCGTPPEEYCVQGTGVTGVSCHL	61	CDA
DB	20	AGMACYDAGRPORCLPVFENAAFGRLAQASHTCGSPDEDFCPHVGAGAGAHQRC	79	CD
QY	62	QPHLQGAFLTDYNNQADTTWQSTMLAGVQYSSINLTLLHGLKAFDITVRLKFT	121	
DB	80	ADPORHNASYLTDFHQBDESTWQSPSMAFGVQYFISVNTILGLKAYITVRLKFT	139	
QY	122	SRPESFAYIKRTREDGPMWIPYQYSSCENTYSKANGFIRTCGDEQOALCTDEFSDIS	181	
DB	140	SRPESFAYIKRSDAGPMWEPYQYVSASCKTYKRGQYLRPGEDERVAFCSEFSDIS	199	
QY	182	LTGQNAFSLTEGRPSAYNFDNSPVLOEWATDITVTLNELNTFGDEVNDPKVLKSY	241	
DB	200	LSGNVAFSLTEGRPSAYNFEESPGLEQWVTSTELLISLDRLNTFGDDITFADPKVLSY	259	
QY	242	YASDFAVGGRCKNGHASECMKNEFKLVNCKNHTYGVDCCKLCPFFNDRPMWRATAE	301	
DB	260	YAVSDFSVGGRCKNGHASECGPDVAGQLACRQHNITGTDRCCLPFFQDRPMWARGTAE	319	
QY	302	SASECLPCDNGRSQECYFPDELYRSTGHGHCNTNCDNTDGAHCRCRNFRLGNNEA	361	
DB	320	AAHECLPCNCSGRSECTFDRELFRSTGHGRCRCHCRDHTAGPHCERCQENFYHWDPM	379	
QY	362	CSSCHCSPVGLSTQCDYGRCSCKPGVMGDKDRCPQGFHSLTEAGRCPCSDPGSID	421	
DB	380	CQPCDQSGSLHLQCDTGTCAKCPVTGKCDCLPGFHSLSGCGRCPCNCPAGSLD	439	
QY	422	ECNVETGRVCCKNVGFCNRCRCKPGFNLESSNPRCTCFCFGHSSVCTNAVGVSY	481	
DB	440	TCDPGRGRCPCKENVEGNLDRCPGTENLQHPNPGACSSCFYGVHSCVASTAQFQVH	499	
QY	482	ISSTFQIDCGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYIAPAKFLGKQVLSYG	541	
DB	500	ILSDFHQAGSWARSVGGSEHSQWSPN----GVLLSPDEEBELTAPGLGDRFSYG	555	
QY	542	QNLSPFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYYVRLH---EAT	598	
DB	556	QPLILTRVPPGDSPLPVQ-LRLEGTGLALS--LRHSSLSGPDARASQGGRAQVPTQET	612	
QY	599	DYFWRPALTPFEQKLLNLTSTIKRTYSERSAG--YLDDEVTLASARPGGVATWVES	656	
DB	613	SEDVAPPLPFPFHFORLLANLTSRLRVSPPSPAGPVFLTEVRLTSARPGLSPASPASWEI	672	

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: May 18, 2004, 14:29:28 ; Search time 42.7526 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-16  
Perfect score: 8544  
Sequence: 1 QAMDECTDEGRPQRCMPE.....EDIRTLPSGCNTPSIEKP 1576

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phase:.\*  
10: sp\_plant:.\*  
11: sp\_rodent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_rvirus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6203	72.6	1593	13 Q8JHV8	Q8JHV8 brachydanio
2	4789	56.1	1007	13 Q90ZN3	Q90ZN3 gallus gall
3	3532.5	41.3	1623	5 Q9U3U7	Q9U3U7 anopheles g
4	2614.5	30.6	1190	6 Q8HZI9	Q8HZI9 equus caball
5	2612.5	30.6	1196	6 Q867A2	Q867A2 canis famil
6	1712	20.0	1785	13 Q8JHV7	Q8JHV7 brachydanio
7	1705	20.0	529	4 Q8N2D6	Q8N2D6 homo sapien
8	1666	19.5	1792	13 Q57484	Q57484 gallus gall
9	1652	19.3	1761	4 Q86XN2	Q86XN2 homo sapien
10	1626.5	19.0	3102	5 Q45614	Q45614 caenorhabdi
11	1566	18.3	319	4 Q96BH6	Q96BH6 homo sapien
12	1562.5	18.3	1799	11 Q8R0Y0	Q8R0Y0 mus musculu
13	1517	17.8	351	11 P97552	P97552 rattus norv
14	1506.5	17.6	2731	5 Q9VJTS	Q9VJTS drosophila
15	1506.5	17.6	3367	5 Q9XZC9	Q9XZC9 drosophila
16	1506.5	17.6	3375	5 Q8IP51	Q8IP51 drosophila

17	1485.5	17.4	1631	4 Q9Y6U6	Q9Y6U6 homo sapien
18	1485.5	17.4	3712	5 Q9VRW0	Q9VRW0 drosophila
19	1476	17.3	1827	13 Q8JHV6	Q8JHV6 brachydanio
20	1394	16.3	3704	5 P91904	P91904 caenorhabdi
21	1295.5	15.2	3695	4 Q8TDF8	Q8TDF8 homo sapien
22	1197	14.0	1168	5 Q967S8	Q967S8 schistocerc
23	1155	13.5	604	11 Q924Z9	Q924Z9 rattus norv
24	1151.5	13.5	603	13 Q42140	Q42140 brachydanio
25	1139.5	13.3	602	13 Q42203	Q42203 brachydanio
26	1137.5	13.3	569	13 Q57339	Q57339 xenopus lae
27	1136	13.3	1026	5 Q8SWY0	Q8SWY0 drosophila
28	1131.5	13.2	464	11 Q61965	Q61965 mus musculu
29	1092	12.8	555	5 Q9NFW6	Q9NFW6 branchiosto
30	1086.5	12.7	1069	5 Q9BPS4	Q9BPS4 bombyx mori
31	1071	12.5	1086	4 Q8TAS6	Q8TAS6 homo sapien
32	1054.5	12.3	1067	5 Q44585	Q44585 caenorhabdi
33	1053.5	12.3	610	5 Q96659	Q96659 hirudo medi
34	1034	12.1	1546	4 Q9NS27	Q9NS27 homo sapien
35	1031	12.1	1461	11 Q9JLTP3	Q9JLTP3 mus musculu
36	1030	12.1	1546	4 Q75445	Q75445 homo sapien
37	979	11.5	1512	11 Q8K3K1	Q8K3K1 rattus norv
38	962.5	11.3	984	11 Q8K271	Q8K271 mus musculu
39	934.5	10.9	1486	4 Q14637	Q14637 homo sapien
40	918.5	10.8	695	11 Q8C9J2	Q8C9J2 mus musculu
41	902.5	10.6	1168	11 Q91V90	Q91V90 mus musculu
42	896	10.5	911	11 Q9CRX6	Q9CRX6 mus musculu
43	879	10.3	667	5 Q9VJ25	Q9VJ25 drosophila
44	862	10.1	580	4 Q00634	Q00634 homo sapien
45	858	10.0	580	11 Q9RIA3	Q9RIA3 mus musculu

ALIGNMENTS

RESULT 1

Q8JHV8 PRELIMINARY; PRT; 1593 AA.  
ID Q8JHV8  
AC Q8JHV8; 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Laminin gamma 1.  
GN LAMC1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_taxID=7955;  
RN [1]\_taxID=7955;  
RP SEQUENCE FROM N.A. PubMed=12070089;  
RX MEDLINE=22065263; PubMed=12070089;  
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,  
RA Hirst E.M., Stemple D.L.;  
RT "Zebrafish mutants identify an essential role for laminins in  
RT notochord formation."  
RL Development 129:3137-3146(2002).  
DR EMBL; AF458048; AM61766.1;  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR InterPro; IPR008212; Lam\_N2.  
DR Pfam; PF00052; Laminin\_B; 1.  
DR Pfam; PF00053; Laminin\_EGF; 10.  
DR Pfam; PF00055; Laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 11.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 7.

```
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Laminin EGF-like domain.
SQ SEQUENCE 1593 AA; 176218 MW; A501F3A8884A411 CRC64;

Query Match
Best Local Similarity 69.7%; Score 6203; DB 13; Length 1593;
Matches 1097; Conservative 212; Mismatches 265; Indels 0; Gaps 0;

QY 3 AMDECTEGGPQCMPEFVNAAFNVTATNTCGTPPEEYCVQGTGVTGKSHCLCDAG 62
DB 20 AMDECTEDDRPQCMPEFVNAAFNVTATNTCGSPPEEFCVQGTGVTGKSHCHCNAA 79
QY 63 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVOYVPSINLTLLHKAFLDITVYRLKPHTS 122
DB 80 DPLRLHGAVALYTDINQVPQPTWQSQTMLAGIQVPSINLTLLHKSFDITVYRLKPHTS 139
QY 123 RPESFAIYKTRDPGPIPYQYSGSCENTYSKANRGFIITGDBEQALCTDFSDISPL 182
DB 140 RPESFAIYKTRSDPGPTPYQYSGSCENTYSKKNRGFIITGDBEQALCTDFSDISPL 199
QY 183 TGGNVAESTLEGPSAFNFDNSPVLQEWATDIRVTNLRLNTFGDEVFNDPVKLASYYY 242
DB 200 YGGNVAESTLEGPSAFNFDNSPVLQEWATDIRVTNLRLNTFGDEVFNDPVKLASYYY 259
QY 243 AISDFAVGGRCKNGHASECMKNBFDKLVNCKNHTYGVDCCKLPFFNDRPWRRTAES 302
DB 260 AISDFAVGGRCKNGHASECMKNBFDKLVNCKNHTYGVDCCKLPFFNDRPWRRTAES 319
QY 303 ASECLPCDCNGRSEOCYFDELVESTGHGHCNTQDNTDGAHCERCFNFFLGNNEAC 362
DB 320 PNECLPCNCKNGHASECMKNBFDKLVNCKNHTYGVDCCKLPFFNDRPWRRTAES 379
QY 363 SSCCHSPVGLSTQDSYGRCSCKPGVNGDKDRCPGFPHSLTEAGRCPCSDPSSIDE 422
DB 380 LSCGNCNPGVLSLSTQDNTGRCSCKPGVNGDKDRCPGFPHSLTEAGRCPCSDPSSIDE 439
QY 423 CNVETGTCVCKNDVNGECCKECPGFNLESNPRGCTPCFCGHSSVCNNAVGSYYSI 482
DB 440 CDVGTGRCCQKBNVDGNCRCCKLGFYFLNLPQNPQGGCTPCFCQHSVCESADGYSHKI 499
QY 483 SSTQIDEDGWRARQDRGSEASLEWSSERODIAVISDSYFPRPIAPAKFLGKQVLSYG 542
DB 500 TSTFDRDDEGKQRODSSVPVQWSPSSGSEISLSEDPYPIYFVAPDKFLHQLLSYG 559
QY 543 NLSFSPVDRDRLSLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVPRLHEATDYP 602
DB 560 NLTLNFIQRHARSLAEDLVLEGAGLRVSVPLIAQNSYPSSETTVKYVPRLHEATDYP 619
QY 603 RPAITPEFQKLLNLSIKIRGYBSRSAGYLDVTLASARPGVGPATWVESCTCPVG 662
DB 620 RPTIKHADFOKLLNLSIKIRGYBSRSAGYLDVTLASARPGVGPATWVESCTCPVG 679
QY 663 YGGFCFECMLSGYRRTFNLGYPFCVLACNGHSETCDPBTGVNCRDNTAGPHCKCS 722
DB 680 YLGQHCQDQGRSRPELRPFETCERCNCNGHSDTCDPBTGMNCQHNATGLSCERCK 739
QY 723 DGYTGDSITAGTSSDQPCPCPGSSCAVPPKTEKWCNTNCTGTGTRKCLCDGDFGDP 782
DB 740 DGFVGDSTVSGSSDCKACPCPAGATCAVPTKNEVCTNCTGTGTRKCLCDGDFGDP 799
QY 783 LGRNGPVLRLCQCSNIDNNAVGNCRNLTGECCLKIYNTAGYCDRCXKDGFGNPLAP 842
DB 800 LGKGPVRAACRACSCNNIEPNAVGNCRNRESGECCLKIYNTAGYCDRCXKDGFGNPLAP 859
QY 843 NPADCKACNCPVGTWQSQSCNPNVTGQCCLPHVTGDCGACDPGFYNLQSGGGERC 902
DB 860 NVADCKPCKCSPYGTVDQRACQVGTQCCLPHVINRDCGACELGFYNLQSGGGERC 919
QY 903 DCHALGTNGQCDINTGQCEQPGITGQHCBCEVNHFGFGECKPCDCHPESLSLQC 962
DB 920 NCNPIGTSNGQCDIVSGQCEQPGITGQHCBCEVNHFGFGECKPCDCHPESLSLQC 979
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## RESULT 2

```
Q90ZN3 ID Q90ZN3 PRELIMINARY; PRT; 1007 AA.
AC Q90ZN3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Laminin gamma 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Halfter W., Dong S., Balasubramani M., Bier M.E.;
RT "aberrant histogenesis after temporary disruption of the retinal basal
RL lamina."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373841; AAK55397.1; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000034; Laminin B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin B; 1.
DR Pfam; PF00053; laminin_EGF; 9.
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 43.5393 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-18  
Perfect score: 8694  
Sequence: 1 MTGGRAALQPRGRWLPL.....EDIKKTLPTGCFNTPSIKPK 1605

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_29Jan04.\*
- 1: Geneseqp1980s.\*
  - 2: Geneseqp1990s.\*
  - 3: Geneseqp2000s.\*
  - 4: Geneseqp2001s.\*
  - 5: Geneseqp2002s.\*
  - 6: Geneseqp2003as.\*
  - 7: Geneseqp2003bs.\*
  - 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8694	100.0	1605	3 AAB19805	Aab19805 Mouse lam
2	8694	100.0	1605	3 AAB48454	Aab48454 Mouse lam
3	8694	100.0	1605	5 ABB81596	Abb81596 Mouse lam
4	8613	99.1	1607	2 AAWS0897	Aaw50897 Mouse lam
5	8527	98.1	1572	3 AAB19806	Aab19806 Mouse lam
6	8527	98.1	1572	3 AAB48455	Aab48455 Mouse lam
7	8527	98.1	1572	5 ABB81597	Abb81597 Mouse lam
8	8148	93.7	1609	3 AAB19801	Aab19801 Human lam
9	8148	93.7	1609	3 AAB48452	Aab48452 Human lam
10	8148	93.7	1609	5 ABB81594	Abb81594 Human lam
11	8148	93.7	1609	7 ADC01887	Adc01887 Human lam
12	8148	93.7	1617	3 AAB19803	Aab19803 Human lam
13	8144	93.7	1609	2 AAWS0898	Aaw50898 Human lam
14	8043	92.5	1576	3 AAB19802	Aab19802 Human lam
15	8043	92.5	1576	3 AAB48453	Aab48453 Human lam
16	8043	92.5	1576	5 ABB81595	Abb81595 Human lam
17	8043	92.5	1584	3 AAB19804	Aab19804 Human lam
18	3598.5	41.4	1587	3 AAB40917	Aab40917 Human ORF
19	3596.5	41.4	1587	5 AAWS0361	Aam50361 Mouse lam
20	3596.5	41.4	1587	6 ABR58467	AbR58467 Human NOV
21	3593.5	41.3	1575	6 ABR58468	AbR58468 Human NOV
22	3476	40.0	1639	4 ABB59807	Abb59807 Drosophil
23	3445.5	39.6	1524	2 AAV15458	Aav15458 Human lam
24	2592	29.8	1193	5 AAE14712	Aae14712 Human lam
25	2592	29.8	1193	6 ABR48214	AbR48214 Human bla

26	2592	29.8	1193	6 ABUS6513	AbUS6513 Lung canc
27	2592	29.8	1193	6 ABUS6696	AbUS6696 Lung canc
28	2592	29.8	1193	6 ABR92103	AbR92103 Human cer
29	2592	29.8	1193	6 ADA74120	Ada74120 Human lam
30	2591	29.8	1193	2 AAR91427	Aar91427 Kalinin/1
31	2591	29.8	1193	3 AAB48468	Aab48468 Human lam
32	2591	29.8	1193	5 AAO14992	Aao14992 Laminin g
33	2584	29.7	1172	3 AAB48469	Aab48469 Human lam
34	2583	29.7	1193	3 AAB48470	Aab48470 Human lam
35	2577.5	29.6	1190	6 ADA74091	Ada74091 Equine la
36	2576	29.6	1172	3 AAB48471	Aab48471 Human lam
37	2477.5	28.5	1111	5 AAE14713	Aae14713 Human lam
38	2476.5	28.5	1111	2 AAR91428	Aar91428 Kalinin/1
39	2476.5	28.5	1111	5 AAO14993	Aao14993 Laminin g
40	2400.5	27.6	1171	3 AAB48473	Aab48473 Mouse lam
41	2400.5	27.6	1192	3 AAB48472	Aab48472 Mouse lam
42	2400.5	27.6	1192	5 AAE14711	Aae14711 Mouse lam
43	2400.5	27.6	1192	5 ADA74121	Ada74121 Murine la
44	2306.5	26.5	1171	2 AAW26583	Aaw26583 Rat hemid
45	1812.5	20.8	3106	3 AAB19795	Aab19795 Mouse lam

ALIGNMENTS

RESULT 1  
AAB19805  
ID AAB19805 standard; protein; 1605 AA.  
XX  
AC AAB19805;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Mouse laminin 2 gamma-1 chain.  
XX  
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..33  
FT Protein /label= Signal\_peptide  
FT /label= Mature\_protein  
XX  
FN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
DR WPI; 2000-687537/67.  
DR N-ESDB; AAA88905.  
XX  
PT Purified laminin 2 protein, useful for research and therapeutic purposes  
including peripheral nerve regeneration, treatment of degenerative muscle  
disorders, angiogenesis regulation, and ex vivo cell therapy.  
PS Claim 5; Page 288-294; 305pp; English.  
XX  
CC The present sequence is that of the gamma-1 chain of mouse laminin 2.  
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
(100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for  
CC preventing apoptosis. Genetic defects in human laminin 2 structure or  
CC expression are associated with a major type of congenital muscular  
CC dystrophy. Laminin 2 is also thought to be important in Schwann  
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
CC polynucleotides encoding them (see AAB8891-906), methods for making  
CC recombinant laminin 2, cells that express recombinant laminin 2, and  
CC methods for using purified laminin 2 for research and therapeutic  
CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX  
SQ Sequence 1605 AA;

Query Match 100.0%; Score 8694; DB 3; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGGRAALALQPRGLWPLLAVALAVAGCVRAAMDECADEGGPQRCMPFVNAAFNVT 60  
Db 1 MTGGRAALALQPRGLWPLLAVALAVAGCVRAAMDECADEGGPQRCMPFVNAAFNVT 60

Qy 61 VVATNTCGTPPEYCVQGTGVTGKSLCHLDAQOHLQGAAPLTDYNNQADTTWQSQT 120  
Db 61 VVATNTCGTPPEYCVQGTGVTGKSLCHLDAQOHLQGAAPLTDYNNQADTTWQSQT 120

Qy 121 MLAGVQVPSNINLTLLHGKAFDITYVLKFTSRPESFALYKTRDGPWIPYQYVSGSC 180  
Db 121 MLAGVQVPSNINLTLLHGKAFDITYVLKFTSRPESFALYKTRDGPWIPYQYVSGSC 180

Qy 181 ENTYSKANRGFIRTGSDQOALCTDFSDISPTGTGNVAFSTLEGPSAYNFNDSFVLOE 240  
Db 181 ENTYSKANRGFIRTGSDQOALCTDFSDISPTGTGNVAFSTLEGPSAYNFNDSFVLOE 240

Qy 241 WVTATDTRVTLNLTGDFVNDPKVLSYVYIAISDFVAGCKCNHGASECVKNERDK 300  
Db 241 WVTATDTRVTLNLTGDFVNDPKVLSYVYIAISDFVAGCKCNHGASECVKNERDK 300

Qy 301 LMCNKENTYGVDCCKLPFFNDPRWRATAESASECLPCDCNCRSQECYFDPPELYRSTG 360  
Db 301 LMCNKENTYGVDCCKLPFFNDPRWRATAESASECLPCDCNCRSQECYFDPPELYRSTG 360

Qy 361 HGHCTNCRDNTGAKCERENFFRLGNTAEACSPCHSPVGLSTOCDSYGRCSCKPGV 420  
Db 361 HGHCTNCRDNTGAKCERENFFRLGNTAEACSPCHSPVGLSTOCDSYGRCSCKPGV 420

Qy 421 MGDKCDRCQPGFSLTEAGCRPCSDPGSGTDCNVETGRVCCKDNVEGFNCERCKPGFF 480  
Db 421 MGDKCDRCQPGFSLTEAGCRPCSDPGSGTDCNVETGRVCCKDNVEGFNCERCKPGFF 480

Qy 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSDYDTSSTFQIDEDGWRYEQRDGEASLEWSS 540  
Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSDYDTSSTFQIDEDGWRYEQRDGEASLEWSS 540

Qy 541 DRQVIATVSDSYFPRYFIAPVKFLGNQVLSYGONLSFSPFVDRDRTRLGAEDLVLEGAGL 600  
Db 541 DRQVIATVSDSYFPRYFIAPVKFLGNQVLSYGONLSFSPFVDRDRTRLGAEDLVLEGAGL 600

Qy 601 RVSVPLIAQNSYSPSETTVKYIFELHEATDYPWRPALSPPEFQKLLNLTSLIKIRTYSE 660  
Db 601 RVSVPLIAQNSYSPSETTVKYIFELHEATDYPWRPALSPPEFQKLLNLTSLIKIRTYSE 660

Qy 661 RSAGVLDVTLQSRARPGVPATWVESCTCPVGGQFCETCLPGYRRRETPSLGYPSPCV 720  
Db 661 RSAGVLDVTLQSRARPGVPATWVESCTCPVGGQFCETCLPGYRRRETPSLGYPSPCV 720

Qy 721 LCTCNHSETCDPTGVCDCRDNATAGPHCKSDGYGSDTLGTSSDCQPCPCPGSSCA 780  
Db 721 LCTCNHSETCDPTGVCDCRDNATAGPHCKSDGYGSDTLGTSSDCQPCPCPGSSCA 780

Qy 781 IVPKTEVWVCHTCPTGTAGKRCCLDDGYFGDPLGNGPVLRCRCPQCNDNIDNAYGNC 840  
Db 781 IVPKTEVWVCHTCPTGTAGKRCCLDDGYFGDPLGNGPVLRCRCPQCNDNIDNAYGNC 840

Qy 841 NRTLGECLKCIYNTAGYCDRCCKEGFFGNPLAPNADKCKACACNYGTVOQSSCNVPTG 900  
Db 841 NRTLGECLKCIYNTAGYCDRCCKEGFFGNPLAPNADKCKACACNYGTVOQSSCNVPTG 900

Qy 901 QCQCLPHVSGRDCGTCDPGYYNLQSGGOCERCDCCHALGSTNGQCDIRTGQCECQPGITGQ 960  
Db 901 QCQCLPHVSGRDCGTCDPGYYNLQSGGOCERCDCCHALGSTNGQCDIRTGQCECQPGITGQ 960

Qy 961 HCERCETNHFGFEGCKPCDCHHEGSLSLQCKDDGRCBCEGFGVGNRCQCEENYFNR 1020  
Db 961 HCERCETNHFGFEGCKPCDCHHEGSLSLQCKDDGRCBCEGFGVGNRCQCEENYFNR 1020

Qy 1021 SWPQCQCEPCACRYLVKDKAAAEHRVKLQELSLIANLTGDDMTDQAFEDRLKEAREVT 1080  
Db 1021 SWPQCQCEPCACRYLVKDKAAAEHRVKLQELSLIANLTGDDMTDQAFEDRLKEAREVT 1080

Qy 1081 DLLREAQEVKDVQDQNLMDRLQRVNSSLHQSISRLONTIRNTIETGILAEARSRVESTEQ 1140  
Db 1081 DLLREAQEVKDVQDQNLMDRLQRVNSSLHQSISRLONTIRNTIETGILAEARSRVESTEQ 1140

Qy 1141 LIETASRELEKAKMAANVSIPTPESTGEPNNMTLLAEARLAEARHKEADDIRVAKTA 1200  
Db 1141 LIETASRELEKAKMAANVSIPTPESTGEPNNMTLLAEARLAEARHKEADDIRVAKTA 1200

Qy 1201 NETSAAEYNLLIRLTLAGENOTALIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260  
Db 1201 NETSAAEYNLLIRLTLAGENOTALIEBELNRKYEQAKNISQDLEKQAAARVHEEAKRAGDKA 1260

Qy 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320  
Db 1261 VEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKNL 1320

Qy 1321 LEKGAEQQTADQLARADAALAEBAEAAKKGSTLQEAANDILNNLKDFORRVNDNKTAA 1380  
Db 1321 LEKGAEQQTADQLARADAALAEBAEAAKKGSTLQEAANDILNNLKDFORRVNDNKTAA 1380

Qy 1381 BEALRRIPAINRTTAEANEKTRAEQALGNAADATATEAKNAHEABEASAAQKNAATSTK 1440  
Db 1381 BEALRRIPAINRTTAEANEKTRAEQALGNAADATATEAKNAHEABEASAAQKNAATSTK 1440

Qy 1441 ADAERTTGEVTDLDNEVNGMLRQLEEAENELKRRQDDADQDMMAGMASQAQAEALNAR 1500  
Db 1441 ADAERTTGEVTDLDNEVNGMLRQLEEAENELKRRQDDADQDMMAGMASQAQAEALNAR 1500

Qy 1501 KAKNSVSSLLSQANLLDQLDQDVTDLNKLNEIEGSLNKAKDEMKASDLDRKVSLESE 1560  
Db 1501 KAKNSVSSLLSQANLLDQLDQDVTDLNKLNEIEGSLNKAKDEMKASDLDRKVSLESE 1560

Qy 1561 ARKQEAALMDYNRDIAETIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605  
Db 1561 ARKQEAALMDYNRDIAETIKDIHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 2  
AAB48454  
ID AAB48454 standard; protein; 1605 AA.  
XX AAB48454;  
AC AAB48454;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 26.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX  
OS Mus musculus.  
XX

PN WO200066732-A2.  
 XX PD 09-NOV-2000.  
 XX 28-APR-2000; 2000WO-US011543.  
 XX 30-APR-1999; 99US-0131720P.  
 XX 21-AUG-1999; 99US-0149730P.  
 XX 24-SEP-1999; 99US-0155945P.  
 XX 11-FEB-2000; 2000US-0182012P.  
 XX (BIOS-) BIOSTRATUM INC.  
 PA Kortessmaa J, Tryggvason K;  
 XX WPI: 2000-687539/67.  
 XX N-PSDB; AAC83715.  
 DR Purified laminin 8 protein, useful for research and therapeutic purposes  
 PT including peripheral nerve regeneration, treatment of degenerative muscle  
 PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
 XX Claim 5; Page 227-232; 245pp; English.  
 CC The present sequence is a laminin 8 polypeptide chain. Laminins are a  
 CC family of heterotrimeric glycoproteins that function via binding  
 CC interactions with neighbouring cell receptors and by forming laminin  
 CC networks. They are signalling molecules which influence cellular  
 CC function. Laminin 8 is useful for treating injuries to tissue of  
 CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
 CC treating injuries to vascular tissue, promoting cell attachment and  
 CC migration, ex vivo cell therapy, improving the biocompatibility of  
 CC medical devices, and preparing improved cell culture devices and media.  
 CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
 CC of vascular injuries, improving the take of grafts, improving the  
 CC biocompatibility of medical devices, treating neural injuries (neural  
 CC regeneration), regulating angiogenesis, and promoting cell attachment and  
 CC migration  
 XX Sequence 1605 AA;  
 SQ Query Match 100.0%; Score 8694; DB 3; Length 1605;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGGGAAALQPRGLWFLAVLAAGVACVRAAMDECADEGGRPQRCMPFVNAAFNVT 60  
 DB 1 MTGGGAAALQPRGLWFLAVLAAGVACVRAAMDECADEGGRPQRCMPFVNAAFNVT 60  
 QY 61 VVATNTCGTPPEYCVQGTGVTGKTSCHLDAQOQHLQHGAAFLTDYNNQADTTWQSQ 120  
 DB 61 VVATNTCGTPPEYCVQGTGVTGKTSCHLDAQOQHLQHGAAFLTDYNNQADTTWQSQ 120  
 QY 121 MLAGVQYVNSINLTLHLGKAFDITVRLKFTSRPESFAIYKRTREDGFWIPYQYSGSC 180  
 DB 121 MLAGVQYVNSINLTLHLGKAFDITVRLKFTSRPESFAIYKRTREDGFWIPYQYSGSC 180  
 QY 181 ENTYSKANRGFRTTGGDEOQALCTPESDISPLTGNVAFSTLEGRPSAYNFDSNVLQ 240  
 DB 181 ENTYSKANRGFRTTGGDEOQALCTPESDISPLTGNVAFSTLEGRPSAYNFDSNVLQ 240  
 QY 241 WYATDIRVTLNRLNTFGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNFDFK 300  
 DB 241 WYATDIRVTLNRLNTFGDEVNDPKVLKSYYYAISDFAVGRCCKNGHASECVKNFDFK 300  
 QY 301 LMCNCKHNTYGVDCBKLPFFNDRPWRATASASECLPCDCNGRSQCYDPBELYRSTG 360  
 DB 301 LMCNCKHNTYGVDCBKLPFFNDRPWRATASASECLPCDCNGRSQCYDPBELYRSTG 360  
 QY 361 HGHGCTNCRDNTDGAKCRRENFFRLGNTEACSPCHGSPVGSLSITQCDSDYGRCSCKPGV 420  
 DB 361 HGHGCTNCRDNTDGAKCRRENFFRLGNTEACSPCHGSPVGSLSITQCDSDYGRCSCKPGV 420

QY 421 MGDKDRCPQPGFHSLTEAGRCPCSDPSGTDENVTGRCVKCNVNEGFCNCEKCPGPF 480  
 DB 421 MGDKDRCPQPGFHSLTEAGRCPCSDPSGTDENVTGRCVKCNVNEGFCNCEKCPGPF 480  
 QY 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSYDLSISTFOIDEDGWRVQDGSSEASLEWS 540  
 DB 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSYDLSISTFOIDEDGWRVQDGSSEASLEWS 540  
 QY 541 DROYIAVISDSYPPRYFIAPVKFLGNQVLSYGNLSFSFRVDRDRDRLSAEDLVLEGAGL 600  
 DB 541 DROYIAVISDSYPPRYFIAPVKFLGNQVLSYGNLSFSFRVDRDRDRLSAEDLVLEGAGL 600  
 QY 601 RVSVPILIAQNSYPSSETTKYIFRLHEATDYPWRPALSPFEPQKLNNLTSIKIRTYSE 660  
 DB 601 RVSVPILIAQNSYPSSETTKYIFRLHEATDYPWRPALSPFEPQKLNNLTSIKIRTYSE 660  
 QY 661 RSAGYLDVDTLQARPGVPATWVESCCTPGVGGQFCETCLPGVRRRTPSLGPYSPCV 720  
 DB 661 RSAGYLDVDTLQARPGVPATWVESCCTPGVGGQFCETCLPGVRRRTPSLGPYSPCV 720  
 QY 721 LCTCNHSETCDPETGVCDRCNNTAGPHCEKSDGYVGDSTLGTSSDCQPCPCGSSCA 780  
 DB 721 LCTCNHSETCDPETGVCDRCNNTAGPHCEKSDGYVGDSTLGTSSDCQPCPCGSSCA 780  
 QY 781 IVPKTKEVWCTHCPTCTAGKCELCDDGYGDPGSGNVPVRLCRPCQCNNDNDPNAVNC 840  
 DB 781 IVPKTKEVWCTHCPTCTAGKCELCDDGYGDPGSGNVPVRLCRPCQCNNDNDPNAVNC 840  
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 DB 841 NRIITGECLKIYNTAGFYCDRCKEGFGNPLNPADKCKACACNYGTVOQSSCNPVTG 900  
 QY 901 QCQCLPHVSRDCTCDPGVYNLSQGGRCERCDHALGSTNGCQDRTQCCECPGQITQ 960  
 DB 901 QCQCLPHVSRDCTCDPGVYNLSQGGRCERCDHALGSTNGCQDRTQCCECPGQITQ 960  
 QY 961 HCRCETNHFPGPECKPCDCHHEGSLSQCKDGRCEGFGVGNRCDCQCEENFYNR 1020  
 DB 961 HCRCETNHFPGPECKPCDCHHEGSLSQCKDGRCEGFGVGNRCDCQCEENFYNR 1020  
 QY 1021 SWFGCECPACVRLVKDAAAEHRVKLQELSLIANLGTGDDMVTDQAFDRLEKEAREVT 1080  
 DB 1021 SWFGCECPACVRLVKDAAAEHRVKLQELSLIANLGTGDDMVTDQAFDRLEKEAREVT 1080  
 QY 1081 DLLREACEVKDQDNLMDRLQVNSLSHSQISRLQNIWNTIETGILAEARARSVESTSQ 1140  
 DB 1081 DLLREACEVKDQDNLMDRLQVNSLSHSQISRLQNIWNTIETGILAEARARSVESTSQ 1140  
 QY 1141 LIEIASRELEKAKAAANVSITQPESTGEFNNMTLLAEAEARLAEHRKQADDIRVAKTA 1200  
 DB 1141 LIEIASRELEKAKAAANVSITQPESTGEFNNMTLLAEAEARLAEHRKQADDIRVAKTA 1200  
 QY 1201 NETSABAYNLLTLAGENQTALEIELNARKYEQAKNISQDLEKQAAHYHEEAKRAGDKA 1260  
 DB 1201 NETSABAYNLLTLAGENQTALEIELNARKYEQAKNISQDLEKQAAHYHEEAKRAGDKA 1260  
 QY 1261 VEIYASVAQLTPVDSSEALNEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHEVKL 1320  
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 DB 1321 LEIGKAEQQTADQLLARADAALAEAAKKGSTLOEANDILNNLKDFDRVNDNKTAA 1380  
 QY 1381 EEALRIPALNRTIAENKTRTREAQALGNAAADATEAKNKAHEARERIASAAQKNATSTK 1440  
 DB 1381 EEALRIPALNRTIAENKTRTREAQALGNAAADATEAKNKAHEARERIASAAQKNATSTK 1440  
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 QY 1501 KAKNSVSSLLSQLNNLLDQLGQDVTDLNKLNIEGSLNKADEMKASDLDRKVSLESE 1560



Db 1501 KAKNSVSSLLSQNLNLDQGLDQTDVLDNKLNEIGSLNKADEMKAASDLDRKVSLESE 1560

Qy 1561 ARKQEAAMIDYNRDIAEIIKD.IHNLSDIKKTLPTGCFNTPSIEKP 1605

Db 1561 ARKQEAAMIDYNRDIAEIIKD.IHNLSDIKKTLPTGCFNTPSIEKP 1605

RESULT 3

AB881596

ID AB881596 standard; protein; 1605 AA.

XX AC AB881596;

XX DT 19-SEP-2002 (first entry)

XX DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.

XX KW Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;

XX KW tissue repair development; laminin; healing; vascular tissue;

XX KW re-endothelialisation; vascular injury; cell attachment; cell stasis;

XX KW proliferation; migration.

XX OS Mus musculus.

XX FH Location/Qualifiers

FT Peptide 1..33

FT Protein 34..1605

FT /label= laminin\_10\_third\_chain

XX W0200250111-A2.

XX PN

XX PD 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX PI Tryggvason K, Doi M, Thyboll J;

XX WPI: 2002-557650/59.

DR N-PSDB; ABQ72914.

XX New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for

PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 191-195; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is

CC an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell

CC growth and differentiation in tissue repair development. Specifically,

CC laminin 10 can be used for accelerating the healing injuries of vascular

CC tissue, improving the biocompatibility of grafts useful for treating such

CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis.

CC proliferation, differentiation, and/or migration. The present sequence

CC represents a third chain protein of laminin 10, from the present

XX invention

XX SQ Sequence 1605 AA;

Query Match 100.0%; Score 8694; DB 5; Length 1605;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGGRAALALQPRGRLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAPNVT 60

Db 1 MTGGRAALALQPRGRLWPLLAVALAAGCVRAAMDECADEGGRPQRCMPEFVNAAPNVT 60

Qy 61 VVATNTCGTTPPEEYCVQGTGVTGTSKCHLQDAGQHLQHGAAFLTDYNNQADTTWQSQT 120

Db 61 VVATNTCGTTPPEEYCVQGTGVTGTSKCHLQDAGQHLQHGAAFLTDYNNQADTTWQSQT 120

Qy 121 MLAGVQYPSNINLTLLHGKAFDITYVRLKPHTRSPSFAIYKRTREDGPMIPYQYSGSC 180

Db 121 MLAGVQYPSNINLTLLHGKAFDITYVRLKPHTRSPSFAIYKRTREDGPMIPYQYSGSC 180

Qy 181 ENTYSKANRGFIRTGDEQQAALCTDEPSDIPLTGGNVAFSTLEGRPSAYNFNSPVLQE 240

Db 181 ENTYSKANRGFIRTGDEQQAALCTDEPSDIPLTGGNVAFSTLEGRPSAYNFNSPVLQE 240

Qy 241 WVTATDIRVTNLRLNTFGDEVFNDPKVLSYVVAISDFAVGGRCKNGHASECVKQEFDK 300

Db 241 WVTATDIRVTNLRLNTFGDEVFNDPKVLSYVVAISDFAVGGRCKNGHASECVKQEFDK 300

Qy 301 LMCNKNTYGVDCCKLPFFNDRPWRATAEASASECLPCDCNCRSOECYDFPELYRSTG 360

Db 301 LMCNKNTYGVDCCKLPFFNDRPWRATAEASASECLPCDCNCRSOECYDFPELYRSTG 360

Qy 361 HGHCTNCRDNTDGAKECRENPFRLGNTAECSPCHCSPVGLSTQDYSYGRCSCKPGV 420

Db 361 HGHCTNCRDNTDGAKECRENPFRLGNTAECSPCHCSPVGLSTQDYSYGRCSCKPGV 420

Qy 421 MGDKCDRCQPGFHSLTEAGRPCSDPSGSDTDECVETGRVCCKDNVEGNCERCKPGFF 480

Db 421 MGDKCDRCQPGFHSLTEAGRPCSDPSGSDTDECVETGRVCCKDNVEGNCERCKPGFF 480

Qy 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVVDISSTFQIDEDGWRVQRDGSSEASLWSS 540

Db 481 NLESSNPKGCTPCFCFGHSSVCTNAVGYSVVDISSTFQIDEDGWRVQRDGSSEASLWSS 540

Qy 541 DROYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPSFVRDRDRLSLAEDLVLEGAGL 600

Db 541 DROYIAVISDSYFPRYFIAPVKFLGNQVLSYQNLSPSFVRDRDRLSLAEDLVLEGAGL 600

Qy 601 RVSVPILIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLSIKIRGTYS 660

Db 601 RVSVPILIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFEFQKLLNLSIKIRGTYS 660

Qy 661 RSAGYLDVTLQOSARPGVPATWVESCPCPVGGGQFCETCLPGYRRETPSLGYPSPCV 720

Db 661 RSAGYLDVTLQOSARPGVPATWVESCPCPVGGGQFCETCLPGYRRETPSLGYPSPCV 720

Qy 721 LCTCNHSETCDPETGVCDCRDNTAGPHCEKSDGYTGDSITGLTSSDCQPCPCGGSSCA 780

Db 721 LCTCNHSETCDPETGVCDCRDNTAGPHCEKSDGYTGDSITGLTSSDCQPCPCGGSSCA 780

Qy 781 IVPKTKVVCVTCPTGTAGKCELCDDGYFGDPPLGNSGVPVLCRCPCCNDNDIDNAGNC 840

Db 781 IVPKTKVVCVTCPTGTAGKCELCDDGYFGDPPLGNSGVPVLCRCPCCNDNDIDNAGNC 840

Qy 841 NRLTGECLKCIYNTAGFYCDRCKEGFGNPLAPNADKCKACACNYGTVOQSSCNVPTG 900

Db 841 NRLTGECLKCIYNTAGFYCDRCKEGFGNPLAPNADKCKACACNYGTVOQSSCNVPTG 900

Qy 901 QQCCLPHVSGRDCGTCDPGYNLQSGQCCERCDCHALGSTNGQCDIRTGQCECOPGITGQ 960

Db 901 QQCCLPHVSGRDCGTCDPGYNLQSGQCCERCDCHALGSTNGQCDIRTGQCECOPGITGQ 960

Qy 961 HCERCETHNFGPBGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCDCQCEENFYNR 1020

Db 961 HCERCETHNFGPBGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCDCQCEENFYNR 1020

Qy 1021 SWPGQCEPCACYRLVKDIAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKAEREV 1080

Db 1021 SWPGQCEPCACYRLVKDIAAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKAEREV 1080

Qy 1081 DLLRRAQEKVDQDNLMDLRQVNSSLHSQISRLQNIANTIEETGILAEARSVESTEQ 1140

Db 1091 DLLRBAEQVKVDQNLMDRLQRVNSLSHSQISRLQINRTIETGTILAEARSRVSTEQ 1140  
QY 1141 LIEIASRELEKAKMAANVSITPESTGEPNNMTLLAEAEARLAEHKKQEAADIVRVAKTA 1200  
Db 1141 LIEIASRELEKAKMAANVSITPESTGEPNNMTLLAEAEARLAEHKKQEAADIVRVAKTA 1200  
QY 1201 NETSBAYNLLRTLAGENOTALEIEELNRKYEQAKNLSODLEKQAAARVHEEAKGDKA 1260  
Db 1201 NETSBAYNLLRTLAGENOTALEIEELNRKYEQAKNLSODLEKQAAARVHEEAKGDKA 1260  
QY 1261 VEIYASVAQLTPVDSSEALNEANKIKKEAADLDRLIDQKLKDYEDLREDMRGKHEVKNL 1320  
Db 1261 VEIYASVAQLTPVDSSEALNEANKIKKEAADLDRLIDQKLKDYEDLREDMRGKHEVKNL 1320  
QY 1321 LEKGAEQOOTDOLLARADAALAEAEAAKGRSTLQEAANDILNNLKDFDRRVNDKTA 1380  
Db 1321 LEKGAEQOOTDOLLARADAALAEAEAAKGRSTLQEAANDILNNLKDFDRRVNDKTA 1380  
QY 1381 BEALRRIPAINRTIAEANEKTRAEQALGNAADATEAKNKAHEAERIASAAQKATSTK 1440  
Db 1381 BEALRRIPAINRTIAEANEKTRAEQALGNAADATEAKNKAHEAERIASAAQKATSTK 1440  
QY 1441 ADAERTFGBVTDLNEVNGMLRQLEAEENELKRGKQDDADODMMAGMASQAQAEALNAR 1500  
Db 1441 ADAERTFGBVTDLNEVNGMLRQLEAEENELKRGKQDDADODMMAGMASQAQAEALNAR 1500  
QY 1501 KAKNSVSSLLSQNLNLLDOLGQDVTDLNKLNEIEGSLNKAKDENKASDLDRKYSDLSE 1560  
Db 1501 KAKNSVSSLLSQNLNLLDOLGQDVTDLNKLNEIEGSLNKAKDENKASDLDRKYSDLSE 1560  
QY 1561 ARKQEAAMVNDYRDIAEIIKDIHNLEIDIKKTLPTGCFNTPPSIEKP 1605  
Db 1561 ARKQEAAMVNDYRDIAEIIKDIHNLEIDIKKTLPTGCFNTPPSIEKP 1605

## RESULT 4

AAW50897  
ID AAW50897 standard; protein; 1607 AA.

AC AAW50897;

XX 07-DEC-1998 (first entry)

XX Mouse laminin G1 chain.

XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW Carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
KW therapy.

XX Mus sp.

XX WO9815179-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.

XX (UNIW ) UNIV WASHINGTON.

XX Castillo G, Snow AD;

XX WPI; 1998-240534/21.

XX Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CJD.

XX Claim 15; Page 102-105; 132pp; English.

XX This is the amino acid sequence of the mouse laminin G1 chain. The  
PS primary object of the invention is to use laminin, laminin-derived  
CC protein fragments and/or laminin-derived polypeptides as potent  
CC inhibitors of amyloid formation, deposition, accumulation and/or  
CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
CC products (see AAW50888-99) may include mouse or human laminin A or A1  
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
CC binding domain of the laminin A chain. A claimed method for treating an  
CC amyloid disease comprises administering a polypeptide having a  
CC conformational similarity to a fragment of a laminin protein. A method  
CC for diagnosing an amyloid disease involves determining levels of laminin  
CC in a sample. Production of laminin or its fourth globular repeat in vivo  
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
CC products and methods can be used for the diagnosis, prognosis, monitoring  
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
CC associated with chronic inflammation, various forms of malignancy and  
CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler  
CC syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis  
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
CC transthyretin amyloid), and the amyloidosis associated with endocrine  
CC tumours such as medullary carcinoma of the thyroid (variant of  
XX procalcitonin)

XX Sequence 1607 AA;

Query Match 99.1%; Score 8613; DB 2; Length 1607;

Best Local Similarity 99.3%; Pred. NO. 0;

Matches 1596; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

Qy 1 MTGGRAALALQPRGLMLPPLAVLAAGVAVRAAMDECADEGGRPORCMPEFVNAAFNVT 60  
Db 1 MTGGRAALALQPRGLMLPPLAVLAAGVAVRAAMDECADEGGRPORCMPEFVNAAFNVT 60  
Qy 61 VVATNTCGTPPEEYCVQTVGTGVTGKCHLCDAGQQLHQAAPLTDYNNQADTTWQSQT 120  
Db 61 VVATNTCGTPPEEYCVQTVGTGVTGKCHLCDAGQQLHQAAPLTDYNNQADTTWQSQT 120  
Qy 121 MLAGVQVPNSINLTLLHGAFTDITYVRLKFTSRPESFAIKYKTRDGPWIPQYVYSGSC 180  
Db 121 MLAGVQVPNSINLTLLHGAFTDITYVRLKFTSRPESFAIKYKTRDGPWIPQYVYSGSC 180  
Qy 181 ENTYSKANRGFIRTGDEQOALCTDFSDISPLTGGNVAFTLEGRPSAYNFNDSVLOE 240  
Db 181 ENTYSKANRGFIRTGDEQOALCTDFSDISPLTGGNVAFTLEGRPSAYNFNDSVLOE 240  
Qy 241 WVTATDIRVTNLNLTFGDEVNDPKVLSYYVAISDFAVGGRCCKNGHASECVKNEFDK 300  
Db 241 WVTATDIRVTNLNLTFGDEVNDPKVLSYYVAISDFAVGGRCCKNGHASECVKNEFDK 300  
Qy 301 LMCNCKHNTYGVDCCKLPFFFNDRPWRRTAEASASCLPCDCNCRSQEQCYFDPELYRSTG 360  
Db 301 LMCNCKHNTYGVDCCKLPFFFNDRPWRRTAEASASCLPCDCNCRSQEQCYFDPELYRSTG 360  
Qy 361 HGGHCTNCRDNTDGAKCERCERENFFRLGNTAEACSPCHGSPVGLSTOCCSYGRCSCKPGV 420  
Db 361 HGGHCTNCRDNTDGAKCERCERENFFRLGNTAEACSPCHGSPVGLSTOCCSYGRCSCKPGV 420  
Qy 421 MGBKDRCPQGFHSLTEAGRCPCSCDPSGSTDENVTGRCVCCKDNVEGFNCERCKPGFF 480  
Db 421 MGBKDRCPQGFHSLTEAGRCPCSCDPSGSTDENVTGRCVCCKDNVEGFNCERCKPGFF 480

QY 481 NLESSNPKGCTPCFCGHSSVCTNAVGYSVYDISSFTQIDEDGWRVEQDGSSEASLEWSS 540  
Db 481 NLESSNPKGCTPCFCGHSSVCTNAVGYSVYDISSFTQIDEDGWRVEQDGSSEASLEWSS 540  
QY 541 DROYIAVSDSYPRPIAPVKELGNQVLSYGONLSFSFRVDRDRLSAEDLVLEGAGL 600  
Db 541 DRODIAVSDSYPRPIAPVKELGNQVLSYGONLSFSFRVDRDRLSAEDLVLEGAGL 600  
QY 601 RVSVPLIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFQKLNLLNLTISKIRGTYS 660  
Db 601 RVSVPLIAQNSYPSSETTVKYIFRLHEATDYPWRPALSPFQKLNLLNLTISKIRGTYS 660  
QY 661 RSAGYLDVTLQARPGVPATWVESCPCVGYGQFCETCLPGYRRTPSLGYPSPCV 720  
Db 661 RTAGYLDVTLQARPGVPATWVESCPCVGYGQFCETCLPGYRRTPSLGYPSPCV 720  
QY 721 LCTCNHSETCDPBTGCDVCDRDNTAGPHCEKSDGYGSDSTLGTSSDCQPCPCGSSCA 780  
Db 721 LCTCNHSETCDPBTGCDVCDRDNTAGPHCEKSDGYGSDSTLGTSSDCQPCPCGSSCA 780  
QY 781 IVPKTEVWCTHCTGTAGKRCCLDDGYGDPGLSGNVPRLCRPCQCNNDTDPNAVNC 840  
Db 781 IVPKTEVWCTHCTGTAGKRCCLDDGYGDPGLSGNVPRLCRPCQCNNDTDPNAVNC 840  
QY 841 NRLTGECLKIYNTAGFYCDRCCKEGFNGPLAENPADKCKACACN-YGTVOQSSCNPTV 899  
Db 841 NRLTGECLKIYNTAGFYCDRCCKEGFNGPLAENPADKCKACACNPGYTVQOQSSCNPTV 900  
QY 900 GQCCPLPHVSGRCGCTCDPVYNLQGGQCCERCDCHALGSTNGQCDIRTGQCECQPGITG 959  
Db 901 GQCCPLPHVSGRCGCTCDPVYNLQGGQCCERCDCHALGSTNGQCDIRTGQCECQPGITG 960  
QY 960 QHCERTNHFPGEGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCDOCEENFYFN 1019  
Db 961 QHCERTNHFPGEGCKPCDCHHEGSLSLQCKDGRCEGFGVGNRCDOCEENFYFN 1020  
QY 1020 RSWFGQCECPACVRLKDKAAERVKLOELESILIANLGTDDMVTDQAEEDLKAEREV 1079  
Db 1021 RSWFGQCECPACVRLKDKAAERVKLOELESILIANLGTDDMVTDQAEEDLKAEREV 1080  
QY 1080 TDLLEAQAQVQDQNLMDRLQVNSLSLSQISRLQNIETIETGILAEARSRVSETE 1139  
Db 1081 TDLLEAQAQVQDQNLMDRLQVNSLSLSQISRLQNIETIETGILAEARSRVSETE 1140  
QY 1140 QLTIEASRELEKAKM-AANVSITQPESTGEPNNMTLLAEARLAEHRKHQADDIRVAK 1198  
Db 1141 QLTIEASRELEKAKMAANVSITQPESTGEPNNMTLLAEARLAEHRKHQADDIRVAK 1200  
QY 1199 TANETSAAENLLRLTAGENOTALIEELNRKYEQAKNISQLEKQAAVHEEAKRAGD 1258  
Db 1201 TANETSAAENLLRLTAGENOTALIEELNRKYEQAKNISQLEKQAAVHEEAKRAGD 1260  
QY 1259 KAVEIYASVAQLTPVDSALENEANKIKKEAADLRLIDQKLDYEDLREDMRGKEHEVK 1318  
Db 1261 KAVEIYASVAQLTPVDSALENEANKIKKEAADLRLIDQKLDYEDLREDMRGKEHEVK 1320  
QY 1319 NLEKGAEOCTADQLLARAADAALAEAAKKGSTLQEAANDILNLLKDFRRVNDNKT 1378  
Db 1321 NLEKGAEOCTADQLLARAADAALAEAAKKGSTLQEAANDILNLLKDFRRVNDNKT 1380  
QY 1379 AAEALRRIPAINRTIAEAENEKTRAEQALAGNAADAATEAKNAKAEARIASAAQKNATS 1438  
Db 1381 AAEALRRIPAINRTIAEAENEKTRAEQALAGNAADAATEAKNAKAEARIASAAQKNATS 1440  
QY 1439 TKADAERTFGEVTDLNEVNGMLRQLEAEANELKRRQDDADQMMWAGASQAQAQAEALN 1498  
Db 1441 TKADAERTFGEVTDLNEVNGMLRQLEAEANELKRRQDDADQMMWAGASQAQAQAEALN 1500  
QY 1499 ARKAKNSVSLLSQNLNLLDQLGOLDTVDLNKLNEIEGSLNKADEKMSKASDLDRKYSIDLE 1558  
Db 1501 ARKAKNSVSLLSQNLNLLDQLGOLDTVDLNKLNEIEGSLNKADEKMSKASDLDRKYSIDLE 1560  
QY 1559 SEARKQEAAMVNDYRDIAEIIKDIHNLEDKIKTLPTGCFNTPSIEKP 1605

Db 1561 SEARKQEAAMVNDYRDIAEIIKDIHNLEDKIKTLPTGCFNTPSIEKP 1607  
RESULT 5  
ASB19806  
ID AAB19806 standard; protein; 1572 AA.  
XX  
AC AAB19806;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Mouse laminin 2 mature gamma-1 chain.  
XX  
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion; degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Mus musculus.  
XX  
PN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Yurchenco P;  
XX  
DR WPI; 2000-687537/67.  
DR N-PSDB; AAA88906.  
XX  
PT Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 302-306; 305pp; English.  
XX  
CC The present sequence is that of mouse laminin 2 gamma-1 chain mature protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media  
XX  
SQ Sequence 1572 AA;  
Query Match 98.1%; Score 8527; DB 3; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 AMDECADEGGPQRCMEFFVNAENVTVAINTCGTTPPEEYCVGTGVTKSHCLCDAG 93  
Db 1 AMDECADEGGPQRCMEFFVNAENVTVAINTCGTTPPEEYCVGTGVTKSHCLCDAG 60  
QY 94 QOHLQHGAAFTDYNNQADTTWQSQTLGAGVQVPSNINLTLLHGKAFDITYVRLKFTS 153

Db 61 QOHLQGAFLDYNNQADTTWQSTMLAGVQVPSINLTLHLGKAFDITYVRLKPTS 120  
QY 154 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRGTGDSQQALCTDEFSDISPL 213  
Db 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRGTGDSQQALCTDEFSDISPL 180  
QY 214 TCGNVAFTLEGRPSAYNFDNSPVLQEWATDITVTLNRLNTFQDEVFNDPKVLKSYYY 273  
Db 181 TCGNVAFTLEGRPSAYNFDNSPVLQEWATDITVTLNRLNTFQDEVFNDPKVLKSYYY 240  
QY 274 ATSDFAVGRCKNGHASCVCNNEFDKLMCNCKHTYGVDCBKLPFFNDPWRATAES 333  
Db 241 ATSDFAVGRCKNGHASCVCNNEFDKLMCNCKHTYGVDCBKLPFFNDPWRATAES 300  
QY 334 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCFRNLGNTAC 393  
Db 301 ASECLPCDCNGRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCFRNLGNTAC 360  
QY 394 SPCHSPVGLSTQCDYSYGRCSCKPGWMDKCDRCQPGFHSITBAGCPSCDPSGSTDE 453  
Db 361 SPCHSPVGLSTQCDYSYGRCSCKPGWMDKCDRCQPGFHSITBAGCPSCDPSGSTDE 420  
QY 454 CNVETGRVCCKNVEGFNCERCKPGFFNLESNPXGCTPCFCFHSSVCTNAVGYSVYDI 513  
Db 421 CNVETGRVCCKNVEGFNCERCKPGFFNLESNPXGCTPCFCFHSSVCTNAVGYSVYDI 480  
QY 514 SSTFOIDEGWRVQDGESEASLEWSSDRQYTAVIDSYFPFRYFIAPVKFLQNVLSYGO 573  
Db 481 SSTFOIDEGWRVQDGESEASLEWSSDRQYTAVIDSYFPFRYFIAPVKFLQNVLSYGO 540  
QY 574 NLSFSPVDRDRLTSLAEDLVLEGAGLRVSVFLIAQNSYPSSETTVKYIFRLHEATDYPW 633  
Db 541 NLSFSPVDRDRLTSLAEDLVLEGAGLRVSVFLIAQNSYPSSETTVKYIFRLHEATDYPW 600  
QY 634 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLQSRPFGVGPATVYESCTCPVG 693  
Db 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVDTLQSRPFGVGPATVYESCTCPVG 660  
QY 694 YGQFCETCLPGVRETPSLGYPVPCVLCTCNHSETCDPETGVCDNRDNTAGPCEKCS 753  
Db 661 YGQFCETCLPGVRETPSLGYPVPCVLCTCNHSETCDPETGVCDNRDNTAGPCEKCS 720  
QY 754 DGYGDSLTGLTSSDCQPCPGSSCAIYVKTKEVVCTHCTPTGTAGKCELCDDGYFGDP 813  
Db 721 DGYGDSLTGLTSSDCQPCPGSSCAIYVKTKEVVCTHCTPTGTAGKCELCDDGYFGDP 780  
QY 814 LGSNGPVRLCRQCNDNDPNAVCNRLTGECLKIYNTAGFYCDRCKEGFFGNPLAP 873  
Db 781 LGSNGPVRLCRQCNDNDPNAVCNRLTGECLKIYNTAGFYCDRCKEGFFGNPLAP 840  
QY 874 NPADKCKACACNYGTVOQSSCNPTVTGQCCLPHVSGRDCGTCDPGYNNLQSGQCERCD 933  
Db 841 NPADKCKACACNYGTVOQSSCNPTVTGQCCLPHVSGRDCGTCDPGYNNLQSGQCERCD 900  
QY 934 CHALGSTNGCCDIRTQCCQCPGITGOHCERCETHFGFPGEGCKPCDCHHSGSLQCK 993  
Db 901 CHALGSTNGCCDIRTQCCQCPGITGOHCERCETHFGFPGEGCKPCDCHHSGSLQCK 960  
QY 994 DGRCEGFGVGNRCDQCEENYFNRSWPGQCEPCACVRLVKDAEHRVKLQLESII 1053  
Db 961 DGRCEGFGVGNRCDQCEENYFNRSWPGQCEPCACVRLVKDAEHRVKLQLESII 1020  
QY 1054 ANLGTGDDMVTOAFEDRLKEAREVTDLLRAQEVKQVQDQNLMDRLQVNSLSHSQISR 1113  
Db 1021 ANLGTGDDMVTOAFEDRLKEAREVTDLLRAQEVKQVQDQNLMDRLQVNSLSHSQISR 1080  
QY 1114 LQNIWNTIETGLAERARSVESTBQLTETIASRELEKAKMAANSITQPESTGEPNNMT 1173  
Db 1081 LQNIWNTIETGLAERARSVESTBQLTETIASRELEKAKMAANSITQPESTGEPNNMT 1140  
QY 1174 LLAEEARLAEHRKQADDIRVAKTANETSABAVNLLRLTAGNQTALTEELNRYKE 1233  
Db 1141 LLAEEARLAEHRKQADDIRVAKTANETSABAVNLLRLTAGNQTALTEELNRYKE 1200

QY 1234 QAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSFALNEANKIKKEAADLD 1293  
Db 1201 QAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLTPVDSFALNEANKIKKEAADLD 1260  
QY 1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLKGAEOQTADQOLLARADAAKALAEAAKGR 1353  
Db 1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLKGAEOQTADQOLLARADAAKALAEAAKGR 1320  
QY 1354 STLQEAANDILNLLKDFDRVNDNKTAAEEALRRIPAINRTIABANEKTRTREAQALGNAAA 1413  
Db 1321 STLQEAANDILNLLKDFDRVNDNKTAAEEALRRIPAINRTIABANEKTRTREAQALGNAAA 1380  
QY 1414 DATEAKKAHEABRIASAAQKATSTKADARTFGEVTDLDNEVNGMLQLEBAEHLKX 1473  
Db 1381 DATEAKKAHEABRIASAAQKATSTKADARTFGEVTDLDNEVNGMLQLEBAEHLKX 1440  
QY 1474 QODDADOMMAGWASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDLDVLDLKNLE 1533  
Db 1441 QODDADOMMAGWASQAQAEALNARKAKNSVSSLLSQNLNLLDQLGQDLDVLDLKNLE 1500  
QY 1534 IEGSLNKADEMKAASDLDRKVSOLSEARKQEAAMINDYNRDIAEIIKDHNLEDIKKTLP 1593  
Db 1501 IEGSLNKADEMKAASDLDRKVSOLSEARKQEAAMINDYNRDIAEIIKDHNLEDIKKTLP 1560  
QY 1594 TGCNTPSIEKP 1605  
Db 1561 TGCNTPSIEKP 1572  
RESULT 6  
AAB48455  
ID AAB48455 standard; protein; 1572 AA.  
AC AAB48455;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 28.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
OS Mus musculus.  
XX  
PN WO200066732-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0162012P.  
XX  
FA (BIOS-) BIOSTRATUM INC.  
XX  
PI Kortessma J, Tryggvason K;  
XX  
DR N-PSDB; AAC83716.  
XX  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 240-245; 245pp; English.  
XX  
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin

CC	networks. They are signalling molecules which influence cellular
CC	function. Laminin 8 is useful for treating injuries to tissue of
CC	mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC	treating injuries to vascular tissue, promoting cell attachment and
CC	migration, ex vivo cell therapy, improving the biocompatibility of
CC	medical devices, and preparing improved cell culture devices and media.
CC	Laminin 8 is also useful for promoting re-endothelialisation at the site
CC	of vascular injuries, improving the take of grafts, improving the
CC	biocompatibility of medical devices, treating neural injuries (neural
CC	regeneration), regulating angiogenesis, and promoting cell attachment and
CC	migration
XX	
SQ	Sequence 1572 AA;
	Query Match 98.1%; Score 8527; DB 3; Length 1572;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	34 AMDECADEGRRCORCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGTSCHLCDAG 93
Db	1 AMDECADEGRRCORCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTGTSCHLCDAG 60
Qy	94 QOHLQGAALFTDYNQADFTWQSOOTMLAGVQPNISLTLHLGKAPDITVRLKFTS 153
Db	61 QOHLQGAALFTDYNQADFTWQSOOTMLAGVQPNISLTLHLGKAPDITVRLKFTS 120
Qy	154 RPESFAIYKRETRDGPWIPQYISGSCENTYSXANRGTINTGDEQOALCTDEFSDISPL 213
Db	121 RPESFAIYKRETRDGPWIPQYISGSCENTYSXANRGTINTGDEQOALCTDEFSDISPL 180
Qy	214 TGGNVAESTLEGPSAYFNPNFVQLQWVTATDIRVTLNRLTFGEVNDPKVLSYYY 273
Db	181 TGGNVAESTLEGPSAYFNPNFVQLQWVTATDIRVTLNRLTFGEVNDPKVLSYYY 240
Qy	274 AISDFAVGGCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATARS 333
Db	241 AISDFAVGGCKNGHASECVKNEFDKLMCNCKHNTYGVDCCKLPFFNDRPWRATARS 300
Qy	334 ASECLPCDCNCRGQECYFDELVRSTGHGCHTNCRDNDTGAKCERENFRPLGNTEAC 393
Db	301 ASECLPCDCNCRGQECYFDELVRSTGHGCHTNCRDNDTGAKCERENFRPLGNTEAC 360
Qy	394 SPCHSPVGSISTOCDSYGRCSCKPVGMDKCDRCOPGFHSLTEAGRCSCDPSGSTDE 453
Db	361 SPCHSPVGSISTOCDSYGRCSCKPVGMDKCDRCOPGFHSLTEAGRCSCDPSGSTDE 420
Qy	454 CNVETGRVCVKNVEGFCNCRKPGFFNLESSNPKGCTPCFCGHSVCTNAVGVSVYDI 513
Db	421 CNVETGRVCVKNVEGFCNCRKPGFFNLESSNPKGCTPCFCGHSVCTNAVGVSVYDI 480
Qy	514 SSTQIDEDGWRVQRDGSSEASLEWSSDRQYIAVISDSYPRYFIAPVKFLGNQVLSYGQ 573
Db	481 SSTQIDEDGWRVQRDGSSEASLEWSSDRQYIAVISDSYPRYFIAPVKFLGNQVLSYGQ 540
Qy	574 NLSFSFRVDRDRLSADLVLGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 633
Db	541 NLSFSFRVDRDRLSADLVLGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600
Qy	634 RPALSPREFQKLLNLSIKIRGYISRSAGYLDVTLQSRPQGPVATWVESCTCPVG 693
Db	601 RPALSPREFQKLLNLSIKIRGYISRSAGYLDVTLQSRPQGPVATWVESCTCPVG 660
Qy	694 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 753
Db	661 YGGQFCETCLPGYRRETPSLGYPSPCVLCTCNHSETCDPETGVCDNRDNTAGPHCEKCS 720
Qy	754 DGYVGDSTLGTSSDCQPCPCGGSSCAIVPKTEWVCTHCTGTAGRCCLCDGDFGDP 813
Db	721 DGYVGDSTLGTSSDCQPCPCGGSSCAIVPKTEWVCTHCTGTAGRCCLCDGDFGDP 780
Qy	814 LGSNGPVLRCPCQCNNDNIDPNAVGNCRNLGTGCKLCIYNTAGFYCDRCCKEGFGNPLAP 873
Db	781 LGSNGPVLRCPCQCNNDNIDPNAVGNCRNLGTGCKLCIYNTAGFYCDRCCKEGFGNPLAP 840

Qy	874 NPADKCKACACNVTGTVQOQSSCHPVTGQCOCPLPHVSGRDGCTCDPGYNNLQSGGCERCD 933
Db	841 NPADKCKACACNVTGTVQOQSSCHPVTGQCOCPLPHVSGRDGCTCDPGYNNLQSGGCERCD 900
Qy	934 CHALGSTNGQCDINTGQCECPQGITGQHCRCRTNHPFGPEGCKPCDCHHESLSLOCK 993
Db	901 CHALGSTNGQCDINTGQCECPQGITGQHCRCRTNHPFGPEGCKPCDCHHESLSLOCK 960
Qy	994 DDGRCECREGFGVNRCDQCEENFYFNSWPGCECPACRYLVKDAAEHVKLQLESLI 1053
Db	961 DDGRCECREGFGVNRCDQCEENFYFNSWPGCECPACRYLVKDAAEHVKLQLESLI 1020
Qy	1054 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAGVQKVDQNDLMDRLQRVNSSLHSQISR 1113
Db	1021 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAGVQKVDQNDLMDRLQRVNSSLHSQISR 1080
Qy	1114 LQNTNTEETGIIAEARSARVESTEQIIEIASRELEKAKMAANVSITQPESTCEPNMT 1173
Db	1081 LQNTNTEETGIIAEARSARVESTEQIIEIASRELEKAKMAANVSITQPESTCEPNMT 1140
Qy	1174 LLAEEARLAEHRHQEADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIEELNRKYE 1233
Db	1141 LLAEEARLAEHRHQEADDIVRVAKTANETSAEAYNLLRLTAGENQTALEIEELNRKYE 1200
Qy	1234 QAKNISQDLEKQAAVHHEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1293
Db	1201 QAKNISQDLEKQAAVHHEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLD 1260
Qy	1294 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLARADAAKALAEAAKGR 1353
Db	1261 RLIDQKLKDYEDLREDMRGKEHEVKNLLEKGAEQQTADQLARADAAKALAEAAKGR 1320
Qy	1354 STLQANDILNLKDFRRVNDKNTAABEALRRTPAINRTIAEANEXTREAQALGNAAA 1413
Db	1321 STLQANDILNLKDFRRVNDKNTAABEALRRTPAINRTIAEANEXTREAQALGNAAA 1380
Qy	1414 DATEAKNKAHEAERIASAAQGNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANELKR 1473
Db	1381 DATEAKNKAHEAERIASAAQGNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEANELKR 1440
Qy	1474 QDDADQDMMAGWASQAQAEALNARKXSVSSLLSOLNLLDQLDQDLYDLNKLNE 1533
Db	1441 QDDADQDMMAGWASQAQAEALNARKXSVSSLLSOLNLLDQLDQDLYDLNKLNE 1500
Qy	1534 IEGSLINKAKDBMKASDLDRKVSLESEARKQEAAMNDYNRDIAEIIKDHNLEDIKKTLP 1593
Db	1501 IEGSLINKAKDBMKASDLDRKVSLESEARKQEAAMNDYNRDIAEIIKDHNLEDIKKTLP 1560
Qy	1594 TGCFTNTPSIEKP 1605
Db	1561 TGCFTNTPSIEKP 1572

RESULT 7

ABB81597	ABB81597 standard; protein; 1572 AA.
ID	ABB81597
XX	
AC	ABB81597;
XX	
DT	19-SEP-2002 (first entry)
XX	
DE	Mouse laminin 10 third chain protein sequence SEQ ID NO:20.
XX	
KW	Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW	tissue repair development; laminin; healing; vascular tissue;
KW	re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW	proliferation; migration.
XX	
OS	Mus musculus.
XX	
PN	WO200250111-A2.
XX	

27-JUN-2002.  
21-DEC-2001; 2001WO-US051035.  
21-DEC-2000; 2000US-0257449P.  
28-MAR-2001; 2001US-0279282P.  
13-NOV-2001; 2001US-00279282.  
(BIOS-) BIOSTRATUM INC.  
Tryggvason K, Doi M, Thyboll J;  
WPI; 2002-557650/59.  
N-PSDB; AB072915.  
New human laminin-10 proteins, useful for accelerating the healing of  
vascular tissue, improving the biocompatibility of grafts, or for  
promoting re-endothelialization at the site of vascular injuries.  
Claim 9; Page 204-209; 231pp; English.  
The present invention describes human laminin alpha 5. Also described is  
an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are  
useful in maintaining cell/tissue phenotype as well as promoting cell  
growth and differentiation in tissue repair development. Specifically,  
laminin 10 can be used for accelerating the healing injuries of vascular  
tissue, improving the biocompatibility of grafts useful for treating such  
injuries, and promoting re-endothelialisation at the site of vascular  
injuries, and promote cell attachment and subsequent cell stasis,  
proliferation, differentiation, and/or migration. The present sequence  
represents a third chain protein of laminin 10, from the present  
invention  
Sequence 1572 AA;  
Query Match 98.1%; Score 8527; DB 5; Length 1572;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
34 AMDECADEGRPORCHPEFNAAFNVVATNTCTGTPPEYCVQGTGVTGTSCHLCDAG 93  
1 AMDECADEGRPORCHPEFNAAFNVVATNTCTGTPPEYCVQGTGVTGTSCHLCDAG 60  
94 QOHLQGAFLTDYNNQADTTWQSTMLAGVOYFNSINLTLHLGKAFDITVRLKFTHS 153  
61 QOHLQGAFLTDYNNQADTTWQSTMLAGVOYFNSINLTLHLGKAFDITVRLKFTHS 120  
154 RPESFAIYKRTREDDGPIWPIYQYSGSCENTYSKANRGFTTGGDEQQALCTDEFSDISPL 213  
121 RPESFAIYKRTREDDGPIWPIYQYSGSCENTYSKANRGFTTGGDEQQALCTDEFSDISPL 180  
214 TGENVAFSTLEGPSAYNFDSNPVQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 273  
181 TGENVAFSTLEGPSAYNFDSNPVQEWVTATDIRVTNLRLNTFGDEVNDPKVLKSYYY 240  
274 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATABS 333  
241 AISDFAVGGRCCKNGHASECVKNEFDKLMCNCKHNTYGVDCBKCLPFFNDRPWRATABS 300  
334 ASECLPCDNGRSOEYFDPYELVYSTGHGCHTNCEDNTDGAACRCRNFRLGNTEAC 393  
301 ASECLPCDNGRSOEYFDPYELVYSTGHGCHTNCEDNTDGAACRCRNFRLGNTEAC 360  
394 SPCHSPVGSLSLTCQDSYGRSCCKPGVMGDKDRCCQPGFHSLTEACRSCDPSGSTDE 453  
361 SPCHSPVGSLSLTCQDSYGRSCCKPGVMGDKDRCCQPGFHSLTEACRSCDPSGSTDE 420  
454 CNVETGRVCVKDNVEGFNCERCKPGFPNLESNPKGCTPCFCGHSSVCTNAGSVYDI 513  
421 CNVETGRVCVKDNVEGFNCERCKPGFPNLESNPKGCTPCFCGHSSVCTNAGSVYDI 480  
514 SSTFQIDEDGWRVEQRDGESEASLEWSSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQG 573

481 SSTFQIDEDGWRVEQRDGESEASLEWSSDRQYIAVISDSYFPFYFIAPVKFLGNQVLSYQG 540  
574 NLSFSPVDRDRRLSAEDLVLEGAGLRVSVPLTAQNSYFSETTVKYIFRLHEATDYPW 633  
541 NLSFSPVDRDRRLSAEDLVLEGAGLRVSVPLTAQNSYFSETTVKYIFRLHEATDYPW 600  
634 RPLSPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAARPGVGPATWVESCTCPVG 693  
601 RPLSPPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQSAARPGVGPATWVESCTCPVG 660  
694 YGGOFCECTCLPGYHRETPSLGYPSPCVLCTCNHSETCDPETGVCDCRDMTAPHCEKCS 753  
661 YGGOFCECTCLPGYHRETPSLGYPSPCVLCTCNHSETCDPETGVCDCRDMTAPHCEKCS 720  
754 DGYGDTLGTSSDCQPCPCPGSSCAIVPKTKXVCTHCTPTGTAGKRCBLCDGDFGDP 813  
721 DGYGDTLGTSSDCQPCPCPGSSCAIVPKTKXVCTHCTPTGTAGKRCBLCDGDFGDP 780  
814 LGSNGPVRLCEPCOCNDNIDPNVAGNCNRLTGELCKCIYNTAGFYCDRCKEGFGNPLAP 873  
781 LGSNGPVRLCEPCOCNDNIDPNVAGNCNRLTGELCKCIYNTAGFYCDRCKEGFGNPLAP 840  
874 NPADKCKACACNYGTVOQSSCNPVTCQCCLPHVSGRDCGTCDPGYNNLQSGGCRCD 933  
841 NPADKCKACACNYGTVOQSSCNPVTCQCCLPHVSGRDCGTCDPGYNNLQSGGCRCD 900  
934 CHALGSTNGQCDINTGQCEQCPGITHGHCRCETNHFPGPEGCKPCDCHHESLSLOCK 993  
901 CHALGSTNGQCDINTGQCEQCPGITHGHCRCETNHFPGPEGCKPCDCHHESLSLOCK 960  
994 DDGCECREGFGVGNRCQCESENYFYNRSWPCQPCACRYLRVLDKAAEHVRVQLQLESLE 1053  
961 DDGCECREGFGVGNRCQCESENYFYNRSWPCQPCACRYLRVLDKAAEHVRVQLQLESLE 1020  
1054 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAEVQVDQDNLMRLQRVNSSLHSQISR 1113  
1021 ANLGTGDDMTDQAFEDRLKEAREVTDLLREAEVQVDQDNLMRLQRVNSSLHSQISR 1080  
1114 LQNTNRTIEETGILAEARSRVSTEOLIEIASRELEKAKAAVNSITQPESTGEPPNMT 1173  
1081 LQNTNRTIEETGILAEARSRVSTEOLIEIASRELEKAKAAVNSITQPESTGEPPNMT 1140  
1174 LLAEARLAEHRKQADDIRVAKTANETSABAYNLLRLTAGENOTALIEBELNRKYE 1233  
1141 LLAEARLAEHRKQADDIRVAKTANETSABAYNLLRLTAGENOTALIEBELNRKYE 1200  
1234 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEANKI KKEAADLD 1293  
1201 QAKNISQDLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALEANEANKI KKEAADLD 1260  
1294 RLIDQKLKDYEDLREDMRGHEHEVNNLEKGAEQQTADQLLAPADAALAEBAAKKR 1353  
1261 RLIDQKLKDYEDLREDMRGHEHEVNNLEKGAEQQTADQLLAPADAALAEBAAKKR 1320  
1354 STLQANDILNNLKDFRRVNDKNTAAEALRIPAINRTIAEANETRAQALGNAAA 1413  
1321 STLQANDILNNLKDFRRVNDKNTAAEALRIPAINRTIAEANETRAQALGNAAA 1380  
1414 DATEAKNKAHEAERIASAAQKNATSTKADAEFTFGEVTDLDNEVNGMLRQLEAEANELKR 1473  
1381 DATEAKNKAHEAERIASAAQKNATSTKADAEFTFGEVTDLDNEVNGMLRQLEAEANELKR 1440  
1474 QDDADQDMMAGVASQAQAEALNARKAKNSVSSLLSQNLNLLDQGLDQDVTDLNKLNE 1533  
1441 QDDADQDMMAGVASQAQAEALNARKAKNSVSSLLSQNLNLLDQGLDQDVTDLNKLNE 1500  
1534 IEGSLINKAKDEMKASDLDRKVSLESEARKQEAALIMDYNRDIAEIIKDHNLEDIKKTLTLP 1593  
1501 IEGSLINKAKDEMKASDLDRKVSLESEARKQEAALIMDYNRDIAEIIKDHNLEDIKKTLTLP 1560  
1594 TGCFTNTSIEKP 1605  
1561 TGCFTNTSIEKP 1572





```
QY 1138 TEQIETIASRELEKAKM--AANVSITQPESTGEPNNMTLLAEAEARLARHRHQEADDIVRV 1196
Db 1141 TERLIETIASRELEKAKVAANVSITQPESTGEPNNMTLLAEAEARLARHRHQEADDIVRV 1200
QY 1197 AKTANETSAAEAYNLLRLTAGENOTALIEELNRYEQAKNISOLEKQKQARVHEBAKRA 1256
Db 1201 AKTANDTSTAYNLLRLTAGENOTALIEELNRYEQAKNISOLEKQKQARVHEBAKRA 1260
QY 1257 GDKAVEIYASVAQTFVDSALENEANKIKKEAADLRLIDOKLKDYEDLREDNRGKHEHE 1316
Db 1261 GDKAVEIYASVAQSPDSLENEANNIKMEAEENLEQLIDOKLKDYEDLREDNRGKHELE 1320
QY 1317 VKNLEKGAQOQTADQLARADAKALAEAAKKGSTLQEAANDILNLIKDPDRRYNDN 1376
Db 1321 VKNLEKGTQQTADQLARADAKALAEAAKKGRTLQEAANDILNLIKDPDRRYNDN 1380
QY 1377 KTAAEALRIRIPAINRTIAEANEKTRQAQLGNAADATEAKNKAHEAEERIASAAQKNA 1436
Db 1381 KTAAEALRKIPAINOTITEANEKTRQAQALGSAADATEAKNKAHEAEERIASAVQKNA 1440
QY 1437 TSTKADAERTTGEVTDLDNEVNGMLRQLEEAENELKPKQDDADQDMMWAGMASQAQEA 1496
Db 1441 TSTKAEARTTFAEVTDLNNEVNNMLKQLEAEKELKPKQDDADQDMMWAGMASQAQEA 1500
QY 1497 INAKKAKNSVSLSQLNNLLDQGLDVTDLNKLNEIEGSLNKADEMKAASDLDRKVS 1556
Db 1501 INAKKAKNSVTSLSIINDLEQLGLDVTDLNKLNEIEGLTNKAKDEMKVSDLDLRKVS 1560
QY 1557 LESEARKQEAAMYNDRIBAHIIKDIHLEDKITLPTGCNTPSIEKP 1605
Db 1561 LENEAKQEAAMYNDRIDIEBKDIRNLEDIRKTLPSGCNTPSIEKP 1609

RESULT 9
AAB48452
ID AAB48452 standard; protein; 1609 AA.
XX
AC AAB48452;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 8 polypeptide, SEQ ID NO: 22.
XX
KW Human; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO2000066732-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOTRATUM INC.
XX
PI Korteemaa J, Tryggvason K;
XX
DR WPI; 2000-687539/67.
DR DR-ESDB; AAC83713.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 202-207; 245pp; English.
```

```
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1609 AA;
Query Match 93.7%; Score 8148; DB 3; Length 1609;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;
QY 1 MTGGGRAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPORCMPEFNAAAFN 58
Db 1 MRGSHRAAPALPRGELWPLVLAALAAAAGCAQAMDECTDEGGRPORCMPEFNAAAFN 60
QY 59 VTVVANTCTGTPEEYCVGTGVTGKTSCHLCDAGQLOHGAFLTDYNNQADTTWQS 118
Db 61 VTVVANTCTGTPEEYCVGTGVTGKTSCHLCDAGQLOHGAFLTDYNNQADTTWQS 120
QY 119 QTMLAGOVQVPSINLTLLHKGAFDITYYRLKPHTRSRPSFALYKRTREDGPMIPQYYS 178
Db 121 QTMLAGOVQVPSINLTLLHKGAFDITYYRLKPHTRSRPSFALYKRTREDGPMIPQYYS 180
QY 179 SCENTYSKANRGFIRTGDEQALCTDFSDISPLTGGNVAFTLGGPSAYNFNSPVL 238
Db 181 SCENTYSKANRGFIRTGDEQALCTDFSDISPLTGGNVAFTLGGPSAYNFNSPVL 240
QY 239 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLSYYVAISDFAVGGRCKNGHASECVKNEF 298
Db 241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLSYYVAISDFAVGGRCKNGHASECMKNEF 300
QY 299 DKLMCNCKHNTYGVDCCKLPFNDRPMRRATAESASECLPCDCKGRSOECYFDPDELYS 358
Db 301 DKLVCMCKRNTYGVDCCKLPFNDRPMRRATAESASECLPCDCKGRSOECYFDPDELYS 360
QY 359 TGHGGHCTNCRDNTDGAHCERCENFRRLGNTEACSPCHSPVGLSLTQCDSYGRCSCKP 418
Db 361 TGHGGHCTNCRDNTDGAHCERCENFRRLGNTEACSPCHSPVGLSLTQCDSYGRCSCKP 420
QY 419 GYMGDKCDRCQPGPHSLTEAGCRPCSDPSGSDSCNVETGRCVKDNGVEGNCERCKPG 478
Db 421 GYMGDKCDRCQPGPHSLTEAGCRPCSDPSGSDSCNVETGRCVKDNGVEGNCERCKPG 480
QY 479 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVDISSTFQIDEDGWRVQRDGSSEASLEW 538
Db 481 FFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVSISSTFQIDEDGWRVQRDGSSEASLEW 540
QY 539 SSDRQYIAVISDSYFPRYPFIAPVKFLGNQVLSYGNQLSFSFRVDRDRRLSADLVLEGA 598
Db 541 SSERODIAVISDSYFPRYPFIAPAKFLGQVLSYGNQLSFSFRVDRDRRLSADLVLEGA 600
QY 599 GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALSPPEFOKLLNLTSLIKIRTY 658
Db 601 GLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPWRPALTPPEFOKLLNLTSLIKIRTY 660
QY 659 SERSAGYLDVTLQSGARPQGPVATWVESCTCPVYGGQFCETCLPGVRRTPPSLGPYSP 718
Db 661 SERSAGYLDVTLQSGARPQGPVATWVESCTCPVYGGQFCETCLPGVRRTPPSLGPYSP 720
QY 719 CVLCTCNHGSERFDEBTGVDCRDNTAGPHCEKSDGYVGDSTLGTSSDCQPCPCPGSS 778
Db 721 CVLCAHGSERFDEBTGVDCRDNTAGPHCEKSDGYVGDSTLGTSSDCQPCPCPGSS 780
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QY 779 CAIYVKTKEVVTCHPTGTAGRCCELCDGDFGDPGLSGNPGVRLCRQCQNDNIDPNAV 838  
 Db 781 CAVVPTKKEVVTCHPTGTAGRCCELCDGDFGDPGLSGNPGVRLCRQCQSDNIDPNAV 840  
 QY 839 NCNRLTGCECLKCIYNTAGFYCDRCKEGFFGNPLAPNADCKACACN-YGTVOQSSCNP 897  
 Db 841 NCNRLTGCECLKCIYNTAGFYCDRCKEGFFGNPLAPNADCKACACNPGYTMKQSSCNP 900  
 QY 898 VTGQOCLPHVSGRDCGTCDFGYNLSGQCECERCDCHALGSTNGQCDIRTGQCECOPGI 957  
 Db 901 VTGQOCLPHVSGRDCGTCDFGYNLSGQCECERCDCHALGSTNGQCDIRTGQCECOPGI 960  
 QY 958 TGQHCERTNHFGPGGCKPCCHHSGSLQCKDDGRCEGFGVGNRCDCQCEENYF 1017  
 Db 961 TGQHCERTNHFGPGGCKPCCHHSGSLQCKDDGRCEGFGVGNRCDCQCEENYF 1020  
 QY 1018 YNRSWPGQCECPACVRLVKDAAEHVVKVQLESLIANLGTGDDMTDQAFEDLKEAER 1077  
 Db 1021 YNRSWPGQCECPACVRLVKDAAEHVVKVQLESLIANLGTGDDMTDQAFEDLKEAER 1080  
 QY 1078 EVDTLLEAQQEVDQNDLRLQVNSLSHQSLSQSLRNIRNTTETGILAEARSRVES 1137  
 Db 1081 EVDTLLEAQQEVDQNDLRLQVNSLSHQSLSQSLRNIRNTTETGILAEARSRVES 1140  
 QY 1138 TEQLEIASRELEKAKM-AANVSTQPESTGEPNNMTLLAEARLAEERHKKQEAADDIVRV 1196  
 Db 1141 TEQLEIASRELEKAKM-AANVSTQPESTGEPNNMTLLAEARLAEERHKKQEAADDIVRV 1200  
 QY 1197 AKTANETSABAVNLLRLTAGENOTALBIEELNKYEQAKNISQLEKQAAVHEERAKRA 1256  
 Db 1201 AKTANETSABAVNLLRLTAGENOTALBIEELNKYEQAKNISQLEKQAAVHEERAKRA 1260  
 QY 1257 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316  
 Db 1261 GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1320  
 QY 1317 VKNLEKKAQOATDOLLARADAKALAEAAKGRSTLOEANDILNNLKQDPRVNDN 1376  
 Db 1321 VKNLEKKAQOATDOLLARADAKALAEAAKGRSTLOEANDILNNLKQDPRVNDN 1380  
 QY 1377 KTAEEALRRIPAINRTIAENETREQAALGNAADATEAKNKAHEAERIASAAQKNA 1436  
 Db 1381 KTAEEALRRIPAINRTIAENETREQAALGNAADATEAKNKAHEAERIASAAQKNA 1440  
 QY 1437 TSTKADARTGEVTDLDNEVNGMLRQLEBAENELKQDDADODMMAGASQAQAEAE 1496  
 Db 1441 TSTKADARTGEVTDLDNEVNGMLRQLEBAENELKQDDADODMMAGASQAQAEAE 1500  
 QY 1497 LNARAKNSVSLLSQNLNLLDQLGQDVTDLNKLNEIEGSLINKAKDEMKASDLDRKVS 1556  
 Db 1501 LNARAKNSVSLLSQNLNLLDQLGQDVTDLNKLNEIEGSLINKAKDEMKASDLDRKVS 1560  
 QY 1557 LESEARKQEAALMDYNRDIAEIIKDIHNELEDIKTLPTGCFNTPSIEKP 1605  
 Db 1561 LESEARKQEAALMDYNRDIAEIIKDIHNELEDIKTLPTGCFNTPSIEKP 1609

RESULT 10  
 ABB81594  
 ID ABB81594 standard; protein; 1609 AA.  
 XX ABB81594;  
 AC ABB81594;  
 XX ABB81594;  
 DT 19-SEP-2002 (first entry)  
 XX Human laminin 10 third chain protein sequence SEQ ID NO:14.  
 DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
 KW tissue repair development; laminin; healing; vascular tissue;  
 KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
 KW proliferation; migration.

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..33  
 FT /label= signal  
 FT Protein 34..1609  
 FT /label= laminin\_10\_third\_chain  
 XX WO200250111-A2.  
 PN 27-JUN-2002.  
 XX 21-DEC-2001; 2001WO-US051035.  
 XX 21-DEC-2000; 2000US-0257449P.  
 PR 28-MAR-2001; 2001US-0279282P.  
 PR 13-NOV-2001; 2001US-00279282.  
 XX (BIOS-) BIOSTRATUM INC.  
 PA Trygsvason K, Doi M, Thyboll J;  
 PI WPI; 2002-557650/59.  
 XX N-PSDB; ABQ72912.  
 DR New human laminin-10 proteins, useful for accelerating the healing of  
 PT vascular tissue, improving the biocompatibility of grafts, or for  
 FT promoting re-endothelialization at the site of vascular injuries.  
 XX Claim 9; Page 165-170; 231pp; English.  
 CC The present invention describes human laminin alpha 5. Also described is  
 CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
 CC useful in maintaining cell/tissue phenotype as well as promoting cell  
 CC growth and differentiation in tissue repair development. Specifically,  
 CC laminin 10 can be used for accelerating the healing of vascular  
 CC tissue, improving the biocompatibility of grafts useful for treating such  
 CC injuries, for promoting re-endothelialisation at the site of vascular  
 CC injuries, and promote cell attachment and subsequent cell stasis,  
 CC proliferation, differentiation, and/or migration. The present sequence  
 CC represents a third chain protein of laminin 10, from the present  
 CC invention  
 XX Sequence 1609 AA;  
 SQ Query Match 93.7%; Score 8148; DB 5; Length 1609;  
 Best Local Similarity 92.8%; Pred. No. 0;  
 Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

QY 1 MTGGGAAALALQPRGLWPLLAFL--AAVAGCVRAAMDECADEGGRCORCMPEFVNAAPN 58  
 Db 1 MRGSHRAAPALPRGRLLWPLAVLAAAAAAGCAQAAAMDECTDEGGRCORCMPEFVNAAPN 60  
 QY 59 VTVVATNTCGTPPEEYCVQTVGTGVTGKCHLDCAGQHLQHGAAFLTDVNOADTTWQS 118  
 Db 61 VTVVATNTCGTPPEEYCVQTVGTGVTGKCHLDCAGQHLQHGAAFLTDVNOADTTWQS 120  
 QY 119 QTMLAGVQVYVNSINLTLLHKGAFDITYVRLKFTSRPESFAYIKYKTRDGPWIPYQYVSG 178  
 Db 121 QTMLAGVQVYVNSINLTLLHKGAFDITYVRLKFTSRPESFAYIKYKTRDGPWIPYQYVSG 180  
 QY 179 SCENTYSKANRGIPTGGDEQOALCTDEPSDISPLTGGVAVSTLEGPSAYNFNSPVL 238  
 Db 181 SCENTYSKANRGIPTGGDEQOALCTDEPSDISPLTGGVAVSTLEGPSAYNFNSPVL 240  
 QY 239 QEWVATDTRVTLNRLNTGDEVFNDPKVLKSYVYVAISDFAVGGRCKNGHASECVKNEF 298  
 Db 241 QEWVATDTRVTLNRLNTGDEVFNDPKVLKSYVYVAISDFAVGGRCKNGHASECVKNEF 300  
 QY 299 DKLMCKNKNTYGVDCCKLPFFNDRPWRATASASECLPCDCNGRSCQCYFDELYRS 358  
 Db 301 DKLMCKNKNTYGVDCCKLPFFNDRPWRATASASECLPCDCNGRSCQCYFDELYRS 360

QY	359	TGHHGCTNCRDNTGAKCERCENPRLGNTACSPCHSPVGSLSSTQCDSTGRCCKP	418
Db	361	TGHHGCTNCRDNTGAKCERCENPRLGNTACSPCHSPVGSLSSTQCDSTGRCCKP	420
QY	419	GVNGDKDRCPQGFHSITAGCPCSDPSGSTDECNVETGRVCVKDNVEGNCERCKPG	478
Db	421	GVNGDKDRCPQGFHSITAGCPCSDPSGSTDECNVETGRVCVKDNVEGNCERCKPG	480
QY	479	FFNLESNPXGCTPCFCFGHSSVCTNAVGSVYD1SSTFQIDBDGWRVQRDSEASLEW	538
Db	481	FFNLESNPXGCTPCFCFGHSSVCTNAVGSVYD1SSTFQIDBDGWRVQRDSEASLEW	540
QY	539	SSROQYIAVSDSYFFRYFIAPVKFLGNVLVYGNLSFSPVRDRTLSAEDLVLEGA	598
Db	541	SSROQYIAVSDSYFFRYFIAPVKFLGNVLVYGNLSFSPVRDRTLSAEDLVLEGA	600
QY	599	GLRVSPLIAQNSYPSSETTKVIFRLHEATDTPWRPALSPFFQKLLNNLTSIKIRGT	658
Db	601	GLRVSPLIAQNSYPSSETTKVIFRLHEATDTPWRPALSPFFQKLLNNLTSIKIRGT	660
QY	659	SERAGYLDVTLQSRAPGVPATWVESCCTPVGYGGQFCETCLPGYRRETSLGYPSP	718
Db	661	SERAGYLDVTLQSRAPGVPATWVESCCTPVGYGGQFCETCLPGYRRETSLGYPSP	720
QY	719	CVLCTNGHSETCPETGVCDRNTAGPHCEKSDGYGDSITLGTSSDCQPCPCGGSS	778
Db	721	CVLCTNGHSETCPETGVCDRNTAGPHCEKSDGYGDSITLGTSSDCQPCPCGGSS	780
QY	779	CAIVPKTKVYVCHTCTGTAGKCELDGDFGDPGLSGNPGVRLRCPQCNDNIDNAV	838
Db	781	CAIVPKTKVYVCHTCTGTAGKCELDGDFGDPGLSGNPGVRLRCPQCNDNIDNAV	840
QY	839	NCNRLTGECLKCIYNTAGFYCDRCCKEFGNPLAPNADKCKACACN-YGTVOQOQSCNP	897
Db	841	NCNRLTGECLKCIYNTAGFYCDRCCKEFGNPLAPNADKCKACNPNYGTMTQOQSCNP	900
QY	898	VTGQCQLPHVSGRDCGTCPGYYNLQSGGGERCDCHALGSTNGQCDITGTGCECQPGI	957
Db	901	VTGQCQLPHVSGRDCGTCPGYYNLQSGGGERCDCHALGSTNGQCDITGTGCECQPGI	960
QY	958	TGQRCERCENHFGFEGCKPCCHHSGSLQCKDDGRCECEGFGVGNRCQCCENYF	1017
Db	961	TGQRCERCENHFGFEGCKPCCHHSGSLQCKDDGRCECEGFGVGNRCQCCENYF	1020
QY	1018	YNRSWPCQCECPACRYLVKQAAEHVKLQLESILIANLGTGDDMTDQAFEDRLKEAR	1077
Db	1021	YNRSWPCQCECPACRYLVKQAAEHVKLQLESILIANLGTGDDMTDQAFEDRLKEAR	1080
QY	1078	EVTDLLEAQVQKVDQNLMDRLQVNSLSHQISRLQNTINTIETGILAEARSVES	1137
Db	1081	EVTDLLEAQVQKVDQNLMDRLQVNSLSHQISRLQNTINTIETGILAEARSVES	1140
QY	1138	TEQLIEIASRELEKAXV-AANVSTQPESTGEPNNMTLLAEAPRLAEHKKQADDIVRV	1196
Db	1141	TEQLIEIASRELEKAXV-AANVSTQPESTGEPNNMTLLAEAPRLAEHKKQADDIVRV	1200
QY	1197	AKTANETSAAEYNLLRTLAGENOTALEIBELNKYFOAKNISQDLKQAAHVHEAKRA	1256
Db	1201	AKTANETSAAEYNLLRTLAGENOTALEIBELNKYFOAKNISQDLKQAAHVHEAKRA	1260
QY	1257	GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADRLIDOKLYEDLREDVRGKEHE	1316
Db	1261	GDKAVEIYASVAQLTPVDSEALENEANKIKKEAADRLIDOKLYEDLREDVRGKEHE	1320
QY	1317	VKNLLEKGAQEQQTADQLLAPADAALAEFAAKKGSTIQEANDIILNNIKOTDRRVNDN	1376
Db	1321	VKNLLEKGAQEQQTADQLLAPADAALAEFAAKKGSTIQEANDIILNNIKOTDRRVNDN	1380
QY	1377	KTAAEEALRRIPALNRTIAENKXETREAQALGANAADATKAKNAHEERIASAOKNA	1436
Db	1381	KTAAEEALRRIPALNRTIAENKXETREAQALGANAADATKAKNAHEERIASAOKNA	1440
QY	1437	TSTRKADABRTFGEVTDLDNEVNGMLRLQLEAEENELKQDDADQDMMAGNASQAQAE	1496
Db	1441	TSTRKADABRTFGEVTDLDNEVNGMLRLQLEAEENELKQDDADQDMMAGNASQAQAE	1500
QY	1497	INARAKAKSVSLLSQNLNLDQLGOLDTVDLNKLNIEGSLNKADEMKAASDLDRKVS	1556
Db	1501	INARAKAKSVSLLSQNLNLDQLGOLDTVDLNKLNIEGSLNKADEMKAASDLDRKVS	1560
QY	1557	LESEARKQBAAIMDYNRDIAEIIKDHNLEDIKKTLPCTGCENTPSIEKP	1605
Db	1561	LESEARKQBAAIMDYNRDIAEIIKDHNLEDIKKTLPCTGCENTPSIEKP	1609
RESULT 11			
Db	ADC01887	ADC01887 standard; protein; 1609 AA.	
AC	ADC01887;		
DT	18-DEC-2003	(first entry)	
DE	Human laminin gamma 1 subunit.		
XX	Cytostatic; human; de; gene; laminin; tumour; laminin-x; beta3 subunit;		
KW	Gammal subunit; alpha4 subunit; angiogenesis.		
OS	Homo sapiens.		
XX	US2003103975-A1.		
PD	05-JUN-2003.		
PF	18-NOV-2002; 2002US-00299058.		
PR	03-NOV-1999; 99US-0163199P.		
PR	03-NOV-2000; 2000US-00706235.		
XX	(JONE/) JONES J C R.		
PA	(GONZ/) GONZALES M.		
PI	Jones JCR, Gonzales M;		
XX	WPI: 2003-755217/71.		
DR	N-PSDB; ADC01886.		
XX	Antigenic fragment of alpha4 laminin, useful for preparing a composition for treating tumor.		
PS	Disclosure; Page 42-46; 52pp; English.		
XX	The invention relates to an antigenic fragment of the human alpha4 laminin subunit appearing as ADC01881. Also included are a chimeric and/or fusion protein comprising the antigenic fragment, an antibody to the antigenic fragment, a cell line that produces the antibody, an isolated laminin complex (laminin-x, comprising an alpha4 subunit, a beta3 subunit or gammal subunit), modulating angiogenesis and a method of inducing tumours. The antigenic fragment of alpha4 laminin subunit is useful for preparing a composition (e.g. the antibody 2A3) for treating a tumour. The present sequence represents the human gamma 1 laminin subunit.		
SQ	Sequence 1609 AA;		
Query Match 93.7%; Score 8148; DB 7; Length 1609;			
Best Local Similarity 92.8%; Pred No. 0;			
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;			
QY	1	MTGGGAAALALQPRGLMPLLAVAL--AAVAGCVRAAMDECADEGGRCORCMPEFVNAAFN	58
Db	1	MRGSHRAAPALPRGLMPLLAVALAAAAAAGCAAMDECTDEGGRCORCMPEFVNAAFN	60
QY	59	VTVVATNTCGTTPPEYCYQVTGTGVTGKSHCLDCAQOHLQHGAAFLTDYNNQADTTWQS	118
Db	61	VTVVATNTCGTTPPEYCYQVTGTGVTGKSHCLDCAQOHLQHGAAFLTDYNNQADTTWQS	120

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QY 119 QTMAGVOVPNSINLTLLHKAFTDITYVRLKPHTSRPSFAIYKTRTREDGFWIPVQYYS 178
Db 121 QTMAGVOVPSSINLTLLHKAFTDITYVRLKPHTSRPSFAIYKTRTREDGFWIPVQYYS 180
QY 179 SCENTYSKANRGFIITGGDEQALCTDFFSDISPLTGGNVAFTSLTLEGRPSYAFNFDNSPVL 238
Db 181 SCENTYSKANRGFIITGGDEQALCTDFFSDISPLTGGNVAFTSLTLEGRPSYAFNFDNSPVL 240
QY 239 QEWVTATDTRVLTNLNLTFGDVFNDPKVLKSYIYAIISDFAVGGCKCNGHASECEKNEF 298
Db 241 QEWVTATDTRVLTNLNLTFGDVFNDPKVLKSYIYAIISDFAVGGCKCNGHASECEKNEF 300
QY 299 DKLMCNCKNTYGVDCXKCLPFNDRPWRRAFAESASECLPCDNGRQBOCYFDPPELYRS 358
Db 301 DKLMCNCKNTYGVDCXKCLPFNDRPWRRAFAESASECLPCDNGRQBOCYFDPPELYRS 360
QY 359 TGHGGHCTNCRDNTDGAECERENFRFLNGTEACSPCHSPVGSLSLTCQDSYGRCSCKP 418
Db 361 TGHGGHCTNCRDNTDGAECERENFRFLNGTEACSPCHSPVGSLSLTCQDSYGRCSCKP 420
QY 419 GVMGDKCDRCQPFHSLTBAECRPSGSDPSGSDTENVETGRVCCKNVGFCNCRCKPG 478
Db 421 GVMGDKCDRCQPFHSLTBAECRPSGSDPSGSDTENVETGRVCCKNVGFCNCRCKPG 480
QY 479 FNLSSNPKGCTPCFCFCHSSVCTNAVGYVYDTSSTFQIDEDGRVQORDGSASLEW 538
Db 481 FNLSSNPKGCTPCFCFCHSSVCTNAVGYVYDTSSTFQIDEDGRVQORDGSASLEW 540
QY 539 SSRQIVAVISDSYFPRYPIAPVKFLGNQVLSYGQNLSPFRVDRDRTRLSEDLVLLEGA 598
Db 541 SSRQIVAVISDSYFPRYPIAPVKFLGNQVLSYGQNLSPFRVDRDRTRLSEDLVLLEGA 600
QY 599 GLRVSVPLIAQNSYSESTVKYIPLHEATYPPRPALSPFEFOKLNNLTSIKIRTY 658
Db 601 GLRVSVPLIAQNSYSESTVKYIPLHEATYPPRPALSPFEFOKLNNLTSIKIRTY 660
QY 659 SERSAGYLDVLTQSRAPGVPATWVESCTCPVGYGQFCETCLPGYRRETSPISLPXSP 718
Db 661 SERSAGYLDVLTQSRAPGVPATWVESCTCPVGYGQFCETCLPGYRRETSPISLPXSP 720
QY 719 CVLCTCNHSETCDPBTGVCDNRDNTAGPHCKSCDGYGDTLGTSSDCQCPGCGSS 778
Db 721 CVLCTCNHSETCDPBTGVCDNRDNTAGPHCKSCDGYGDTLGTSSDCQCPGCGSS 780
QY 779 CATVPKTEWVCTHCTGTAGKCBELCDDGYFGDPLGNSGVPRLCRPCOCNNIDPNNAV 838
Db 781 CATVPKTEWVCTHCTGTAGKCBELCDDGYFGDPLGNSGVPRLCRPCOCNNIDPNNAV 840
QY 839 NCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACN-YGTVOQSSCNP 897
Db 841 NCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACN-PYGTWKQSSCNP 900
QY 898 VTGQCQCLPHVSGRDCGTCDPGYVNLQSGGECRCDCHALGSTNGOCDIRTCQCEQGI 957
Db 901 VTGQCQCLPHVSGRDCGTCDPGYVNLQSGGECRCDCHALGSTNGOCDIRTCQCEQGI 960
QY 958 TGHQRCERTNHFPGPEGCKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCQCENYF 1017
Db 961 TGHQRCERTNHFPGPEGCKPCDCHHEGSLSLQCKDDGRCCEGFGVGNRCDCQCENYF 1020
QY 1018 YNRSWPGQCEPCACRYLKVDAEHRVKLQELSLIANLGTGDDMVYDQAFEDRLKEAR 1077
Db 1021 YNRSWPGQCEPCACRYLKVDAEHRVKLQELSLIANLGTGDDMVYDQAFEDRLKEAR 1080
QY 1078 EVTDLLREAGEVDVQNLMDRLQVRNSSLHSGISRLQINRTIETGILAEARSRVBS 1137
Db 1081 EVDMLLEAGVDVQNLMDRLQVRNSSLHSGISRLQINRTIETGILAEARSRVBS 1140
QY 1138 TEOLIEIASRELEKAKV-AANVSIPOESTGEGNNMTLLAEARLAEHRKQEADDIVRY 1196
Db 1141 TERLIEIASRELEKAKVAAANVSIPOESTGEGNNMTLLAEARLAEHRKQEADDIVRY 1200
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QY 1197 AKTANETSABAYNLLRTLAGENQTALEIEELNRYKYOAKNISQDLEKQAAVHEEAKRA 1256
Db 1201 AKTANDTSEAYNLLRTLAGENQTALEIEELNRYKYOAKNISQDLEKQAAVHEEAKRA 1260
QY 1257 GDKAVIYASVAQLTPVDSEALENEANKTKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316
Db 1261 GDKAVIYASVAQLSPDSETLENEANNIKMEAEINLEQLIDQKLKDYEDLREDMRGKELE 1320
QY 1317 VKNLLSKGKAEQOTADOLLARADAALAEBAKGRSTLOEANDILNNLKDFDRVNDN 1376
Db 1321 VKNLLSKGTEQOTADOLLARADAALAEBAKGRSTLOEANDILNNLKDFDRVNDN 1380
QY 1377 KTAAEALRRIPAINRTIAEANEKTRAEQALALCNAADAATEAKNVKAHEAERIASAAQKNA 1436
Db 1381 KTAAEALRRIPAINRTIAEANEKTRAEQALALCNAADAATEAKNVKAHEAERIASAAQKNA 1440
QY 1437 TSTKADAERTFGEVTDLDNEVGNMLQLEBAENELKRGQDDADODMMAGMASQAQAEAE 1496
Db 1441 TSTKADAERTFAEVTDLDNEVGNMLQLEBAENELKRGQDDADODMMAGMASQAQAEAE 1500
QY 1497 LNARKAKNSVSSLLSOLLNLLDQGLDQTDVLDNKLNEIGSLNKAKDEMKASDLDRKVS 1556
Db 1501 LNARKAKNSVSSLLSOLLNLLDQGLDQTDVLDNKLNEIGSLNKAKDEMKASDLDRKVS 1560
QY 1557 LESEARKQEAAMDYNRDIAEIIKQIHNLIEDIKKTLPTGCFNTPSIEKP 1605
Db 1561 LESEARKQEAAMDYNRDIAEIIKQIHNLIEDIKKTLPTGCFNTPSIEKP 1609

RESULT 12
AAB19803
ID AAB19803 standard; protein; 1617 AA.
XX
AC AAB19803;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
XX
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
KW degenerative muscle disorder; muscular dystrophy; cell therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..33 Location/Qualifiers
FT Protein 34..1609 /label= Signal_peptide
FT Peptide 1610..1617 /label= Mature_protein
FT Peptide 1610..1617 /label= FLAG
XX
PN WO200066730-A2.
XX
PD 09-NOV-2000.
XX
PP 28-APR-2000; 2000WO-US011378.
XX
PR 30-APR-1999; 99US-0131720P.
PR 15-JUN-1999; 99US-0139198P.
PR 12-JUL-1999; 99US-0143289P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Yurchenco P;
XX
DR WPI; 2000-687537/67.
DR N-PSDB; AAA88903.
XX
PT Purified laminin 2 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
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XX	Claim 5; Page 263-268; 305pp; English.	
XX	The present sequence is that of the gamma-1 chain of human laminin 2, with an additional C-terminal FLAG epitope, resulting from expression in transfected cells from mammalian expression vectors. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAB8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell regulation, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media	
XX	Sequence 1617 AA;	
SQ	Query Match 93.7%; Score 8148; DB 3; Length 1617; Best Local Similarity 92.8%; Pred. No. 0; Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;	
QY	1 MTGGRAALALQPRGLWPLAVL--AAVAGCVRAAMDECADEGRPQRCMPFVNAAFN 58	
DB	1 MRGSHRAAPALRPRGLWPLVLAALAAAGCAQAAMDECTDEGRPQRCMPFVNAAFN 60	
QY	59 VTVAATTCGTPPEEYCVQTVGVTKSCHLDAGQOHQGAFLTDVNNQADTTWMS 118	
DB	61 VTVAATTCGTPPEEYCVQTVGVTKSCHLDAGQPHLQGAFLTDVNNQADTTWMS 120	
QY	119 QTMLAGVQYFNSINLTLHGKAFDITVRLKFTSRPESFALYKRTREDGFWIPYQYSG 178	
DB	121 QTMLAGVQYFSSINLTLHGKAFDITVRLKFTSRPESFALYKRTREDGFWIPYQYSG 180	
QY	179 SCENTYKANRGFTRTGGDSQOALCTDFSDISPLTGCNVAFSTLEGRPSAYNFDSPLV 238	
DB	181 SCENTYKANRGFTRTGGDSQOALCTDFSDISPLTGCNVAFSTLEGRPSAYNFDSPLV 240	
QY	239 QEWTAIDIRVTNLNLTFGDEVFNDPKVLKSYIYAI SDPAVGRCCKNGHASECVKNEF 298	
DB	241 QEWTAIDIRVTNLNLTFGDEVFNDPKVLKSYIYAI SDPAVGRCCKNGHASECVKNEF 300	
QY	299 DKLMCNCKHNTYGVDCSKCLPFFNDRPWRRTAESASECLPCDCNGRSQECYFDPPELYRS 358	
DB	301 DKLVNCKHNTYGVDCSKCLPFFNDRPWRRTAESASECLPCDCNGRSQECYFDPPELYRS 360	
QY	359 TGHGCHCTCNDTGDGAKCERCENFFRLGNTEACSPCHSPVGSLSSTQCDSYGRCSCKP 418	
DB	361 TGHGCHCTCNDTGDGAKCERCENFFRLGNTEACSPCHSPVGSLSSTQCDSYGRCSCKP 420	
QY	419 GVMGDKCDRCQPGFHSLTEAGRCPCSDPGSGTDECNVETGRVCVKDNVEGFNCRCCKPG 478	
DB	421 GVMGDKCDRCQPGFHSLTEAGRCPCSDPGSGTDECNVETGRVCVKDNVEGFNCRCCKPG 480	
QY	479 FPNLESNPKGCTPCFCGHSSVCTNAGVSVYDISSTFOIDEDGWEVORDGSEASLEW 538	
DB	481 FPNLESNPKGCTPCFCGHSSVCTNAGVSVYDISSTFOIDEDGWEVORDGSEASLEW 540	
QY	539 SSDRQYIAVSDSYFFRYFAPVFLGNQVLSYQNLFSFVRVDRDRTRLSAEDLVLEGA 598	
DB	541 SSERQYIAVSDSYFFRYFAPVFLGNQVLSYQNLFSFVRVDRDRTRLSAEDLVLEGA 600	
QY	599 GLRVSVPLIAQGNYPSETTVKYIFRLHEATDYWRPALSPFFPQKLNNLTIKIRGTY 658	
DB	601 GLRVSVPLIAQGNYPSETTVKYIFRLHEATDYWRPALSPFFPQKLNNLTIKIRGTY 660	
QY	659 SERSAGYLDLDTLQSRPFGVPATWVESCTCPVGGYQFCETCLPYRRETSLPGYPSP 718	
DB	661 SERSAGYLDLDTLQSRPFGVPATWVESCTCPVGGYQFCETCLPYRRETSLPGYPSP 720	
QY	719 CVLCTCNHSHSTCDPETHGVCDNDTAGPHCEKCSGDIYDSTLGTSSDQCPQCPGSS 778	
DB	721 CVLCAHGHSTCDPETHGVCDNDTAGPHCEKCSGDIYDSTLGTSSDQCPQCPGSS 780	
QY	779 CAIVPKTEVVTCHPTGTGTAGRCLEDDGDFGDLPSNGPVLRCPCQCNNDNDPNAV 838	
DB	781 CAIVPKTEVVTCHPTGTGTAGRCLEDDGDFGDLPSNGPVLRCPCQCNNDNDPNAV 840	
QY	839 NCNRLTGBCLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACACN-YGTVOQSSCNP 897	
DB	841 NCNRLTGBCLKCIYNTAGFYCDRCKEGFFGNPLAPNADKCKACNCPYGTMTKQSSCNP 900	
QY	898 VTGQCCLPHVSGRCGTCDFGYNLSGQGCRCDCDHALGSTNGQCDIRTGQCECQPGI 957	
DB	901 VTGQCCLPHVSGRCGTCDFGYNLSGQGCRCDCDHALGSTNGQCDIRTGQCECQPGI 960	
QY	958 TGOHCERCETHVHFGPGPCGKPCDCHHGSLSLCKDGRCECEGFGVGNRCDCQENYF 1017	
DB	961 TGOHCERCETHVHFGPGPCGKPCDCHHGSLSLCKDGRCECEGFGVGNRCDCQENYF 1020	
QY	1018 YNRSWPGQCECPACYRLVVKDAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKBAER 1077	
DB	1021 YNRSWPGQCECPACYRLVVKDAEHRVKLQELSLIANLGTGDDMTDQAFEDRLKBAER 1080	
QY	1078 EYTDLLRRAQVQKVDQNLMDLQVNSLSHQSISRLQNIQNTIETGILAEARSVES 1137	
DB	1081 EYMDLLRRAQVQKVDQNLMDLQVNSLSHQSISRLQNIQNTIETGILAEARSVES 1140	
QY	1138 TEQLTETIASRELEKAKM-AANVSITQPESTGEPNNMTLLAEAEARLAEHRKQEAADDIVRV 1196	
DB	1141 TERLIEIASRELEKAKVAAANVSITQPESTGDPNNMTLLAEAEARLAEHRKQEAADDIVRV 1200	
QY	1197 AKTANETSABAYNLLRTLAGENQTALEIEBELNKRYQAKNISODLEKQAAARVHEAKRA 1256	
DB	1201 AKTANDTSTAYNLLRTLAGENQTALEIEBELNKRYQAKNISODLEKQAAARVHEAKRA 1260	
QY	1257 GDKAVEIIVASVAQLTPVDSEALENEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316	
DB	1261 GDKAVEIIVASVAQLSPDSELENEANNIKMEAEENLSQLIDQKLKDYEDLREDMRGKEHE 1320	
QY	1317 VKNLLEKKAQOQTADQLLARADAALAEAAKKGASTLQEAANDILNLLKDFRRVNDN 1376	
DB	1321 VKNLLEKKGTEQQTADQLLARADAALAEAAKKGASTLQEAANDILNLLKDFRRVNDN 1380	
QY	1377 KTAASEALRRIPAINRTTAEANEKTRAEALAGNAADATAEAKKAHEAEIRASAAQKVA 1436	
DB	1381 KTAASEALRRIPAINQTTTEANEKTRAEALAGNAADATAEAKKAHEAEIRASAVQKVA 1440	
QY	1437 TSTKADAERTTGEVTDLDNEVNGMLRQLAEABNELAKRKQDDADQDMMWAGVASQAQSAE 1496	
DB	1441 TSTKAEARTTFAEVTDLNEVNNMLKQLQEAELKRRKQDDADQDMMWAGVASQAQSAE 1500	
QY	1497 LNARKAKNSVSLLSQLANNLLDQLDQTLVDLKLNETEGSLNKAKOSMKASDLDKVSVD 1556	
DB	1501 INARKAKNSVSLLSIINDLLEQLQGLDQTLVDLKLNETEGTLNKAKOSMKASDLDKVSVD 1560	
QY	1557 LESEARKQEAALMDYNRDIAEIIKDIHNLEDIKKTLPFGCFNTPSIEKP 1605	
DB	1561 LENEAKQEAALMDYNRDIEIIMKDINLEDIRKTLPSGCFNTPSIEKP 1609	
XX	RESULT 13	
XX	AAW50898	
XX	ID AAW50898 standard; protein; 1609 AA.	
XX	XX	
XX	AAW50898;	
XX	XX	
XX	DT 07-DEC-1998 (first entry)	
XX	DE Human laminin G1 chain.	

XX	Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;	59	VTVAATNTGTPPEYCVQTVGTGVTGKSHCLDCAQOHLQGAFLTDNNQADTTWQS	118
KW	Down's syndrome; hereditary cerebral haemorrhage; inflammation;	61	VTVAATNTGTPPEYCVQTVGTGVTGKSHCLDCAQOHLQGAFLTDNNQADTTWQS	120
KW	maligancy; Familial Mediterranean fever; multiple myeloma;	119	QTMLAGVQVPSNLTNHLKAFDITVYRLKPHSRPSPFALYKTRDGDGWPVQYYS	178
KW	type II diabetes; prion disease; Creutzfeldt-Jacob disease; CUD;	121	QTMLAGVQVPSNLTNHLKAFDITVYRLKPHSRPSPFALYKTRDGDGWPVQYYS	180
KW	Gertsman-Straussler syndrome; kuru; scrapie; haemodialysis;	179	SCENTYSKANRGFIRTGDEQOALCTDFSDISPLTGNVAFSTILEGRPSYFNPNPVL	238
KW	carpal tunnel syndrome; senile cardiac amyloid polynuropathy;	181	SCENTYSKANRGFIRTGDEQOALCTDFSDISPLTGNVAFSTILEGRPSYFNPNPVL	240
KW	Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;	239	QEWVTATDIRVTNLRNTFTGDEVFNDPKVLSYYVIAISDPVAGRCCKNGHASECVKNEF	298
XX	therapy.	241	QEWVTATDIRVTNLRNTFTGDEVFNDPKVLSYYVIAISDPVAGRCCKNGHASECVKNEF	300
OS	Homo sapiens.	299	DKLMCNCKHNTYGVDCCKLPFNDRPWRATAESASCLPCDCNCRGQECVDFDELAYS	358
XX		301	DKLMCNCKHNTYGVDCCKLPFNDRPWRATAESASCLPCDCNCRGQECVDFDELAYS	360
XX	WO9815179-A1.	359	TGHGHCTNCRDNTDGAKECRENFRNGTEACSPCHCSPVGLSTQCSYGRCSCKP	418
XX	16-APR-1998.	361	TGHGHCTNCRDNTDGAKECRENFRNGTEACSPCHCSPVGLSTQCSYGRCSCKP	420
XX	08-OCT-1997; 9TWO-US018145.	419	GVNCKDCRCQPGFHSLEAGRCPCSDPSGSDSCNVTGRCVCKDNVGVNCRCKP	478
XX	08-OCT-1996; 96US-0027981P.	421	GVNCKDCRCQPGFHSLEAGRCPCSDPSGSDSCNVTGRCVCKDNVGVNCRCKP	480
PR	(UNIW ) UNIV WASHINGTON.	479	FFNLESSNPKGCTPCFCFHSVCTNAVGSYVYDTSITFQIDEDGWRVQRDGSASLEW	538
XX	Castillo G, Snow AD;	481	FFNLESSNPKGCTPCFCFHSVCTNAVGSYVYDTSITFQIDEDGWRVQRDGSASLEW	540
XX	WPI; 1998-240534/21.	539	SSDRQVIAVISYPRPIAPVKTGNQVLSYGNLSPFSFRVDRDRTRLSAEDLVLSGA	598
XX	Use of laminin and fragments - for developing products for use in the	541	SSDRQVIAVISYPRPIAPVKTGNQVLSYGNLSPFSFRVDRDRTRLSAEDLVLSGA	600
PT	diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or	599	GLRVSVPVLAQNSYPSSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTISIKIRTY	658
PT	CUD.	601	GLRVSVPVLAQNSYPSSETTVKYIFRLHEATDYPWRPALSPPEFQKLLNLTISIKIRTY	660
XX	Claim 15; Page 106-109; 132pp; English.	659	SERSAGYLDVLTQASRPGVPAWBSCTCPVGGQFCFCTCLPGVRRTPSPGKXP	718
CC	This is the amino acid sequence of the human laminin G1 chain. The	661	SERSAGYLDVLTQASRPGVPAWBSCTCPVGGQFCFCTCLPGVRRTPSPGKXP	720
CC	primary object of the invention is to use laminin, laminin-derived	719	CVLCTCNHSETCDPBTGVCDCRDNTAGPHCKSDGYYGDSITLGTSSDCQPCPCGSS	778
CC	protein fragments and/or laminin-derived polypeptides as potent	721	CVLCTCNHSETCDPBTGVCDCRDNTAGPHCKSDGYYGDSITLGTSSDCQPCPCGSS	780
CC	inhibitors of amyloid formation, deposition, accumulation and/or	779	CAIVPTKEVWCHTGTGTAGRCCELCDGYFGDPLGSGNPVRLCRPCCNNDNIDPNAV	838
CC	peristence in Alzheimer's disease and other amyloidoses. The laminin	781	CAIVPTKEVWCHTGTGTAGRCCELCDGYFGDPLGSGNPVRLCRPCCNNDNIDPNAV	840
CC	products (see AA50888-98) may include mouse or human laminin A or A1	839	NCNRLTGECLKCIYNTAGFYCDCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP	897
CC	chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1	841	NCNRLTGECLKCIYNTAGFYCDCKEGFFGNPLAPNADKCKACACN-YGTVQQSSCNP	900
CC	chain, the globular repeats of the laminin A1 chain and the beta-amyloid	898	VTQCCQCLPHVSGRDCGTCDPGYNNLQSGQGERCDCHALGSTNGQCDTRTGCCEQPGI	957
CC	binding domain of the laminin A chain. A claimed method for treating an	901	VTQCCQCLPHVSGRDCGTCDPGYNNLQSGQGERCDCHALGSTNGQCDTRTGCCEQPGI	960
CC	amyloid disease comprises administering a polypeptide having a	958	TGQHCERCEVNHFGFEGCKPCDCHHEGSLQCKDDGRCCEGFGVGNRCDCQCENYF	1017
CC	conformational similarity to a fragment of a laminin protein. A method	961	TGQHCERCEVNHFGFEGCKPCDCHHEGSLQCKDDGRCCEGFGVGNRCDCQCENYF	1020
CC	for diagnosing an amyloid disease involves determining levels of laminin	1018	YNRSWPGQCECPACYRLVKDAAEHVKVQLQESLIANLGTDDMTVDQAFEDRLKEAR	1077
CC	in a sample. Production of laminin or its fourth globular repeat in vivo	1021	YNRSWPGQCECPACYRLVKDAAEHVKVQLQESLIANLGTDDMTVDQAFEDRLKEAR	1080
CC	provides a method for in vivo inhibition of beta-amyloid amyloidosis. The	1078	EVTDLLEAEQVNDQNLMDRLQRYNSSLHSQISRLQINRTIETGTILAEARSRVES	1137
CC	products and methods can be used for the diagnosis, prognosis, monitoring	1081	EVTDLLEAEQVNDQNLMDRLQRYNSSLHSQISRLQINRTIETGTILAEARSRVES	1140
CC	and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome			
CC	and hereditary cerebral haemorrhage with amyloidosis of the Dutch type			
CC	(where the specific amyloid is the beta-amyloid protein), the amyloidosis			
CC	associated with chronic inflammation various forms of malignancy and			
CC	Familial Mediterranean fever (AA amyloid or inflammation-association			
CC	amyloidosis), the amyloidosis associated with multiple myeloma and other			
CC	B-cell abnormalities (AL amyloid), the amyloidosis associated with type			
CC	II diabetes (amylin or islet amyloid), the amyloidosis associated with			
CC	prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler			
CC	syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis			
CC	associated with long-term haemodialysis and carpal tunnel syndrome (beta			
CC	2-microglobulin amyloid), the amyloidosis associated with senile cardiac			
CC	amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or			
CC	transferrin amyloid), and the amyloidosis associated with endocrine			
CC	tumours such as medullary carcinoma of the thyroid (variant of			
CC	procalcitonin)			
XX				
SQ	Sequence 1609 AA;			
	Query Match 93.7%; Score 8144; DB 2; Length 1609;			
	Best Local Similarity 92.7%; Pred. No. 0;			
	Matches 1492; Conservative 59; Mismatches 54; Indels 4; Gaps 3;			
QY	1 MTGGGAALALOPRGLWPLAVL--AAVAGCVRAAMDECADEGGRCQRCMPFVNAAPN 58			
DB	1 MRGSHRAAPALRPRGLWPLAVLAAAGCAQAAMDECTDEGGRCQRCMPFVNAAPN 60			

1138 TEQIETASRELEKAKM-AANVSITQPESTGEPMNTLLAEAEARRLAERHKQADIVRV 1196  
 1141 TERLIETASRELEKAKVAAANVSITQPESTGDPNNMTLLAEAEARKLAERHKQADIVRV 1200  
 1197 AKTANETSAEAYNLLLTLAGENOTALIEIELNKKYEQAKNISODLEKQAAARVHEAKRA 1256  
 1201 AKTANDUSTEAYNLLLTLAGENOTALIEIELNKKYEQAKNISODLEKQAAARVHEAKRA 1260  
 1257 GDKAVEIYASVAQLTPVDSBALNEANKIKKEAADLRLIDQKLKDYEDLREDMRGKEHE 1316  
 1261 GDKAVEIYASVAQLSPDSETLENEANNIKWEAENLEQLIDQKLKDYEDLREDMRGKELE 1320  
 1317 VKNLLBKGAQCOQTADQLARADAKALAEAAKKGSTLQEAANDILNNLKDFDRVNDN 1376  
 1321 VKNLLBKGTQOQTADQLARADAKALAEAAKKGSTLQEAANDILNNLKDFDRVNDN 1380  
 1377 KTAEEALRIPAINRTIABANETKREAQALGNAADATEAKNKAHEARIASAAQKNA 1436  
 1381 KTAEEALRKIPAINQITTEANETKREAQALGSAADATEAKNKAHEARIASAVQKNA 1440  
 1437 TSTKADARTFGEVTDLDNEVNGMLROLBEAENELKEKODDADQDDMMAGWASQAQAEAE 1496  
 1441 TSTKAEARTFAEVTDLJNEVNNMLKQLEAEKELKKKODDADQDDMMAGWASQAQAEAE 1500  
 1497 LNARKAKNSVSLLSQLNNLLDQLGQDVTVDLNLKLINEIEGSLNKADEMKASDLDRKVS 1556  
 1501 INARKAKNSVSLLSIINDLLEQLGQDVTVDLNLKLINEIEGTLNKADEMKVSDLRKVS 1560  
 1557 LESAPKQEAAMDYNDRIABEIKDHNLEDIKTLTGCGFNTPSIEKP 1605  
 1561 LENEAKQEAAMDYNDRIEIMKDIRNLEDIRKTLPSGCGFNTPSIEKP 1609

RESULT 14  
 AAB19802  
 ID AAB19802 standard; protein; 1576 AA.  
 XX AC AAB19802;  
 XX DT 05-MAR-2001 (first entry)  
 XX DE Human laminin 2 mature gamma-1 chain.  
 XX KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
 XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
 XX OS Homo sapiens.  
 XX PN WO200066730-A2.  
 XX FD 09-NOV-2000.  
 XX PF 28-APR-2000; 2000WO-US011378.  
 XX PR 30-APR-1999; 99US-0131720P.  
 XX PR 15-JUN-1999; 99US-0139198P.  
 XX PR 12-JUL-1999; 99US-0143289P.  
 XX PR 24-SEP-1999; 99US-0155945P.  
 XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 XX PI Yurchenco P;  
 XX WPI; 2000-687537/67.  
 XX N-PSDB; AAA88902.  
 XX PT Purified laminin 2 protein, useful for research and therapeutic purposes  
 XX PT including peripheral nerve regeneration, treatment of degenerative muscle  
 XX PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
 XX PS Claim 5; Page 251-256; 305pp; English.  
 XX CC The present sequence is that of human laminin 2 gamma-1 chain mature

CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and  
 CC gamma-1 (100 kDa) chains. It is thought to be specifically required for  
 CC stabilizing myotubes during skeletal muscle development, and for  
 CC preventing apoptosis. Genetic defects in its structure or expression are  
 CC associated with a major type of congenital muscular dystrophy. Laminin 2  
 CC is also thought to be important in Schwann cell/basal lamina  
 CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-  
 CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding  
 CC them (see AAA8891-906), methods for making recombinant laminin 2, cells  
 CC that express recombinant laminin 2, and methods for using purified  
 CC laminin 2 for research and therapeutic purposes including peripheral  
 CC nerve regeneration, treatment of degenerative muscle disorders,  
 CC angiogenesis regulation, promoting cell attachment and migration, ex vivo  
 CC cell therapy, improving the take of grafts, improving the  
 CC biocompatibility of medical devices and preparing improved culture  
 CC devices and media  
 XX Sequence 1576 AA;  
 SQ

Query Match 92.5%; Score 8043; DB 3; Length 1576;  
 Best Local Similarity 93.3%; Pred. No. 0;  
 Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;

QY 32 RAAMDECADEGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGTSKCHLCD 91  
 DB 1 QAAMDECTDEGRPORCMPEFVNAAFNVTVATNTCGTPPEEYCVQGTGVTGTSKCHLCD 60  
 QY 92 AQOQLHQAALFTDYNNOADTTWQSOTMLAGVQPSINLTLLHKGAFITTVRLKFX 151  
 DB 61 AQOPLHQAALFTDYNNOADTTWQSOTMLAGVQPSINLTLLHKGAFITTVRLKFX 120  
 QY 152 TSPRSFAIYKTRTDGPMWIPYQYVSGSCENTYSKANRGFTRTGGDEQOALCTDEFSDIS 211  
 DB 121 TSPRSFAIYKTRTDGPMWIPYQYVSGSCENTYSKANRGFTRTGGDEQOALCTDEFSDIS 180  
 QY 212 PLTGGNVAFSTLEGRPSAYNFDSNVLOEWTATDIRVTNLRLNTFGDEVNDPKVLSY 271  
 DB 181 PLTGGNVAFSTLEGRPSAYNFDSNVLOEWTATDIRVTNLRLNTFGDEVNDPKVLSY 240  
 QY 272 YYAISDFAVGGRCKCNHASECVKNEFDKJMCNKHNTYGVDCCKLPFFNDPWRARATA 331  
 DB 241 YYAISDFAVGGRCKCNHASECVKNEFDKJMCNKHNTYGVDCCKLPFFNDPWRARATA 300  
 QY 332 EASCLPCDCNGRQECYFDPPELYRSTGHGHCNTCDNDTGAKCERCNFRFLNGTE 391  
 DB 301 EASCLPCDCNGRQECYFDPPELYRSTGHGHCNTCDNDTGAKCERCNFRFLNGNE 360  
 QY 392 ACSPCHCSPVSGSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLSLTAACRCPSCDPSGST 451  
 DB 361 ACSSCHCSPVSGSLSTQCDSYGRCSCKPGVMGDKDCRCQPGFHSLSLTAACRCPSCDPSGSI 420  
 QY 452 DECNVETRCVCKDNVEGFNCERCKPFFNLESSNPKCTPCFCFCHSSVCTNAVGYSY 511  
 DB 421 DECNVETRCVCKDNVEGFNCERCKPFFNLESSNPKCTPCFCFCHSSVCTNAVGYSY 480  
 QY 512 DISSTFQIDEDGWRVQORDGSEASLEWSSDRQYIAVISDSYFPPRYFIAPVKFLGNQVLSY 571  
 DB 481 SISSTFQIDEDGWRVQORDGSEASLEWSSERQDIAVISDSYFPPRYFIAPVKFLGNQVLSY 540  
 QY 572 GONLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSTTVKYIFRLHEADY 631  
 DB 541 GONLSFSFRVDRDTRLAEDLVLEGAGLRVSVPLIAQNSYPSSTTVKYIFRLHEADY 600  
 QY 632 PWRPALSPFEFOKLNNLTISKIRGTYSERSAGYLDVDTLOSARGPGVPATWVESCTCP 691  
 DB 601 PWRPALTPFEFOKLNNLTISKIRGTYSERSAGYLDVDTLOSARGPGVPATWVESCTCP 660  
 QY 692 VGYGQFCETCLPGYRRTPPSLGPYSPCVLTCNCHSETCDDETGVCDNRDNTAGPHECK 751  
 DB 661 VGYGQFCETCLPGYRRTPPSLGPYSPCVLTCNCHSETCDDETGVCDNRDNTAGPHECK 720  
 QY 752 CSDGYVGDSTLGTSSDCPCPCPGSSCAIVPKTKEVVTCTPTAGKRCCLCDGCFG 811



Db 721 CSDGYGSGTAGTSSDQCPFCPGSSCAVVPKTKVWVNCNPTGTTGKRCCLCDDGYFG 780  
Qy 812 DPLGNSGVRVLCRCPCQCNNDIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKEFGFNPL 871  
Db 781 DPLGRNGFVRLCRLCCSDNIDPNAVGNCRNLTGECCLKIYNTAGFYCDRCCKDGFNPL 840  
Qy 872 APNPADKCKACACN-YGTVOQSSCNVPTGQCQCLPHVSGRDCGTCDPGYINLOSOGCE 930  
Db 841 APNPADKCKACNCPYGTMTQSSCNVPTGQCCELPHTVGTQDCGACDPGFYINLOSOGCE 900  
Qy 931 RCDCHALGSTNGQCDIRTGQCECOPGITGQCHERCETNHFQGPGECKPCDCHHEGSLSL 990  
Db 901 RCDCHALGSTNGQCDIRTGQCECOPGITGQCHERCETNHFQGPGECKPCDCHHEGSLSL 960  
Qy 991 QCKDGRCEGREGFVGNRCDCQENYFYNRWPQSCQCPACRYLVKDKAAEHRVKLOELE 1050  
Db 961 QCKDGRCEGREGFVGNRCDCQENYFYNRWPQSCQCPACRYLVKDKAAEHRVKLOELE 1020  
Qy 1051 SLIANLGGDMVTDQAFEDRLKABREVTDLLREAOEVKDVDDNLDRLQVRNSSLHSQ 1110  
Db 1021 SLIANLGGDMVTDQAFEDRLKABREVTDLLREAOEVKDVDDNLDRLQVRNSSLHSQ 1080  
Qy 1111 ISRLQNIERTIETGILAEARARSVESTEQIETIASRELEKAKM-AANVSITQPESTGEP 1169  
Db 1081 ISRLQNIERTIETGILAEARARSVESTEQIETIASRELEKAKM-AANVSITQPESTGEP 1140  
Qy 1170 NMNTLLAEARLAEHRHKEADDIVRVAKTANETSAAAYNLLRTLAGENOTALIEBELN 1229  
Db 1141 NMNTLLAEARLAEHRHKEADDIVRVAKTANETSAAAYNLLRTLAGENOTALIEBELN 1200  
Qy 1230 RRYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPYDSPALENANKIKKEA 1289  
Db 1201 RRYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPYDSPALENANKIKKEA 1260  
Qy 1290 ADLDELIDOKLKYEDIEDNRGKEHEVNNLEKGAECQOTADOLLARADAALAEAA 1349  
Db 1261 ENLEQIDOKLKYEDIEDNRGKEHEVNNLEKGAECQOTADOLLARADAALAEAA 1320  
Qy 1350 KKGRTSLQEAANDILNNLKDFFRVNDNKTAAEALRIPAINRTIABANEXTREQAALG 1409  
Db 1321 KKGRTSLQEAANDILNNLKDFFRVNDNKTAAEALRIPAINRTIABANEXTREQAALG 1380  
Qy 1410 NAADATAEAKNAKHAERIASAAQKATSTYADAEERTFGEVTDLDNEVNGMLRQLEAEN 1469  
Db 1381 SAADATAEAKNAKHAERIASAAQKATSTYADAEERTFGEVTDLDNEVNGMLRQLEAEN 1440  
Qy 1470 ELKRGQDDADODMMWAGMASQAQAEALNARKAKNSVSSLLSOLNLLDOLGQDVTVDLN 1529  
Db 1441 ELKRGQDDADODMMWAGMASQAQAEALNARKAKNSVSSLLSOLNLLDOLGQDVTVDLN 1500  
Qy 1530 KLNIEGSLINKAKDEMKASDLDRKVSQDLESEARKQEAAMINDYNRDIAETIKDHNLEDIK 1589  
Db 1501 KLNIEGSLINKAKDEMKASDLDRKVSQDLESEARKQEAAMINDYNRDIAETIKDHNLEDIK 1560  
Qy 1590 KTLPGTCENTPSIEKP 1605  
Db 1561 KTLPGTCENTPSIEKP 1576

RESULT 15  
ID AAB48453  
XX AAB48453 standard; protein; 1576 AA.  
AC AAB48453;  
XX AAB48453;  
DT 02-MAR-2001 (first entry)  
XX Human laminin 8 polypeptide, SEQ ID NO: 24.  
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX

OS Homo sapiens.  
XX WO200066732-A2.  
PN 09-NOV-2000.  
PD 28-APR-2000; 2000WO-US011543.  
PF 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
PI WPI; 2000-687539/67.  
XX N-PSDB; AAC83714.  
DR Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 214-218; 245pp; English.  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration  
XX Sequence 1576 AA;

Query Match 92.5%; Score 8043; DB 3; Length 1576;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1470; Conservative 57; Mismatches 47; Indels 2; Gaps 2;  
Qy 32 RAAMDECADEGGRPCORCMPEFVNAAFNVTVATNTCGTPPEYCVQTVGTVKSKCHLCD 91  
Db 1 QAAMDECTDEGGRPCORCMPEFVNAAFNVTVATNTCGTPPEYCVQTVGTVKSKCHLCD 60  
Qy 92 AQQHLQHGAAPLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYRLKPH 151  
Db 61 AQQHLQHGAAPLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLGKAFDITYRLKPH 120  
Qy 152 TSPSPFALYKTRTDGPMIPYQYSGSCENTYKXNRGFIRTGDEQALCTDEFSDIS 211  
Db 121 TSPSPFALYKTRTDGPMIPYQYSGSCENTYKXNRGFIRTGDEQALCTDEFSDIS 180  
Qy 212 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVNDPKVLKSY 271  
Db 181 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTNLNLTFGDEVNDPKVLKSY 240  
Qy 272 YYAISDFAVGGCKNGHASECKNEFDKLMCKNKHNTYGVDCCKLCPFFNDRPWRATA 331  
Db 241 YYAISDFAVGGCKNGHASECKNEFDKLMCKNKHNTYGVDCCKLCPFFNDRPWRATA 300  
Qy 332 ESASECLPDCNCRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFFRLGNTE 391  
Db 301 ESASECLPDCNCRSQECYFDPPELYRSTGHGHCNTCRDNTDGAKCERCENFFRLGNTE 360  
Qy 392 ACSPCCHSVGSLSTQCSYGRCSCKPGVMGDKCRCPGHSLETAGCRPCSCDPSGST 451  
Db 360 ACSPCCHSVGSLSTQCSYGRCSCKPGVMGDKCRCPGHSLETAGCRPCSCDPSGST 420

Db 361 ACSSCHCSPVGLSTQCDYSYGRCSCKPGVMGDXCDRCQCFHFSLTBAGCRPCSCDPGSGI 420  
Qy 452 DECNVETGRVCNDVGEFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVY 511  
Db 421 DECNVETGRVCNDVGEFNCERCKPGFFNLESSNPKGCTPCFCFGHSSVCTNAVGSYVY 480  
Qy 512 DISSTFQIDEDGWRVGEORDGSEASLEWSSDRQVIAVISYPPRYPIAPVKELGNOLSY 571  
Db 481 SISSTFQIDEDGWRVGEORDGSEASLEWSSDRQVIAVISYPPRYPIAPVKELGNOLSY 540  
Qy 572 QONLSFSFRVDRDRLTRLSAEDLVLEGAGLAVSVPLIAQNSYPSSETTVKYIPFLHEATDY 631  
Db 541 QONLSFSFRVDRDRLTRLSAEDLVLEGAGLAVSVPLIAQNSYPSSETTVKYIPFLHEATDY 600  
Qy 632 PWRPALSPFFQKLLNNLTSIKIRGTYSERSAGYVLDVTLQSRPQPGVPATWVESCTCP 691  
Db 601 PWRPALTPFFQKLLNNLTSIKIRGTYSERSAGYVLDVTLQSRPQPGVPATWVESCTCP 660  
Qy 692 VYGGQCFCECLPGYRRETPSLGYPSCVLCTCNHGHSETCDPETGVCDNRDNTAGPHEK 751  
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Qy 752 CSBGYYGDSITLGTSSDCQPCPGSSCAIVPTKKEVWVTHCTPTAGKCELCDDGYFG 811  
Db 721 CSBGYYGDSITLGTSSDCQPCPGSSCAIVPTKKEVWVTHCTPTAGKCELCDDGYFG 780  
Qy 812 DPLGSGFVRLCRPCQNDNIDNAVGNCHRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 871  
Db 781 DPLGSGFVRLCRPCQNDNIDNAVGNCHRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 840  
Qy 872 APNPAKCKACACH-YGTVOQSSCNPVTCOCCLPHVSGRDGCTDPGYVNLQSGQGC 930  
Db 841 APNPAKCKACACH-YGTVOQSSCNPVTCOCCLPHVSGRDGCTDPGYVNLQSGQGC 900  
Qy 931 RCDCHALGSTNGQCDITGTQCEQCPGITGHCERCEVNFHFGPGECKPCDCHHGSLSL 990  
Db 901 RCDCHALGSTNGQCDITGTQCEQCPGITGHCERCEVNFHFGPGECKPCDCHHGSLSL 960  
Qy 991 QCKDDGCECEGFGVNRCDCEVNFYNSWPCQCPACRYLVKDKAAEHVVKLQELJ 1050  
Db 961 QCKDDGCECEGFGVNRCDCEVNFYNSWPCQCPACRYLVKDKAAEHVVKLQELJ 1020  
Qy 1051 SLIANLGTGDDMTVDQAFEDRLKEAREVTDLLFEAQEVKDVQNDLMDRLQRYVNSLSHQ 1110  
Db 1021 SLIANLGTGDDMTVDQAFEDRLKEAREVTDLLFEAQEVKDVQNDLMDRLQRYVNSLSHQ 1080  
Qy 1111 ISRLQNTNTEETGIIAERARSVESTEQIETASRELEKAKM-AANVSITQPESTGE 1169  
Db 1081 ISRLQNTNTEETGIIAERARSVESTEQIETASRELEKAKM-AANVSITQPESTGE 1140  
Qy 1170 NNMTLLAEARLAEKHAERKQADDDIVRVAKTANETSAEAYNLLRTLAGENQTALEIEELN 1229  
Db 1141 NNMTLLAEARLAEKHAERKQADDDIVRVAKTANETSAEAYNLLRTLAGENQTALEIEELN 1200  
Qy 1230 RKYEQAKNI SODLEKQAAHVHEEAKRAGDKAVEIYASVAQITPVDSEALENEANKIKKEA 1289  
Db 1201 RKYEQAKNI SODLEKQAAHVHEEAKRAGDKAVEIYASVAQITPVDSEALENEANKIKKEA 1260  
Qy 1290 ADLRLIDQKLDYEDLREDMRGHEHEVKNLLEKGAEQQTADOLLARADAAKALAEAEA 1349  
Db 1261 ENLEQLIDQKLDYEDLREDMRGHEHEVKNLLEKGAEQQTADOLLARADAAKALAEAEA 1320  
Qy 1350 KKGSTIQEANDIILNNLKDFRRVNDKTAABEALRIPAINRTIABANEKTBREAQALG 1409  
Db 1321 KKGSTIQEANDIILNNLKDFRRVNDKTAABEALRIPAINRTIABANEKTBREAQALG 1380  
Qy 1410 NAADATAEAKNAHEAERIASAAOKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEN 1469  
Db 1381 SAADATAEAKNAHEAERIASAAOKNATSTKADAERTFGEVTDLDNEVNGMLRQLEAEN 1440  
Qy 1470 ELKQKQDDADQDMMWAGVAGQAAQAEALNAPKAKNSVSSLSLQNLNLLDQLGOLDTVDLN 1529  
Db 1441 ELKQKQDDADQDMMWAGVAGQAAQAEALNAPKAKNSVSSLSLQNLNLLDQLGOLDTVDLN 1500

Qy 1530 KLNIEGSLNKADEMKAASDLDRKVSLESEARKQEAAMNDYNDIAEIIKDIHNLESDIK 1589  
Db 1501 KLNIEGTLNKADEMKAASDLDRKVSLESEARKQEAAMNDYNDIAEIIKDIHNLESDIR 1560  
Qy 1590 KTLPTGCENTPSIEKP 1605  
Db 1561 KTLPSGCCFNTPSIEKP 1576

Search completed: May 18, 2004, 14:42:31  
Job time : 49.6393 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 15.8753 Seconds  
(without alignments)

10452.141 Million cell updates/sec

Title: US-10-037-182-12

Perfect score: 9429

Sequence: 1 EPYGVSHLQDKKCFICDS.....EVRSLXDKSEKVAVSTCL 1725

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: Pirl.\*

2: Pirl.\*

3: Pirl.\*

4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9429	100.0	1786	MMMSB1	laminin beta-1 cha
2	8873	94.1	1786	MMHUB1	laminin beta-1 cha
3	4936	52.3	1801	MMKRTS	laminin beta-2 cha
4	4892	51.9	1798	S53869	laminin beta-2 cha
5	4746.5	50.3	1797	A55677	laminin beta-2 cha
6	3733.5	39.6	1790	MMFFB1	laminin beta-1 cha
7	3646	38.7	1808	T15099	hypothetical prote
8	1730	18.3	3672	T23433	hypothetical prote
9	1730	18.3	3704	T37316	probable laminin a
10	1675.5	17.8	1639	MMFFB2	laminin gamma-1 ch
11	1649	17.5	3712	S18253	laminin alpha-1 ch
12	1618.5	17.2	1609	MMHUR2	laminin gamma-1 ch
13	1610.5	17.1	1607	MMMSB2	laminin gamma-1 ch
14	1608	17.1	1597	T28811	hypothetical prote
15	1584	16.8	3635	T10053	laminin alpha 5 ch
16	1575	16.7	303	B45027	laminin B1 chain -
17	1535	16.3	3075	S44458	laminin alpha-1 ch
18	1497.5	15.9	3106	S53868	laminin alpha-2 ch
19	1482	15.7	3084	MMMSA	laminin alpha-1 ch
20	1428.5	15.2	1170	A53612	laminin B1k chain
21	1395.5	14.8	1168	S15695	kalinin B1 - mouse
22	1276.5	13.5	2823	T23064	hypothetical prote
23	1276.5	13.5	2823	T37908	protein T22A3.8 [i
24	1276.5	13.5	3102	T43291	laminin alpha cha
25	978.5	10.4	616	I38231	S-laminin - human
26	858.5	9.1	1193	T44018	laminin B2t chain
27	850.5	9.0	1192	S69000	laminin gamma 2 ch
28	682.5	7.2	1620	T27283	hypothetical prote
29	680	7.2	1574	T13954	MSGF6 protein - ra

## ALIGNMENTS

### RESULT 1

MMMSB1

laminin beta-1 chain precursor - mouse

N;Alternate names: laminin chain B1

C;Species: Mus musculus (House mouse)

C;Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543

R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.

Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987

A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein

A;Reference number: A26413; MUID:87147212; PMID:3493487

A;Accession: A26413

A;Molecule type: mRNA

A;Residues: 1-1786 <SAS>

A;Cross-references: EMBL:M15525; NID:G198700

A;Note: translation in GenBank has additional 48 residues at the amino end

R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A;Title: Structure and distribution of N-linked oligosaccharide chains on various domains

A;Reference number: S02678; MUID:88326259; PMID:2458101

A;Accession: S02679

A;Molecule type: protein

A;Residues: 28-42;932-946 <FUJ>

R;Hartl, L.; Oberbauer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A;Title: The N terminus of laminin A chain is homologous to the B chains.

A;Reference number: S00624; MUID:189225080; PMID:3267223

A;Accession: S05326

A;Molecule type: protein

A;Residues: 457-466;854-868;932-946 <HAR>

R;Mann, K.; Deutzmann, R.; Timpl, R.

Eur. J. Biochem. 178, 71-80, 1988

A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and the

A;Reference number: S08895; MUID:89078415; PMID:2462498

A;Accession: S14877

A;Molecule type: protein

A;Residues: 590-620 <MAN>

R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a)

A;Reference number: A02870; MUID:85051302; PMID:6209134

A;Accession: A02871

A;Molecule type: mRNA

A;Residues: 1292-1530; 'MEMP', 1535-1691; 'C', 1693-1748; 'N', 1750-1786 <BAR>

A;Cross-references: EMBL:X05212; NID:G52861; PIDN:CAA28839.1; PID:G809042

R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter

A;Reference number: S01790; MUID:89030693; PMID:3181157

A;Accession: S02036

A;Molecule type: protein

A;Residues: 1561-1587 <DEU>

R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
EMBO J. 4, 309-316, 1985  
A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
A;Reference number: S13543; MID:85257455; PMID:3848400  
A;Accession: S13543  
A;Molecule type: protein  
A;Residues: 1700-1748, 'N', 1750-1759 <PAU>  
C;Genetics:  
A;Gene: Lamb-1  
A;Map position: 12  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-1786/Product: laminin beta-1 chain #status predicted <WAT>  
F;22-270/Domain: VI <DOM6>  
F;271-340/Domain: V <DOM5>  
F;371-332/Domain: laminin-type EGF-like homology <LE01>  
F;335-395/Domain: laminin-type EGF-like homology <LE02>  
F;398-455/Domain: laminin-type EGF-like homology <LE03>  
F;458-507/Domain: laminin-type EGF-like homology <LE04>  
F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;541-772/Domain: IV <DOM4>  
F;773-1182/Domain: III <DOM3>  
F;773-818/Domain: laminin-type EGF-like homology <LE06>  
F;821-864/Domain: laminin-type EGF-like homology <LE07>  
F;867-914/Domain: laminin-type EGF-like homology <LE08>  
F;917-973/Domain: laminin-type EGF-like homology <LE09>  
F;976-1025/Domain: laminin-type EGF-like homology <LE10>  
F;1028-1084/Domain: laminin-type EGF-like homology <LE11>  
F;1084-1129/Domain: laminin-type EGF-like homology <LE12>  
F;1132-1176/Domain: laminin-type EGF-like homology <LE13>  
F;1183-1397/Domain: II <DOM2>  
F;1183-1397/Region: heptad repeats  
F;1398-1430/Domain: alpha <ALP>  
F;1431-1786/Region: heptad repeats  
F;1431-1786/Domain: I <DOM1>  
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F;30-35/Disulfide bonds: #status predicted  
F;120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra  
F;1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 9429; DB 1; Length 1786;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPYCIVSHLOEDKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWQSENGVENV 60  
DB 62 EPYCIVSHLOEDKCFICDSRDPYHETLNPDShLIENVVTFAPNRLKIWQSENGVENV 121  
QY 61 TIQDLAEAPHFTHLIMTFKTFRAAMLIERSSDFGKTGWYRYFAYDCSSPFGISTGP 120  
DB 122 TIQDLAEAPHFTHLIMTFKTFRAAMLIERSSDFGKTGWYRYFAYDCSSPFGISTGP 181  
QY 121 MKKYDDIICDSRYSDIEPSTEGEVIIPALDPAPKIEDIPYSPRIQNLKILNFKVKLH 180  
DB 182 MKKYDDIICDSRYSDIEPSTEGEVIIPALDPAPKIEDIPYSPRIQNLKILNFKVKLH 241  
QY 181 TLGNLLDSRMEIREKYYAYVDMVAGNCFCYGHASECAPDGVNVEEGVGHCMCR 240  
DB 242 TLGNLLDSRMEIREKYYAYVDMVAGNCFCYGHASECAPDGVNVEEGVGHCMCR 301  
QY 241 HNTKGLNCELQWDFYHDLFWPAPGRNSNACKKCNNEHSSCHFDMAVELATGNVSGV 300  
DB 302 HNTKGLNCELQWDFYHDLFWPAPGRNSNACKKCNNEHSSCHFDMAVELATGNVSGV 361  
QY 301 CDNQHNTMGRNCQKPFYQHFERDIRDNLCEPCTCPAGSENGGICDGYTDFSVGL 360  
DB 362 CDNQHNTMGRNCQKPFYQHFERDIRDNLCEPCTCPAGSENGGICDGYTDFSVGL 421  
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNCDSETGYCYC 420

422 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGGNCDSETGYCYC 481  
QY 421 KRLVTGRCDOCLPQHNLGSLNDLDCRCPDCLGGLNNSCEDSGSCCLPHMIGRCQN 480  
DB 482 KRLVTGRCDOCLPQHNLGSLNDLDCRCPDCLGGLNNSCEDSGSCCLPHMIGRCQN 541  
QY 481 EVESGYFTTLDHYIYEAEEANLPGVVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 540  
DB 542 EVESGYFTTLDHYIYEAEEANLPGVVVERQYIQDRIPSWTGPFRVPEGAYLEFFI 601  
QY 541 DNIYPSMEYELIYEPQLPDHWEKAVITVORPKIPASSRCGNTPDDNQVVSLSFGS 600  
DB 602 DNIYPSMEYELIYEPQLPDHWEKAVITVORPKIPASSRCGNTPDDNQVVSLSFGS 661  
QY 601 RYVVLPRVPCFEKGMNTVLELPOYTASGSDVESPYTFIDSLVLMPCYKSLDIFTVGG 660  
DB 662 RYVVLPRVPCFEKGMNTVLELPOYTASGSDVESPYTFIDSLVLMPCYKSLDIFTVGG 721  
QY 661 GDGEVTSAMETFORYLENSRVVKTMTDVCENIIFISALIHOTGLACEDCPGSL 720  
DB 722 GDGEVTSAMETFORYLENSRVVKTMTDVCENIIFISALIHOTGLACEDCPGSL 781  
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLOGSASAFCAITQCH 780  
DB 782 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLOGSASAFCAITQCH 841  
QY 781 CFQGIYARQCDRCCLPGYWGFPSCPCQCNHGLDCTVTGECCLSCDYTTGHCNCRCLAG 840  
DB 842 CFQGIYARQCDRCCLPGYWGFPSCPCQCNHGLDCTVTGECCLSCDYTTGHCNCRCLAG 901  
QY 841 YYGPIIGSGDHCRPCPCPDGSDGROFARSCYQDPVTLQACVCDPYGSRCDCCASG 900  
DB 902 YYGPIIGSGDHCRPCPCPDGSDGROFARSCYQDPVTLQACVCDPYGSRCDCCASG 961  
QY 901 PFGNPSDFGSCQPCQCHNIDTTDPEACDKTORCLKCLYHTEGDHCOLCGYVYGDAL 960  
DB 962 PFGNPSDFGSCQPCQCHNIDTTDPEACDKTORCLKCLYHTEGDHCOLCGYVYGDAL 1021  
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DB 1022 QDCRKCVCNVLGTWKEHNGSDCHDKATQSCSCLPNVIGQNCDCRCAPTNQLASGTGC 1081  
QY 1021 GPCNNAHSPGSCNEFTGQCQCPGFGRTGTCSECBELFWGDDPVECRACDPRGIET 1080  
DB 1082 GPCNNAHSPGSCNEFTGQCQCPGFGRTGTCSECBELFWGDDPVECRACDPRGIET 1141  
QY 1081 PQDQSTGQCVGVEGPRCDKTRGVSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140  
DB 1142 PQDQSTGQCVGVEGPRCDKTRGVSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1201  
QY 1141 EKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEAEKLTQDVT 1200  
DB 1202 EKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEAEKLTQDVT 1261  
QY 1201 EKQAOVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFKNSDIQALDSI 1260  
DB 1262 EKQAOVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFKNSDIQALDSI 1321  
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDVEDLMLERESPFKEQEQEARLDEL 1320  
DB 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDVEDLMLERESPFKEQEQEARLDEL 1381  
QY 1321 AGKLOSLDI-SAAAQMTCTPPGADCESECCGPNCRDTDEGKCKGCGGGLVTVHSAW 1380  
DB 1382 AGKLOSLDI-SAAAQMTCTPPGADCESECCGPNCRDTDEGKCKGCGGGLVTVHSAW 1441  
QY 1381 QKAMDFDRDLVSALAEVQLSKVSEAKVRADEAKQNAQDVLTKTNATKVKYDKSNEDLR 1440  
DB 1442 QKAMDFDRDLVSALAEVQLSKVSEAKVRADEAKQNAQDVLTKTNATKVKYDKSNEDLR 1501  
QY 1441 NLIKQIRPLFEDSADLDSIEAVANVLKSGNASTPQOLQNTEDIRERVTLSOVEVIL 1500

Db 1502 NLIKQIRNPLTSDSADLOSIEAVANEVLKSGNASTPQOLQNLITDIRBVRTLSQVEVIL 1561  
Qy 1501 QOSADIAAEALLLEAKRASKSATDVKTADMKVKEALEEAEKAAQVAEKAQKQADEIQ 1560  
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Db 1742 DLERYEDNQKYLEKQAEVLNLEGEVRSLLKXIDISEKVAVYSTCL 1786

RESULT 2  
NMHUB1  
N:Altein beta-1 chain precursor - human  
N:Alternate names: laminin chain B1  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text\_change 19-Jan-2001  
C:Accession: S13547; A26994; S23566  
R:Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.  
J. Biol. Chem. 265, 15611-15616, 1990  
A:Title: Structure of the human laminin B1 chain gene.  
A:Reference number: S13547; MUID:90368768; PMID:1975589  
A:Accession: S13547  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1786 <VUO>  
A:Cross-references: GB:M61953; GB:J02778; NID:g186911; PID:AAAS9486.1; PID:g186913  
A:Note: The nucleotide sequence was submitted to GenBank, February 1991  
R:Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Syers, M.; Shows, T.; Pihlajaniemi, T.; Sara  
J. Biol. Chem. 262, 10454-10462, 1987  
A:Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2  
A:Reference number: A28483; MUID:87280097; PMID:3611077  
A:Accession: A28483  
A:Molecule type: mRNA  
A:Residues: 1-1786 <PIK>  
A:Cross-references: GB:M61953; GB:J02778; NID:g186911; PID:AAAS9486.1; PID:g186913  
R:Jay, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.  
Am. J. Hum. Genet. 41, 605-615, 1987  
A:Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localization  
A:Reference number: A26994; MUID:88021029; PMID:3661559  
A:Accession: A26994  
A:Molecule type: mRNA  
A:Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>  
A:Cross-references: EMBL:M20206; NID:g186914; PID:AAAS9487.1; PID:g186915  
R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P  
A:Title: Genes for the human laminin B1 and B2 chains.  
A:Reference number: S23566  
A:Accession: S23566  
A:Molecule type: DNA  
A:Residues: 762-1786 <VU2>  
A:Note: mRNA was also sequenced  
C:Genetics:  
A:Gene: GDB:LAMB1  
A:Cross-references: GDB:119357; OMIM:150240  
A:Map position: 7q31.1-7q31.3  
A:Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/3; 293/3; 334/1; 397/1; 457/1; 494/3; 52  
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F:22-270/Domain: VI <DOM6>  
F:271-548/Domain: V <DOM5>  
F:271-332/Domain: laminin-type EGF-like homology <LE01>  
F:335-395/Domain: laminin-type EGF-like homology <LE02>  
F:398-455/Domain: laminin-type EGF-like homology <LE03>  
F:458-507/Domain: laminin-type EGF-like homology <LE04>  
F:463-468/Region: cell adhesion #status predicted  
F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:549-774/Domain: IV <DOM4>  
F:662-668/Region: cell adhesion #status predicted  
F:773-818/Domain: laminin-type EGF-like homology <LE06>  
F:775-1178/Domain: III <DOM3>  
F:821-864/Domain: laminin-type EGF-like homology <LE07>  
F:867-914/Domain: laminin-type EGF-like homology <LE08>  
F:917-973/Domain: laminin-type EGF-like homology <LE09>  
F:923-927/Region: cell adhesion #status predicted  
F:930-954/Region: cell adhesion #status predicted  
F:976-1025/Domain: laminin-type EGF-like homology <LE10>  
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>  
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>  
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>  
F:1179-1397/Domain: II <DOM2>  
F:1179-1397/Region: heptad repeats  
F:1398-1430/Domain: alpha <ALP>  
F:1431-1786/Domain: I <DOM1>  
F:1431-1786/Region: heptad repeats  
F:30-35/Disulfide bonds: #status predicted  
F:120,356,519,677,985,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate  
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 94.1%; Score 8873; DB 1; Length 1786;

Best Local Similarity 92.9%; Pred. No. 0;

Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy 1 EPYCIYSHLOEDKKCTCDSDRDYHETLAPDSDSLIENVTTPAPNLKIWQSENV 60  
Db 62 EPYCIYSHLOEDKKCTCDSDRDYHETLAPDSDSLIENVTTPAPNLKIWQSENV 121  
Qy 61 TIQLDLEAEHPHFLHMTFKTPAAMLIERSDFKGTWGVYFYAYDCESFPFGISTGP 120  
Db 122 TIQLDLEAEHPHFLHMTFKTPAAMLIERSDFKGTWGVYFYAYDCESFPFGISTGP 181  
Qy 121 MKKVDDIICDSRYSDIEPTEGEVIFRALDPAPKIEDDPSRIQNLKLTNRIRKVKLH 180  
Db 182 MKKVDDIICDSRYSDIEPTEGEVIFRALDPAPKIEDDPSRIQNLKLTNRIRKVKLH 241  
Qy 181 TLGNLLDSMEIREKYVAVYDMVVRGNCFCYGHASECAPVDGVNVEVEGVHGHCMCR 240  
Db 242 TLGNLLDSMEIREKYVAVYDMVVRGNCFCYGHASECAPVDGVNVEVEGVHGHCMCR 301  
Qy 241 HNTKGLNCELMDYHDLPMRPAEGNSNACKKCNNEHSSCHPDMAYFLATGNVSGV 300  
Db 302 HNTKGLNCELMDYHDLPMRPAEGNSNACKKCNNEHSSCHPDMAYFLATGNVSGV 361  
Qy 301 CDNCQHTMGRCNCEQCKPFVQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
Db 362 CDNCQHTMGRCNCEQCKPFVQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421  
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPPGCKSCANPLGTIPGGNCPDSETCYVC 420  
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPPGCKSCANPLGTIPGGNCPDSETCYVC 481  
Qy 421 KRLVTGRCDOCLPOHWGLSNDLDGRCPCDCLGGALNNSSCEDSGCCCLPMIGRCQN 480  
Db 482 KRLVTGRCDOCLPOHWGLSNDLDGRCPCDCLGGALNNSSCEDSGCCCLPMIGRCQN 541  
Qy 481 EVESGYVFTFDHYIYEAEANLPGVGVVVERQYIQDIRIPSWTGPQFVRVPEGALEFFI 540  
Db 542 EVESGYVFTFDHYIYEAEANLPGVGVVVERQYIQDIRIPSWTGPQFVRVPEGALEFFI 601  
Qy 541 DNPYSMEVILLIRYEPQLPDHWEKAVITVORPGKIPASSRCQNTVPDDNQVSLSPGS 600  
Db 602 DNPYSMEVILLIRYEPQLPDHWEKAVITVORPGKIPASSRCQNTVPDDNQVSLSPGS 661

601 RYVVLPRVCFEKMNYTVLELPOYTASGDVSESYTFIDSLVLMPYCKSLDIFTVGGS 660  
662 RYVVLPRVCFEKMNYTVLELPOYTASGDVSESYTFIDSLVLMPYCKSLDIFTVGGS 721  
661 GDGEVTSNASETFQRYVRECLNSVSVKTPMTDVCNRIIFSIISALIHQTGLACECDPQGS 720  
722 GDGWVTSNASETFQRYVRECLNSVSVKTPMTDVCNRIIFSIISALLHQTGLACECDPQGS 781  
721 SSVCDPNNGGOCQPNVVGTCNRCAPGTGFGPNCKPCDCHLQASAFCDATGQCH 780  
782 SSVCDPNNGGOCQPNVVGTCNRCAPGTGFGPNCKPCDCHLQASAFCDATGQCH 841  
781 CFQGIYARQCDRCCLPGYWGFPSPQPCOCNGHALDCTVTGECILSCQDYTTGHCNCRCLAG 840  
842 CFQGVYARQCDRCCLPGYWGFPSPQPCOCNGHADCDPVTGECILNCQDYTMGHCNCRCLAG 901  
841 YGDPPIIGSDHRCPCPCPGPSGRQFARSCVQDPVTIQLACVCPGPGVIGSRCDCCASG 900  
902 YGDPPIIGSDHRCPCPCPGPSGRQFARSCVQDPVTIQLACVCPGPGVIGSRCDCCASG 961  
901 FFGNPSDFGSCQPCQCHNIDTDPEACDKDGRCLKCLYHTEGHDHCLQVGGYGDAL 960  
962 YFGNPSDFGSCQPCQCHNIDTDPEACDKDGRCLKCLYHTEGHDHCLQVGGYGDAL 1021  
961 RQCRKVCVNYLGTVKGHNGSDCHCDKATGQSCSLPNVIGQNCDCAPNTWOLASGTGC 1020  
1022 RQCRKVCVNYLGTVKGHNGSDCHCDKATGQSCSLPNVIGQNCDCAPNTWOLASGTGC 1081  
1021 GPCNCAAHFGSCNFTGQCCMGFGGRTSCEQELFWGDPDVECRACDPRGIGT 1080  
1082 DPCNCAAHFGSCNFTGQCCMGFGGRTSCEQELFWGDPDVECRACDPRGIGT 1141  
1081 PQCDQSTGQCVGVGEGPRCKDTRGYSGVFPDCTPHQCPALWDAIIGELNTRHKEFL 1140  
1142 PQCDQSTGQCVGVGEGPRCKDTRGYSGVFPDCTPHQCPALWDAIIGELNTRHKEFL 1201  
1141 EKAKALXISGIVGYRTVDSVRKYNIEKDIIAQSPAAPLKNIGLFEAEKLTQDVT 1200  
1202 EKAKALXISGIVGYRTVDSVRKYNIEKDIIAQSPAAPLKNIGLFEAEKLTQDVT 1261  
1201 EKAAQVVKLTDTASQNSSTAGELGALQABEALDKTVKELASQLEBFINKNSDIOGALDSI 1260  
1262 EKAAQVVKLTDTASQNSSTAGELGALQABEALDKTVKELASQLEBFINKNSDIOGALDSI 1321  
1261 TKYFQMSLEAKRVNASTTDPNSTVEQSALTTRVEDLMLERSPKQEEOEARLLDEL 1320  
1322 TKYFQMSLEAKRVNASTTDPNSTVEQSALTTRVEDLMLERSPKQEEOEARLLDEL 1381  
1321 AGKQSLDLGAAQOMTCGTPPGADCSBEGGPNCRDTEGKCGGPGCGGLVTVAHSAW 1380  
1382 AGKQSLDLGAAQOMTCGTPPGADCSBEGGPNCRDTEGKCGGPGCGGLVTVAHSAW 1441  
1381 QKAMDFRDVLALAEVEQLSKVSEAKVRADEAKQNAQDVLLKTNATKSKVDKSNEDLR 1440  
1442 QKAMDLQDVLALAEVEQLSKVSEAKVRADEAKQNAQDVLLKTNATKSKVDKSNEDLR 1501  
1441 NLIQKINFLTEDSADLSDTEAVANEVKSNGASTPQOLQNTLDRERVETLSQVEVIL 1500  
1502 NLIQKINFLTEDSADLSDTEAVANEVKSNGASTPQOLQNTLDRERVETLSQVEVIL 1561  
1501 QQSAAIDARAEELLEAKRASKSATDVKVTADVMKEALEAEAKAQAQAEKAIQOADEIQ 1560  
1562 QQSAAIDARAEELLEAKRASKSATDVKVTADVMKEALEAEAKAQAQAEKAIQOADEIQ 1621  
1561 GTQNLISIESETAASBETLTNASORISKLERNVEELKRAQNSGEAEYIEKVVVSVKQ 1620  
1622 GTQNLISIESETAASBETLTNASORISKLERNVEELKRAQNSGEAEYIEKVVVSVKQ 1681  
1621 NADVDKTLQDELDEKVKVSELSIAQKTESADARRKAEALLONEAKTLLAQAANSKLQLE 1680  
1682 SAEDVKTLQDELDEKVKVSELSIAQKTESADARRKAEALLONEAKTLLAQAANSKLQLLK 1741

QY 1681 DLERYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
DB 1742 DLERYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786  
RESULT 3  
MURTS  
Laminin beta-2 chain precursor - rat  
N:Alternate names: laminin chain B3; S-laminin  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C:Accession: S03539  
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
N:ature 338, 229-234, 1989  
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A:Reference number: S03539; MUID:89159410; PMID:2922051  
A:Accession: S03539  
A:Molecule type: RNA  
A:Residues: 1-1801 <HUN>  
A:Cross-references: ENBL:X14563; NID:G57250; PID:CAA4561.1; PID:G57251  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
C:Description: interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F:36-285/Domain: VI <DOM6>  
F:286-555/Domain: V <DOM5>  
F:286-347/Domain: laminin-type EGF-like homology <LE01>  
F:350-410/Domain: laminin-type EGF-like homology <LE02>  
F:413-470/Domain: laminin-type EGF-like homology <LE03>  
F:473-522/Domain: laminin-type EGF-like homology <LE04>  
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:556-784/Domain: IV <DOM4>  
F:786-831/Domain: laminin-type EGF-like homology <LE06>  
F:788-1196/Domain: III <DOM3>  
F:834-877/Domain: laminin-type EGF-like homology <LE07>  
F:880-927/Domain: laminin-type EGF-like homology <LE08>  
F:930-986/Domain: laminin-type EGF-like homology <LE09>  
F:989-1038/Domain: laminin-type EGF-like homology <LE10>  
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F:1197-1412/Domain: II <DOM2>  
F:1197-1412/Region: heptad repeats  
F:1413-1445/Domain: alpha <ALP>  
F:1446-1801/Region: heptad repeats  
F:1446-1801/Domain: I <DOM1>  
F:45-50/Disulfide bonds: #status predicted  
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status P  
F:1193,1196,1800/Disulfide bonds: interchain #status predicted  
Query Match 52.3%; Score 4936; DB 1; Length 1801;  
Best Local Similarity 51.2%; Pred. No. 1.2e-181;  
Matches 887; Conservative 297; Mismatches 530; Indels 20; Gaps 8;  
QY 1 EPYCIIVSHQDEKCKFCICDSRDPYHETLNPDSHLIENVVTFAPNRLKIHWQSENGVENV 60  
DB 77 QPYCIIVSHQDEKCKFCICDSRDPYHETLNPDSHLIENVVTFAPNRLKIHWQSENGVENV 136  
QY 61 TTOLDLEAEFHTLIMTFKTRFAAMLIERSSDPGTWGYRYFAYDVCESSFGIGSTGP 120  
DB 137 TTOLDLEAEFHTLIMTFKTRFAAMLIVERSDPGRTRWYRIFSYDCGADFGIPLAP 196  
QY 121 MKKVDITICDSRYSDIEPSTEGEVIFFALDPAFKIEDPYSPIQNLLKITNLRKFVKLH 180  
DB 197 PRWDVVCESRYSEIEPSTEGEVIYRVLDPAIPDPYSSRIQNLLKITNLRVNLTRLH 256  
QY 181 TLGDMLLDSRMEIRKYYIAYVDMVVRGNCFCYHASECAPVDGVNEEVEGWHGHCNCR 240  
DB 257 TLGDMLLDSRMEIRKYYIAYVDMVVRGNCFCYHASECAPVDGVNEEVEGWHGHCNCR 316

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.80775 seconds

(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-12

Perfect score: 9429

Sequence: 1 EPCIVSHLQEDKKCFICDS.....EVRSLKDISKVAIVSTCL 1725

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9429	100.0	1786	1	LMB1_MOUSE	P02469 mus musculus
2	8873	94.1	1786	1	LMB1_HUMAN	P07942 homo sapien
3	4936	52.3	1801	1	LMB2_RAT	P15800 rattus norv
4	4914	52.1	1799	1	LMB2_MOUSE	P61292 mus musculus
5	4890	51.9	1798	1	LMB2_HUMAN	P55268 homo sapien
6	3734.5	39.6	1790	1	LMB1_DROME	P11046 drosophila
7	1730	18.3	3672	1	LMB2_CAEEL	Q21313 caenorhabdi
8	1682.5	17.8	1639	1	LMG1_DROME	P15215 drosophila
9	1649	17.5	3712	1	LMA_DROME	Q00174 drosophila
10	1618.5	17.2	1609	1	LMG1_HUMAN	P11047 homo sapien
11	1610.5	17.1	1607	1	LMG1_MOUSE	P02468 mus musculus
12	1608	17.1	1535	1	LML1_CAEEL	Q18823 caenorhabdi
13	1584	16.8	3718	1	LMA5_MOUSE	Q61001 mus musculus
14	1575	16.7	303	1	LMB1_CHICK	Q01835 gallus gall
15	1550	16.4	3695	1	LMA5_HUMAN	O15230 homo sapien
16	1535	16.3	3075	1	LMAL_HUMAN	P25391 homo sapien
17	1527.5	16.2	3110	1	LMA2_HUMAN	P24043 homo sapien
18	1497.5	15.9	3106	1	LMA2_MOUSE	C60675 mus musculus
19	1484	15.7	1587	1	LMG3_HUMAN	Q9Y666 homo sapien
20	1482	15.7	3084	1	LMAL_MOUSE	P19337 mus musculus
21	1476.5	15.7	1581	1	LMG2_MOUSE	Q9R066 mus musculus
22	1438.5	15.3	1172	1	LMB3_HUMAN	Q13751 homo sapien
23	1394.5	14.8	1168	1	LMB3_MOUSE	Q61087 mus musculus
24	1330	14.1	3333	1	LMA3_MOUSE	C61079 mus musculus
25	875	9.3	1191	1	LMG2_MOUSE	C61092 mus musculus
26	862.5	9.1	1193	1	LMG2_HUMAN	Q13753 homo sapien
27	668.5	7.1	604	1	NET1_HUMAN	Q95631 homo sapien
28	667	7.1	604	1	NET1_MOUSE	O09118 mus musculus
29	659.5	7.0	606	1	NET1_CHICK	Q90922 gallus gall
30	656	7.0	3707	1	PGBM_MOUSE	Q05793 mus musculus
31	647.5	6.9	4391	1	PGBM_HUMAN	P98160 homo sapien
32	593	6.3	581	1	NET2_CHICK	Q90923 gallus gall
33	583	6.2	612	1	UNC5_CAEEL	P34710 caenorhabdi

34	566.5	6.0	727	1	NETA_DROME	Q24567 drosophila
35	565.5	6.0	1816	1	LMA4_HUMAN	Q16363 homo sapien
36	559.5	5.9	1816	1	LMA4_MOUSE	P97927 mus musculus
37	537	5.7	2319	1	NTC3_RAT	Q91772 rattus norv
38	532	5.6	400	1	LMB_HIRME	Q25092 hirudo medi
39	531	5.6	2524	1	NOTC_XENLA	P21783 xenopus lae
40	527	5.6	2321	1	NTC3_HUMAN	Q9UM47 homo sapien
41	511.5	5.4	2703	1	NOTC_DROME	P07207 drosophila
42	510	5.4	3375	1	UN52_CAEEL	Q06561 caenorhabdi
43	506	5.4	2318	1	NTC3_MOUSE	Q61982 mus musculus
44	497	5.3	2471	1	NTC2_RAT	Q9QW30 rattus norv
45	495.5	5.3	2556	1	NTC1_HUMAN	P46531 homo sapien

ALIGNMENTS

RESULT: LMB1\_MOUSE STANDARD; PRT; 1786 AA.  
ID AC P02469.  
DC LMB1\_MOUSE  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin beta-1 chain precursor (Laminin B1 chain).  
GN LAMB1-1 OR LAMB-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87147212; PubMed=3493487;  
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;  
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a  
RT multidomain protein containing cysteine-rich repeats."  
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).  
RN [2]  
RP SEQUENCE OF 1292-1786 FROM N.A.  
RX MEDLINE=85051302; PubMed=6209134;  
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
RT coiled-coil alpha-helix."  
RL EMBO J. 3:2355-2362(1984).  
RN [3]  
RP SEQUENCE OF 165-172; 539-547 AND 712-719.  
RC STRAIN=BALB/c; TISSUE=Endothelial cells;  
RX MEDLINE=97363207; PubMed=9219532;  
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,  
RA Sorokin L.M.;  
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of  
RT endothelium."  
RL Eur. J. Biochem. 246:727-735(1997).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),  
CC laminin-2 (merosin), and laminin-6 (K-laminin).  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major  
CC component).  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 1 laminin IV domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its



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EMBL; M15525; AAA39407.1; ALT\_INIT.

EMBL; X05212; CAA28839.1; -.

PIR; A28413; MMSBL.

HSP; P02468; IKLO.

MGI; P06743; Lamb1-1.

InterPro; IPR006209; EGF like.

InterPro; IPR002049; Laminin\_EGF.

InterPro; IPR008211; LamNT.

Pfam; PF00053; laminin\_EGF; 13.

Pfam; PF00055; laminin\_Nterm; 1.

PRINTS; PR00011; EGF\_LAMININ.

SMART; SM00180; EGF Lam; 11.

SMART; SM00136; LamNT; 1.

PROSITE; PS00022; EGF-2; 2.

PROSITE; PS01186; EGF-1; 9.

PROSITE; PS01248; LAMININ TYPE EGF; 11.

Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1 21

FT CHAIN 22 1786

FT DOMAIN 22 270

FT DOMAIN 271 334

FT DOMAIN 335 397

FT DOMAIN 398 457

FT DOMAIN 458 509

FT DOMAIN 510 540

FT DOMAIN 541 772

FT DOMAIN 773 820

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FT DOMAIN 1448 1778

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FT DISULFID 300 309

FT DISULFID 312 332

FT DISULFID 335 344

FT DISULFID 337 362

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FT DISULFID 377 395

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FT DISULFID 400 426

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FT DISULFID 806 818

FT DISULFID 821 833

FT DISULFID 823 840

FT DISULFID 842 851

FT DISULFID 854 864

FT DISULFID 867 876

FT DISULFID 883 895

FT DISULFID 886 895

FT DISULFID 898 914 BY SIMILARITY.

FT DISULFID 917 933 BY SIMILARITY.

FT DISULFID 944 955 BY SIMILARITY.

FT DISULFID 946 955 BY SIMILARITY.

FT DISULFID 958 973 BY SIMILARITY.

FT DISULFID 976 990 BY SIMILARITY.

FT DISULFID 978 997 BY SIMILARITY.

FT DISULFID 1000 1009 BY SIMILARITY.

FT DISULFID 1012 1025 BY SIMILARITY.

FT DISULFID 1084 1096 BY SIMILARITY.

FT DISULFID 1086 1103 BY SIMILARITY.

FT DISULFID 1105 1114 BY SIMILARITY.

FT DISULFID 1117 1129 BY SIMILARITY.

FT DISULFID 1132 1144 BY SIMILARITY.

FT DISULFID 1134 1151 BY SIMILARITY.

FT DISULFID 1153 1162 BY SIMILARITY.

FT DISULFID 1165 1176 BY SIMILARITY.

FT DISULFID 1179 1182 INTERCHAIN (PROBABLE).

FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).

FT DISULFID 1185 1185 INTERCHAIN (PROBABLE).

FT CARBOHYD 120 120 N-LINKED (GLCNAC. .)

FT CARBOHYD 356 356 N-LINKED (GLCNAC. .)

FT CARBOHYD 519 519 N-LINKED (GLCNAC. .)

FT CARBOHYD 677 677 N-LINKED (GLCNAC. .)

FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. .)

FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. .)

FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. .)

FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. .)

FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. .)

FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. .)

FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. .)

FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. .)

FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. .)

FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).

FT CONFLICT 1749 1749 D -> N (IN REF. 2).

SQ SEQUENCE 1786 AA; 136904 MW; 846671B7BF41A474 CRC64;

Query Match

Best Local Similarity

Matches 1725; Conservative

100.0%; Score 9429; DB 1; Length 1786;

100.0%; Pred. No. 0;

Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQDKKFCICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV 60

DB 62 EPYCIIVSHLQDKKFCICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV 121

QY 61 TIQLDLAEFHTLIMTKFRPAAMLIERSDFGKTGWYRYFAYDCSSFFGISTGP 120

DB 122 TIQLDLAEFHTLIMTKFRPAAMLIERSDFGKTGWYRYFAYDCSSFFGISTGP 181

QY 121 MKKVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRKIFVKLH 180

DB 182 MKKVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRKIFVKLH 241

QY 181 TLGDNLLDSRMREIKRYYYAVDMVVRGNCFCYGHASECAPVDGVNEVEGWHGCMCR 240

DB 242 TLGDNLLDSRMREIKRYYYAVDMVVRGNCFCYGHASECAPVDGVNEVEGWHGCMCR 301

QY 241 HNTKGLNCELQMDPYHDLWPAPAGRNNAKCKNCNEHSSCHFDMAVFLATGNVSGGV 300

DB 302 HNTKGLNCELQMDPYHDLWPAPAGRNNAKCKNCNEHSSCHFDMAVFLATGNVSGGV 361

QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPTCTDPAGSENGICDGYTDFSVGL 360

DB 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDNLCEPTCTDPAGSENGICDGYTDFSVGL 421

QY 361 IAGQCRCKLHVEGERCDVCKSGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCYC 420

DB 422 IAGQCRCKLHVEGERCDVCKSGFYDLSAEDPYGCKSCACNPLGTIPGNGPCDSETGYCYC 481

QY 421 KELVTGQRCDQCLPQHWGLSNDLQCRPCDCLGALNNSSCSGQSCCLPHMIGROCN 480

DB 482 KELVTGQRCDQCLPQHWGLSNDLQCRPCDCLGALNNSSCSGQSCCLPHMIGROCN 541

481 EVESGYFTTLDHYIYEAEANLPGVVVVERQIQRIPSWTGPFGFVRVPEGAYLEFFI 540  
 Db EVESGYFTTLDHYIYEAEANLPGVVVVERQIQRIPSWTGPFGFVRVPEGAYLEFFI 601  
 QY DNPISMEYELIRYEPQLPDHWEKAVITVOPGKI PASSRCGNTVPDDNQVLSLSPGS 600  
 Db DNPISMEYELIRYEPQLPDHWEKAVITVOPGKI PASSRCGNTVPDDNQVLSLSPGS 661  
 QY RYVVLPRVPCPEKGMNVTYRLELPQYTAGSGDVSPYTFIDSLVLMFYCKSLDIFTVGGG 660  
 Db RYVVLPRVPCPEKGMNVTYRLELPQYTAGSGDVSPYTFIDSLVLMFYCKSLDIFTVGGG 721  
 QY GGEVNTSAWETFORYRCLNSRSVVKTPMTDVCNIIIFSIHALIHTGLACECDPOGSL 720  
 Db GGEVNTSAWETFORYRCLNSRSVVKTPMTDVCNIIIFSIHALIHTGLACECDPOGSL 781  
 QY SSVCDPNGGQCCRNVRVGRTCNRCAPGTFFGPGNGCKPCDCHLOGSASAFCDAITGQCH 780  
 Db SSVCDPNGGQCCRNVRVGRTCNRCAPGTFFGPGNGCKPCDCHLOGSASAFCDAITGQCH 841  
 QY CFQGIYARQCDRLCPGNGFSPCQPCQNGHALDQDVTGSCLSQDVTTHGNCERCLAG 840  
 Db CFQGIYARQCDRLCPGNGFSPCQPCQNGHALDQDVTGSCLSQDVTTHGNCERCLAG 901  
 QY YGDFPIIGSGDHCRCPCPDGPDGRQFARSQYQDPVTLQACVCPGYIGSRCDCCASG 900  
 Db YGDFPIIGSGDHCRCPCPDGPDGRQFARSQYQDPVTLQACVCPGYIGSRCDCCASG 961  
 QY PFGNPSDFGSGCOPCQCHNIDTTPDCAKDTGSKCLVHTGHDHQLQCYGYGDAL 960  
 Db PFGNPSDFGSGCOPCQCHNIDTTPDCAKDTGSKCLVHTGHDHQLQCYGYGDAL 1021  
 QY RODRCKVCNLYGTVEKNGSGDCHDKATGSCCLPNVIGONCDRCAPNTWQASGTGC 1020  
 Db RODRCKVCNLYGTVEKNGSGDCHDKATGSCCLPNVIGONCDRCAPNTWQASGTGC 1081  
 QY GPCNCAHNSFGPSNEFTGQCCMPFGGRTSCSEQLFWGDPDVECRACDPCPRGIET 1080  
 Db GPCNCAHNSFGPSNEFTGQCCMPFGGRTSCSEQLFWGDPDVECRACDPCPRGIET 1141  
 QY PQCDOSTGCVGVEGPRCDKTRGYSVGFDPDCTPCHQCFALMDAIIIGLTHRTKFL 1140  
 Db PQCDOSTGCVGVEGPRCDKTRGYSVGFDPDCTPCHQCFALMDAIIIGLTHRTKFL 1201  
 QY EKAKALKISGVIPYRETVDSEKVKNEIKOILAQSPAAEPLKNTGILFEEAEKLTQDVT 1200  
 Db EKAKALKISGVIPYRETVDSEKVKNEIKOILAQSPAAEPLKNTGILFEEAEKLTQDVT 1261  
 QY EKMAQVEVKLTDTASQNSNITAGELGALQAEBSLDTVKELAEQLEFINKSDIQALDSI 1260  
 Db EKMAQVEVKLTDTASQNSNITAGELGALQAEBSLDTVKELAEQLEFINKSDIQALDSI 1321  
 QY TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEQEQLLDEL 1320  
 Db TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQEQEQLLDEL 1381  
 QY AGKLSLDLSAAQNTCGTPPGADGSEBEGCPNCRDTEGKCGGCGGLVTVHSAW 1380  
 Db AGKLSLDLSAAQNTCGTPPGADGSEBEGCPNCRDTEGKCGGCGGLVTVHSAW 1441  
 QY QKAMPDFRDLVLSALAEVEQLSRWSEAKVRDEAKONAQDVLKTNATKEKVDKSNEDLR 1440  
 Db QKAMPDFRDLVLSALAEVEQLSRWSEAKVRDEAKONAQDVLKTNATKEKVDKSNEDLR 1501  
 QY NLIKQIRNFLTDSADLSIEAVANEVLKSGNASTPQQLQNTEDIRREVETLSQVEVIL 1500  
 Db NLIKQIRNFLTDSADLSIEAVANEVLKSGNASTPQQLQNTEDIRREVETLSQVEVIL 1561  
 QY QOSADIAEAEKLLLEAKBSASDVTVDWVKEALEEAEKVAEAKAIKQADEDIQ 1560  
 Db QOSADIAEAEKLLLEAKBSASDVTVDWVKEALEEAEKVAEAKAIKQADEDIQ 1621  
 QY GTQNLITSIETASAEETLTNASORISKLEENVEFELKRAAQNSEGEAYIEKVVYSVKO 1620

RESULT 2

LMBI\_HUMAN STANDARD; PRT; 1786 AA.  
 ID LMB1\_HUMAN AC P07942;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Laminin beta-1 chain precursor (Laminin B1 chain).  
 GN LMB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90368768; PubMed=1975589;  
 RA Vuolteenaho R., Chow L.I., Tryggvason K.;  
 RT "Structure of the human laminin B1 chain gene.";  
 RL J. Biol. Chem. 265:15611-15616(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87280097; PubMed=3611077;  
 RA Pikkaraenen T., Bddy R., Fukushima Y., Byers M., Shows T.,  
 RA Phalajaniemi T., Saraste M., Tryggvason K.;  
 RT "Human laminin B1 chain. A multidomain protein with gene (LMB1)  
 RT locus in the q22 region of chromosome 7.";  
 RL J. Biol. Chem. 262:10454-10462(1987).  
 RN [3]  
 RP SEQUENCE OF 1276-1709 FROM N.A.  
 RX MEDLINE=98021029; PubMed=3661559;  
 RA Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,  
 RA Drohan W.N.;  
 RT "Isolation of a cDNA clone for the human laminin-B1 chain and its  
 RT gene localization.";  
 RL Am. J. Hum. Genet. 41:605-615(1987).  
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
 CC is thought to mediate the attachment, migration and organization  
 CC of cells into tissues during embryonic development by interacting  
 CC with other extracellular matrix components.  
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
 CC different polypeptide chains (alpha, beta, gamma), which are bound  
 CC to each other by disulfide bonds into a cross-shaped molecule  
 CC comprising one long and three short arms with globules at each  
 CC end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),  
 CC laminin-2 (merosin), and laminin-6 (K-laminin).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major  
 CC component).  
 CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact  
 CC with other laminin chains to form a coiled coil structure.  
 CC -!- DOMAIN: Domains VI and IV are globular.  
 CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
 CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.  
 CC -!- SIMILARITY: Contains 1 laminin IV domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)



QY 1 EPYCIVSHLOEDKKCFICDSDDPHETLNPDHSHLIENVVTFEAPNRUKIWWQSENGYV 60  
DB 2 EPYCIVSHLOEDKKCFICNSQDPHETLNPDHSHLIENVVTFEAPNRUKIWWQSENGYV 121  
QY 61 TIQDLEAFHFTLIMTKTFRPAAMLIERSSDFGKTGWYRYPAYDCBSSPFGISTGP 120  
DB 122 TIQDLEAFHFTLIMTKTFRPAAMLIERSSDFGKTGWYRYPAYDCBSSPFGISTGP 181  
QY 121 MKKYDDIICDSRYSDIBPSTGEVIFRALDPAFKIEDPYSPRIQNLKJITNLRKFVKLH 180  
DB 182 MKKYDDIICDSRYSDIBPSTGEVIFRALDPAFKIEDPYSPRIQNLKJITNLRKFVKLH 241  
QY 181 TLGNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGCMCR 240  
DB 242 TLGNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGCMCR 301  
QY 241 HNTGLNCELQMDPYHDLPRWPAGRNSACKKCNCHESCHDFDPAFLATGNVSGGV 300  
DB 302 HNTGLNCELQMDPYHDLPRWPAGRNSACKKCNCHESCHDFDPAFLATGNVSGGV 361  
QY 301 CDNCQHNMTGNRCQCKPFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 362 CDNCQHNMTGNRCQCKPFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421  
QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGNCPCDSETHCYC 420  
DB 422 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGNCPCDSETHCYC 481  
QY 421 KRLVTGQRCDOCLPOHWGLSNDLQRCPCDCLGGALNNSCESDSGCSCLPHMIGROCN 480  
DB 482 KRLVTGQRCDOCLPOHWGLSNDLQRCPCDCLGGALNNSCESDSGCSCLPHMIGROCN 541  
QY 481 EVESGYFTTLDHYIYEAEANLGGVVRVVERQYIQDRIPSWTQPGFVRVPEGALEYFFI 540  
DB 542 EVESGYFTTLDHYIYEAEANLGGVVRVVERQYIQDRIPSWTQPGFVRVPEGALEYFFI 601  
QY 541 DNIPIYSMEYDILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDNQVVSLSPGS 600  
DB 602 DNIPIYSMEYDILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDNQVVSLSPGS 661  
QY 601 RYVVLPRVCFEKGNYTVRLELPQYTAGSDVSPYTFIDSLVLMPCYKSLDIFTVGS 660  
DB 662 RYVVLPRVCFEKGNYTVRLELPQYTAGSDVSPYTFIDSLVLMPCYKSLDIFTVGS 721  
QY 661 GDGEVTSNAWETFORYLENSRSVVKTPMTDVCNRIIFISALIHOTGLACEDCPGSL 720  
DB 722 GDGEVTSNAWETFORYLENSRSVVKTPMTDVCNRIIFISALIHOTGLACEDCPGSL 781  
QY 721 SSVCDPNNGGQCRPNVVRGTRCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 780  
DB 782 SSVCDPNNGGQCRPNVVRGTRCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 841  
QY 781 CFQGIYARQDRCLPGYWGFPSCQPCQNGHALDCDVTGECISCDQYTTGHCNRCCLAG 840  
DB 842 CFQGIYARQDRCLPGYWGFPSCQPCQNGHALDCDVTGECISCDQYTTGHCNRCCLAG 901  
QY 841 YGDPPIGSGHCHPCPCPDGPDGSRGFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
DB 902 YGDPPIGSGHCHPCPCPDGPDGSRGFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 961  
QY 901 PFGNPSDFGSCQPCQCHHNITDTPBACDKOTGRCLKCLYHTEGDHCLQCYGYGYGDAL 960  
DB 962 YFGNPSDFGSCQPCQCHHNITDTPBACDKOTGRCLKCLYHTEGDHCLQCYGYGYGDAL 1021  
QY 961 RQDCRKCVCNVLGTVKEHNGSDCHCKATGQCSCLPNVIGQNCDCRCPAPNTWLASTGC 1020  
DB 1022 RQDCRKCVCNVLGTVKEHNGSDCHCKATGQCSCLPNVIGQNCDCRCPAPNTWLASTGC 1081  
QY 1021 GPCNCAHSPGSCNEFTGQCQCMQPGFGGRTGTCSECQELFWGDPDVECRACDCDPRGIET 1080  
DB 1082 DPCNCAHSPGSCNEFTGQCQCMQPGFGGRTGTCSECQELFWGDPDVECRACDCDPRGIET 1141  
QY 1081 PQDQSTGQCVCVSGVEGPRCKCTRGYSVGVFPDCTPCHQCFALWDIAIIGELNTRHKFL 1140

DB 1142 PQDQSTGQCVCVSGVEGPRCKCTRGYSVGVFPDCTPCHQCFALWDIAIIGELNTRHKFL 1201  
QY 1141 EKAKALKISGVIGPYRETVDVSEKVKNEIKDILASPAEPLKNIGILFEBAEKLTQV 1200  
DB 1202 EKAKALKISGVIGPYRETVDVSEKVKNEIKDILASPAEPLKNIGILFEBAEKLTQV 1261  
QY 1201 EKMAQVEVKLTDTASQSNSTAGELQALQAEBSLQTKVLAELQEFIKNSDIRGALDSI 1260  
DB 1262 EKMAQVEVKLTDTASQSNSTAGELQALQAEBSLQTKVLAELQEFIKNSDIRGALDSI 1321  
QY 1261 TKYFQMSLEAEKVRNASTTDPNSTVQEGALTRDRVEDLMLERESPCKQBEQALDEL 1320  
DB 1322 TKYFQMSLEAEKVRNASTTDPNSTVQEGALTRDRVEDLMLERESPCKQBEQALDEL 1381  
QY 1321 AGKLSLDLSAAAOQTCGTPPGADCSGEGCGPCNCTDEGEKKCGGPGCGGLTVVAHSAW 1380  
DB 1382 AGKLSLDLSAAAOQTCGTPPGADCSGEGCGPCNCTDEGEKKCGGPGCGGLTVVAHSAW 1441  
QY 1381 QKAMPDRDVLASALAEVQSLSKVSEAKVRADEAKQNAQDVLKTNATKVKDKNEDLR 1440  
DB 1442 QKAMPDRDVLASALAEVQSLSKVSEAKVRADEAKQNAQDVLKTNATKVKDKNEDLR 1501  
QY 1441 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVELTSQVEVIL 1500  
DB 1502 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVELTSQVEVIL 1561  
QY 1501 QOSADIAEAEALLBEAKRSATDVKVTADMVKEALEEAKQVAAEKAQKQADEDIQ 1560  
DB 1562 QOSADIAEAEALLBEAKRSATDVKVTADMVKEALEEAKQVAAEKAQKQADEDIQ 1621  
QY 1561 GTONLLTSTESSTAASEETLTNASQRISEKERNVEELKRAAQNSEGEAYIEKVYVYVKQ 1620  
DB 1622 GTONLLTSTESSTAASEETLTNASQRISEKERNVEELKRAAQNSEGEAYIEKVYVYVKQ 1681  
QY 1621 NADDVKTLDGDELDEKYYKVKESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLE 1680  
DB 1682 NADDVKTLDGDELDEKYYKVKESLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLE 1741  
QY 1681 DLERYEDNQYLEDKAEQELVLEGEVSLKQDISEKVAVYSTCL 1725  
DB 1742 DLERYEDNQYLEDKAEQELVLEGEVSLKQDISEKVAVYSTCL 1786

RESULT 3  
LMB2\_RAT  
ID LMB2\_RAT STANDARD; PRT; 1801 AA.  
AC P15800;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).  
GN LAMB2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]\_TaxID=10116;  
RP SEQUENCE FROM N.A.  
RC Tissue=Liver;  
RX MEDLINE=89159410; PubMed=2922051;  
RA Hunter D.D.; Shah V.; Merlie J.P.; Sares J.R.;  
RT "A laminin-like adhesive protein concentrated in the synaptic cleft  
of the neuromuscular junction."  
RL Nature 338:229-234(1989).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each



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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 46.7946 Seconds

(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-12

Perfect score: 9429

Sequence: 1 EFCYVSHLQEDKCFICDS.....EVRSLKDISEKAVYSTCL 1725

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6600	70.0	1785	13	Q8JHV7 brachydanio
2	5434	57.6	1086	4	Q8TAS6
3	5195	55.1	984	11	Q8K271
4	5162	54.7	1792	13	Q57484
5	4934	52.3	1799	11	Q8R0Y0
6	4790	50.8	911	11	Q9CRX6
7	3712.5	39.4	1761	4	Q86XN2
8	3631.5	38.5	1827	13	Q8JHV6
9	3506.5	37.2	1631	4	Q9Y6U6
10	2741	29.1	1067	5	Q44565
11	2271.5	24.1	1168	5	Q96758
12	1936	20.5	1026	5	Q8SWY0
13	1914	20.3	761	4	Q9UH12
14	1832	19.4	1069	5	Q9BP52
15	1730	18.3	3704	5	P91904
16	1645	17.4	3712	5	Q9VRW0

17 1623 17.2 1593 13 Q8JHV8  
18 1615 17.1 1623 5 Q9U3U7  
19 1558 16.5 3695 4 Q8TDF8  
20 1402.5 14.9 1168 11 Q91V90  
21 1342 14.2 1007 13 Q90ZK3  
22 1276.5 13.5 3102 5 Q45614  
23 1206.5 12.8 2731 5 Q9VJTS  
24 1206.5 12.8 3367 5 Q9XZ29  
25 1206.5 12.8 3375 5 Q8IP51  
26 1101 11.7 1546 4 Q9NS27  
27 1099 11.7 1546 4 Q75445  
28 1064 11.3 1486 4 Q14637  
29 1041 11.0 1461 11 Q9JLP3  
30 1032 10.9 750 4 Q86TP7  
31 978.5 10.4 616 4 Q15483  
32 964 10.2 1512 11 Q8K3K1  
33 932 9.9 628 11 Q9J133  
34 925 9.8 628 4 Q9HB63  
35 925 9.8 628 4 Q9BZP1  
36 910 9.7 605 4 Q7Z5B6  
37 875.5 9.3 1190 6 Q8HZ19  
38 872.5 9.3 1196 6 Q867A2  
39 863.5 7.2 1664 5 Q9TVQ2  
40 680 7.2 1574 11 Q88281  
41 666 7.1 604 11 Q92429  
42 664 7.0 1140 4 Q96KG7  
43 663 7.0 529 4 Q8N2D6  
44 661.5 7.0 1045 5 Q8T3A6  
45 661.5 7.0 1070 5 Q8T3A7

#### ALIGNMENTS

#### RESULT 1

Q8JHV7 PRELIMINARY; PRT; 1785 AA.  
AC Q8JHV7;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Laminin beta 1.  
GN LAMBL.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22065263; PubMed=12070089;  
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,  
RA Hirst E.M., Stemple D.L.;  
RT "Zebrafish mutants identify an essential role for laminins in  
RT notochord formation";  
RL Development 129:3137-3146(2002).  
DR EMBL; AF488049; AAM61767.1; -;  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00053; laminin\_EGF; 13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PRO0011; EGF\_LAMININ.  
DR SMART; SM00180; EGF\_Lam; 13.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
KW Laminin EGF-like domain.  
SQ SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;

Query Match	70.0%	Score	6600	DB	13	Length	1785
Best local Similarity	67.2%	Pred. No.	1.9e-282				
Matches 1162; Conservative	242	Mismatches	319	Indels	6	Gaps	6

QY	1	EPYCIVSHLQEDKKKCFICRSRDPYHETLNP-DSHLIENVVTTTAPNRLKTIWQSENGVEN	59
DB	58	EPYCIVSHLQEEKCFVCDSRQAYNETAHQVTSHTSIENVVTTTAPNRLKTIWQSENGLEN	117
QY	60	VTIQLDLAEAFHFTHTLIIMTKTTPRAPMLIERSDFGKTGWVRYRYPAYCESSFPDIOSTG	119
DB	118	VTIQLDLAEAFHFTHTLIIMTKTTPRAPAMVLIERSADFGNTMQVRYRYPAYCESSFPFVSVG	177
QY	120	PMKKVDDIICDSVSDIEPSTEGEVIFRALDPFAFKIEDPYSPRIQNLKLTINLIRIKFVKL	179
DB	178	PMTKVDDVICDTRYSDIEPSTEGEVIFRLDPAFRIEDPYSPRIQNLKLTINLIRVAFETKL	237
QY	180	HTLGDNLLDSRMIREKYYIYAVDMVVRGNCFCYGHASECAPVDGVNVEVGHVGHGCMC	239
DB	238	HTLGDNLLDSRIEIKETKYYIYALDMVVRGNCFCYGHASECAPVDGTGEAVEGVGHGCMC	297
QY	240	RHNTKGLNCLCNDVFHDLPRWPAEGRNSNACKKCNNEHSSSCHFDMAVELATGNVSGG	299
DB	298	NHNTIGLNCERCQDFYHDLPRWPAEGRNNTNACKKCNHSHSCHFDMAVYRASGNVSGG	357
QY	300	VCNQCQNTWGRNCEQCKPPYFQHPERDIRDPNLCPCTCDPAGSENGGICDGYTDFPSVG	359
DB	358	VCDDCQNTWGNCEQCKPPFHQPEKDIRDPNICPCNDPVGSLNGGVCDDPMTDVSIG	417
QY	360	LIAGOCCKLHVGERCOVCKEGFYDLSADBPVGCKSCACNPLGTTIPGNGPCDSEGTGYC	419
DB	418	LISGQCRCKPNVGERCDQCQKHGYGLS-BDPLGCQPCTCNAUGTPVGGSPCDTDSGNCY	476
QY	420	CKRLVTGORCDQLPQHWGLSNDLGDRCPCDCLGGALNNSCSDSGQSCSLPHMIGROC	479
DB	477	CKRLVTGRNCDQLPQHWGLSNDWDGCRPCDDHGGAINNCCSPVSGQCCQCEHMFGRRC	536
QY	480	NEVESGYFTTLDHYIYEAEBANLGPQVVVERQYIQDRIPSWTGSGFVVRPGAVLEFF	539
DB	537	DOVESGYFTALDHYTYEABEAXFGPGVTVVRPNHPQDRSPTWTGTGFVNVPEGAFLEPS	596
QY	540	IDNIPIYSMEIILIRYEBPOLPDHWEKAVITVQRPKIPASSRGCNTVPDDDNQVSLSPG	599
DB	597	IDNIPIYSMEDLIRIYEPQIPQEWEEVLMVIVPRVITADSRCAINTMPDDDNQVSLHPG	656
QY	600	SRVYVLP RPVCYCFKGMNYYVRLPEQYTAGS DVEGSPYTFIDSLVLMPYCKSLDITVVG	659
DB	657	SRVYVLP RPVCYCFBEGNLYVRLSLYSAL-SDVQSPYTLIDSLVLMPHCKNLIDIFSGSG	715
QY	660	SGDGE-VTNSAMETFORVRCLENSRSVVKTPMTDVCRNIIFSALIHOTGLACEDCDPOG	718
DB	716	TEGNLVNTNSAWENFORVRCLENSQAVVVKTPMTDICKRNIYFSVALLHGVKACQCDPOG	775
QY	719	SLSSVCDPNEGQCCQCRPNVYGRITCNRCAPGTGFGPNCGKPCBCHLQGSASAFCDATIGQ	778
DB	776	SLSTVCDPSGQCCQCRPNVYGRNCDRCAPATELFXPOGCRPCDCSPGSHVSYCHEATGQ	835
QY	779	CHCFQGIYARQCDRLGIYGVGFSCQPCQNGHALDDOTVTGECLSODYTTGHCNCRCL	838
DB	836	CECTIAGAYGRQCDRLFGYGVGFNCRCTCNHABEQCDPQTGQCLSCDRDHTTGHNCERCL	895
QY	839	AGYVGDPIIIGSDHRCRCPCPDGDSGRQPARSCYQDPVTILQACVCDPGYIGSRCDCCA	898
DB	896	GGYVGDPIVLSGDHRCRCQPCPDGDSGRQPSGACYKSPDSSQVFCVNCQYKGARCECA	955
QY	899	SGFFGNPDSDFGGSQPCQCOCHNITDTPDPAKDDTGTGCLKCLYHTEGDHQLCQGYIGD	958
DB	956	PGYVGNPHEVGECRPCQCNSIIMDMDPESCDARTGACVCKLHYHTEGESCNRCRLGYIGN	1015
QY	959	ALRQDCKRCVNYLTGVKEHC-NGSDCHCDKATGQSCCLPNVLIGONCDRCAPNTWOLASG	1017
DB	1016	ALTQSCRKVCVNCQMGTVEMECPSGNCNCDLTSQCLCLPNVVGQHQDCCAPDTWNASG	1075
QY	1018	TGCGFCPCNNAHSFGPSCNEFTGQCQWMPFGGRTCECELEFPWGDPDFECRACDDPGR	1077



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 / Search time 43.6478 seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-14  
Perfect score: 8713  
Sequence: 1 MEGSHRAAPALPRGRLLWPV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLCUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8713	100.0	1609	3 AAB19801	Aab19801 Human lam
2	8713	100.0	1609	3 AAB48452	Aab48452 Human lam
3	8713	100.0	1609	5 ABB81594	Abb81594 Human lam
4	8713	100.0	1609	7 ADC01887	Adc01887 Human lam
5	8713	100.0	1617	3 AAB19803	Aab19803 Human lam
6	8709	100.0	1609	2 AAW50898	Aaw50898 Human lam
7	8544	98.1	1576	3 AAB19802	Aab19802 Human lam
8	8544	98.1	1576	3 AAB48453	Aab48453 Human lam
9	8544	98.1	1576	5 ABB81595	Abb81595 Human lam
10	8544	98.1	1584	3 AAB19804	Aab19804 Human lam
11	8148	93.5	1605	3 AAB19805	Aab19805 Mouse lam
12	8148	93.5	1605	3 AAB48454	Aab48454 Mouse lam
13	8148	93.5	1605	5 ABB81596	Abb81596 Mouse lam
14	8147	93.5	1607	2 AAW50897	Aaw50897 Mouse lam
15	8038	92.3	1572	3 AAB19806	Aab19806 Mouse lam
16	8038	92.3	1572	3 AAB48455	Aab48455 Mouse lam
17	8038	92.3	1572	5 ABB81597	Abb81597 Mouse lam
18	3613	41.5	1587	3 AAB40917	Aab40917 Human ORF
19	3611	41.4	1587	5 AAM50361	Aam50361 Mouse lam
20	3611	41.4	1587	6 ABR58467	Abr58467 Human NOV
21	3609	41.4	1575	6 ABR58468	Abr58468 Human NOV
22	3463.5	39.8	1524	6 AAY15458	Aay15458 Human lam
23	3440	39.5	1639	4 ABB59807	Abb59807 Drosophil
24	2637	30.3	1193	2 AAR91427	Aar91427 Kalinin/1
25	2637	30.3	1193	3 AAB48468	Aab48468 Human lam

26	2637	30.3	1193	5 AAE14712	Aae14712 Human lam
27	2637	30.3	1193	5 AAO14992	Aao14992 Laminin g
28	2637	30.3	1193	6 ABR48214	Abr48214 Human bla
29	2637	30.3	1193	6 ABUS6696	Abus6696 Lung canc
30	2637	30.3	1193	6 ABUS6696	Abus6696 Lung canc
31	2637	30.3	1193	6 ABR92103	Abr92103 Human cer
32	2637	30.3	1193	6 ADA74120	Ada74120 Human lam
33	2630	30.2	1172	3 AAB48469	Aab48469 Human lam
34	2629	30.2	1193	3 AAB48470	Aab48470 Human lam
35	2622	30.1	1172	3 AAB48471	Aab48471 Human lam
36	2612.5	30.0	1190	6 ADA74091	Ada74091 Equine la
37	2516.5	28.9	1111	2 AAR91428	Aar91428 Kalinin/1
38	2516.5	28.9	1111	5 AAE14713	Aae14713 Human lam
39	2516.5	28.9	1111	5 AAO14993	Aao14993 Laminin g
40	2454.5	28.2	1171	3 AAB48473	Aab48473 Mouse lam
41	2454.5	28.2	1192	3 AAB48472	Aab48472 Mouse lam
42	2454.5	28.2	1192	5 AAE14711	Aae14711 Mouse lam
43	2454.5	28.2	1192	6 ADA74121	Ada74121 Murine la
44	2355.5	27.0	1171	2 AAW26583	Aaw26583 Rat hemid
45	1783.5	20.5	3122	7 ADB61794	Adb61794 Human Pro

ALIGNMENTS

RESULT 1  
AAB19801  
ID AAB19801 standard; protein; 1609 AA.

XX AC AAB19801;  
XX DT 05-MAR-2001 (first entry)  
XX DE Human laminin 2 gamma-1 chain.  
XX KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
XX KM degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..33  
FT Protein /label= Signal\_peptide  
FT Protein 34..1609  
FT Protein /label= Mature\_protein  
XX PN WC200066730-A2.

XX PD 09-NOV-2000.  
XX PF 28-APR-2000; 2000MO-US011378.  
XX PR 30-APR-1999; 99US-0131720P.  
XX PR 15-JUN-1999; 99US-0139198P.  
XX PR 12-JUL-1999; 99US-0143289P.  
XX PR 24-SEP-1999; 99US-0155945P.  
XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX PI Yurchenco P;  
XX DR WPI; 2000-687537/67.  
XX DR N-PSDB; AAA88901.

XX PT Purified laminin 2 protein, useful for research and therapeutic purposes  
XX PT including peripheral nerve regeneration, treatment of degenerative muscle  
XX PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX PS Claim 5; Page 239-244; 305pp; English.  
XX CC The present sequence is that of the gamma-1 chain of human laminin 2.  
XX CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
XX CC (100 kDa) chains. It is thought to be specifically required for

CC	stabilizing myotubes during skeletal muscle development, and for
CC	preventing apoptosis. Genetic defects in its structure or expression are
CC	associated with a major type of congenital muscular dystrophy. Laminin 2
CC	is also thought to be important in Schwann cell/basal lamina
CC	interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-
CC	1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding
CC	them (see AA48891-906), methods for making recombinant laminin 2, cells
CC	that express recombinant laminin 2, and methods for using purified
CC	laminin 2 for research and therapeutic purposes including peripheral
CC	nerve regeneration, treatment of degenerative muscle disorders,
CC	angiogenesis regulation, promoting cell attachment and migration, ex vivo
CC	cell therapy, improving the take of grafts, improving the
CC	biocompatibility of medical devices and preparing improved culture
CC	devices and media
XX	
SQ	Sequence 1609 AA;
	Query Match 100.0%; Score 8713; DB 3; Length 1609;
	Best Local Similarity 100.0%; Fred. No. 0;
	Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 MRGSRAAPALPRGLMPVLAVLAAAAAACAQAAMDECTDGGRPQRCPEFVNAAFN 60
Db	1 MRGSRAAPALPRGLMPVLAVLAAAAAACAQAAMDECTDGGRPQRCPEFVNAAFN 60
Qy	61 VTVVATNTCGTPPEYCYQTVGTGYSKCHLCDAGPHLOHGAFLTDYNNQADTTWMS 120
Db	61 VTVVATNTCGTPPEYCYQTVGTGYSKCHLCDAGPHLOHGAFLTDYNNQADTTWMS 120
Qy	121 QTMLAGVQVPSSINLTLLHGAFTDITYVRLKFHTSRPESFALYKRTREDGFWIPYQYSG 180
Db	121 QTMLAGVQVPSSINLTLLHGAFTDITYVRLKFHTSRPESFALYKRTREDGFWIPYQYSG 180
Qy	181 SCENTYSKANRGFIRTGDEQQALCTDFSDISPLTGNVAFSTLEGRSPAYNFDNSPVL 240
Db	181 SCENTYSKANRGFIRTGDEQQALCTDFSDISPLTGNVAFSTLEGRSPAYNFDNSPVL 240
Qy	241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNFF 300
Db	241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNFF 300
Qy	301 DKLVCKNKNTYGVDCCKLPFPNDPRPWRATASASECLPCDNGSQRCEYDPELYXS 360
Db	301 DKLVCKNKNTYGVDCCKLPFPNDPRPWRATASASECLPCDNGSQRCEYDPELYXS 360
Qy	361 TGHGGHCTNQDNTGAHCERENRFFRLGNNEACSSCHSPVGLSTQCDSYGRCSCKP 420
Db	361 TGHGGHCTNQDNTGAHCERENRFFRLGNNEACSSCHSPVGLSTQCDSYGRCSCKP 420
Qy	421 GVMGDKCDRCQPGFSLHTAGCRPCSDPPSGSIDECNVETGRVCYKDNTEGFNCERCKPG 480
Db	421 GVMGDKCDRCQPGFSLHTAGCRPCSDPPSGSIDECNVETGRVCYKDNTEGFNCERCKPG 480
Qy	481 FFNLESNNRGCTPFCFCFHSSVCNTNAVGVSYVISSTTFQIDEDGWRABQRDGEASLEW 540
Db	481 FFNLESNNRGCTPFCFCFHSSVCNTNAVGVSYVISSTTFQIDEDGWRABQRDGEASLEW 540
Qy	541 SSRQDIAVISDSYFPFYPIAFAKFLGQVLSYGNLSPFRVDRDRTRLASDLVLEGA 600
Db	541 SSRQDIAVISDSYFPFYPIAFAKFLGQVLSYGNLSPFRVDRDRTRLASDLVLEGA 600
Qy	601 GLRVSPFLIAQGNYSYSESTTVKYVFLRHEATDYPWRPALTPFEFQKLNLLNTSIKIRGTY 660
Db	601 GLRVSPFLIAQGNYSYSESTTVKYVFLRHEATDYPWRPALTPFEFQKLNLLNTSIKIRGTY 660
Qy	661 SERSAGVLDVTLASARPGGVPATWBSCTCPVYGQFCFCEMLCSGYRRETNLGPYSP 720
Db	661 SERSAGVLDVTLASARPGGVPATWBSCTCPVYGQFCFCEMLCSGYRRETNLGPYSP 720
Qy	721 CVLACACNGHSETCDPETGVCNCRDNTAGPHEKCSGDGYIGDSTAGTSDCQPCPCGGSS 780
Db	721 CVLACACNGHSETCDPETGVCNCRDNTAGPHEKCSGDGYIGDSTAGTSDCQPCPCGGSS 780

[illegible]

Db 1501 INARRAKQSVTSLSIINDLLQLQGLDVTDLNKLNEIEGLTNKAKEMKVSDDLDRKUSD 1560  
QY 1561 LENEAKQBAAMDMYNDIIEIMKDINLEDIRKTLPSGCGNTSPSIEKP 1609  
Db 1561 LENEAKQBAAMDMYNDIIEIMKDINLEDIRKTLPSGCGNTSPSIEKP 1609

RESULT 3  
ID ABB81594  
XX ABB81594 standard; protein; 1609 AA.  
AC ABB81594;  
XX DT 19-SEP-2002 (first entry)  
XX Human laminin 10 third chain protein sequence SEQ ID NO:14.  
DE Laminin alpha 5; laminin 10; vulnarary; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..33  
FT /label= signal  
FT Protein 34..1609  
FT /label= laminin\_10\_third\_chain  
XX WO200250111-A2.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P.  
XX 28-MAR-2001; 2001US-0279282P.  
XX 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
XX WPI; 2002-557650/59.  
XX N-PSDB; ABQ72912.  
XX New human laminin-10 proteins, useful for accelerating the healing of  
XX vascular tissue, improving the biocompatibility of grafts, or for  
XX promoting re-endothelialization at the site of vascular injuries.  
XX Claim 9; Page 165-170; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
XX an isolated laminin 10. Laminin 10 has vulnarary activity. Laminins are  
XX useful in maintaining cell/tissue phenotype as well as promoting cell  
XX growth and differentiation in tissue repair development. Specifically,  
XX laminin 10 can be used for accelerating the healing injuries of vascular  
XX tissue, improving the biocompatibility of grafts useful for treating such  
XX injuries, for promoting re-endothelialisation at the site of vascular  
XX injuries, and promote cell attachment and subsequent cell stasis,  
XX proliferation, differentiation, and/or migration. The present sequence  
XX represents a third chain protein of laminin 10, from the present  
XX invention  
XX Sequence 1609 AA;  
XX  
XX Query Match 100.0%; Score 8713; DB 5; Length 1609;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX 1 MRGSHRAAPALPRGRWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60

Db 1 MRGSHRAAPALPRGRWPVLAVLAAAAAGCAQAAMDECTDEGGRPQRCMPFVNAAFN 60  
QY 61 VTVATNTCGTPPEYCVQGTGVTGKSKCHLSDAGOPHLQHGAAFLTDVNNQADTTWQOS 120  
Db 61 VTVATNTCGTPPEYCVQGTGVTGKSKCHLSDAGOPHLQHGAAFLTDVNNQADTTWQOS 120  
QY 121 QTMLAGVOYSSINLTLHLKGAEDITYRLKFTSPESFAIYKRTREDGPMIPYIYSG 180  
Db 121 QTMLAGVOYSSINLTLHLKGAEDITYRLKFTSPESFAIYKRTREDGPMIPYIYSG 180  
QY 181 SCENTYSKANRGFTIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSPVL 240  
Db 181 SCENTYSKANRGFTIRTGDEQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNDSPVL 240  
QY 241 QEWMTATDITVTLNRLNTPGDEVNDPKVLKSYVYAIISDFAVGGRCKNGHASECKMNEF 300  
Db 241 QEWMTATDITVTLNRLNTPGDEVNDPKVLKSYVYAIISDFAVGGRCKNGHASECKMNEF 300  
QY 301 DKLVCNCKHNTYGVDCBKLPFFNDRPMRRATAESASECLPCDCNGRSQECYFDPPELYRS 360  
Db 301 DKLVCNCKHNTYGVDCBKLPFFNDRPMRRATAESASECLPCDCNGRSQECYFDPPELYRS 360  
QY 361 TGHGHCNTCODNTDGAHCERENFRGLNNEACSSCHSPVGSLSSTOCDSYGRCSCKP 420  
Db 361 TGHGHCNTCODNTDGAHCERENFRGLNNEACSSCHSPVGSLSSTOCDSYGRCSCKP 420  
QY 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDIECNVETGRVCCKNVEGFNCRCRKP 480  
Db 421 GVMGDKCDRCQPGFHSLTEAGCRPCSDPSGSDIECNVETGRVCCKNVEGFNCRCRKP 480  
QY 481 FFNLESSNPGCTPCFCFHSSTVCTNAVGVSYVTSSTFQDDEGWRAEQDGSASLEW 540  
Db 481 FFNLESSNPGCTPCFCFHSSTVCTNAVGVSYVTSSTFQDDEGWRAEQDGSASLEW 540  
QY 541 SSERQDIAVISDSYPPRYFIAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA 600  
Db 541 SSERQDIAVISDSYPPRYFIAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA 600  
QY 601 GLRVSVPLIAQNSYPSSETTVKVFRLHEATDYPWRPALTPFEFQKLNNTLSIKIRGTY 660  
Db 601 GLRVSVPLIAQNSYPSSETTVKVFRLHEATDYPWRPALTPFEFQKLNNTLSIKIRGTY 660  
QY 661 SERSAGYLDVTLASARPQGVPAATWVESCTCPVGGQFCMCLSGYRRRTNLPYSP 720  
Db 661 SERSAGYLDVTLASARPQGVPAATWVESCTCPVGGQFCMCLSGYRRRTNLPYSP 720  
QY 721 CVLCAKNGHSETCDPETGVNCRDNTAGPHCEKSDGYGSDTAGTSDDCQPCPCGSS 780  
Db 721 CVLCAKNGHSETCDPETGVNCRDNTAGPHCEKSDGYGSDTAGTSDDCQPCPCGSS 780  
QY 781 CAVVPTKEVVTCTNCPGTGTRKCBELCDDGYPGDPLGRNGPVRCLCQCSDNIDPNAVG 840  
Db 781 CAVVPTKEVVTCTNCPGTGTRKCBELCDDGYPGDPLGRNGPVRCLCQCSDNIDPNAVG 840  
QY 841 NCNRLTGECLKICYNTAGFYCDRCXGDPNFPADKCKACNCPYGTWKQSSCNP 900  
Db 841 NCNRLTGECLKICYNTAGFYCDRCXGDPNFPADKCKACNCPYGTWKQSSCNP 900  
QY 901 VTQCCCLPHVTGQDCGACDPFYNLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGI 960  
Db 901 VTQCCCLPHVTGQDCGACDPFYNLQSGGGERCDCHALGSTNGQCDIRTGQCECQPGI 960  
QY 961 TGQHCERCEVNHFGFGEGCKPCDCHPEGSLSLQCKDDGRCEGFGVGNCDQCEENYF 1020  
Db 961 TGQHCERCEVNHFGFGEGCKPCDCHPEGSLSLQCKDDGRCEGFGVGNCDQCEENYF 1020  
QY 1021 YNRSWFGQCECPACVRLVKDVADHRVKLOBESLIANLGTGDEMTVDQAFEDLKAER 1080  
Db 1021 YNRSWFGQCECPACVRLVKDVADHRVKLOBESLIANLGTGDEMTVDQAFEDLKAER 1080  
QY 1081 EYMDLLREAAQDVKDQDQMLMDRLQVNTLTSSQSRLOINRTIETETGNLAEQARAVEN 1140

RESULT 4	
ADC01887	
ID	ADC01887 standard; protein; 1609 AA.
XX	
XX	
AC	ADC01887;
AC	
XX	
XX	
DT	18-DEC-2003 (first entry)
XX	
XX	
DE	Human laminin gamma 1 subunit.
XX	
XX	
KW	Cytostatic; human; ds; gene; laminin; tumour; laminin-x; beta3 subunit;
KW	gamal subunit; alpha4 subunit; angiogenesis.

AC ADC01887;

18-DEC-2003 (first entry)

Human laminin gamma 1 subunit

gamma1 subunit; alpha4 sub

XX  
PN  
US2003103975-A1.

XX  
PF  
18-NOV-2002; 2002US-002990

PR 03-NOV-2000; 2000US-007062  
XX

FA (GONZ) / GONZALEZ M.  
XX  
DT TOROS ICB GONZALEZ M.

DR WPL; 2003-75521771.  
DR N-PSDB; ADC01886.

PT for treating tumor.  
XX

CC The invention relates to a

1	QY	MRGSHRAAPALRPRGRLPVLVLA	AAAAAGCAQAMDECTDEGR	PQCMPEFVNAAFN	60
	Db	1	MRGSHRAAPALRPRGRLPVLVLA	AAAAAGCAQAMDECTDEGR	60
61	QY	VTVATNTCTPTPEEYCVGTGVT	KCHLCDACQPHLOHGAAPLTD	YNNQADTTWQOS	120
61	Db	VTVATNTCTPTPEEYCVGTGVT	KCHLCDACQPHLOHGAAPLTD	YNNQADTTWQOS	120
121	QY	QTMLAGVQVPESSINLTLHLGKA	FDITYVRLKPHETSRPESFAL	YKKTREDDGPMIPVQYVYG	180
121	Db	QTMLAGVQVPESSINLTLHLGKA	FDITYVRLKPHETSRPESFAL	YKKTREDDGPMIPVQYVYG	180
181	QY	SCENTYSKANRGFIRITGSGDEQ	QALCTDFESDISPJTGGNVA	PSLUEGRPSAYNFDNSPVL	240
181	Db	SCENTYSKANRGFIRITGSGDEQ	QALCTDFESDISPJTGGNVA	PSLUEGRPSAYNFDNSPVL	240
241	QY	QEWWTATDIRVTLNRLNTFGDE	VFNDDPKVLKSYYYIAISDFA	VGGRCCKNGHASECMKNEF	300
241	Db	QEWWTATDIRVTLNRLNTFGDE	VFNDDPKVLKSYYYIAISDFA	VGGRCCKNGHASECMKNEF	300
301	QY	DKLVNCKHNTYGVDEKCLPPND	RPWRAATAESASECLPCDCN	GRSQBCYFPPELYRS	360
301	Db	DKLVNCKHNTYGVDEKCLPPND	RPWRAATAESASECLPCDCN	GRSQBCYFPPELYRS	360
361	QY	TGHGHCCTNQDNTDGAHCER	CENFRFLGNNEACSSCHSPV	GSLSLTCQDSYGRCSCKP	420
361	Db	TGHGHCCTNQDNTDGAHCER	CENFRFLGNNEACSSCHSPV	GSLSLTCQDSYGRCSCKP	420
421	QY	GVMGDKDRCPQGFHSLUTEAG	RPCDCPSGSDIBCNVETGR	CYCKDNVGFNCERCKPG	480
421	Db	GVMGDKDRCPQGFHSLUTEAG	RPCDCPSGSDIBCNVETGR	CYCKDNVGFNCERCKPG	480
481	QY	FPNLESSNPRGCTPCFCGHSS	VYVCTNAVGYSVYSISSTFQ	IDEDGWRAEQRDGSEASLEW	540
481	Db	FPNLESSNPRGCTPCFCGHSS	VYVCTNAVGYSVYSISSTFQ	IDEDGWRAEQRDGSEASLEW	540
541	QY	SSEQRQDIATVSDSYFPRYFT	APAKFJGKQVLSYGQNLSPS	FRVDRREDTFLSAEDLVLEGA	600
541	Db	SSEQRQDIATVSDSYFPRYFT	APAKFJGKQVLSYGQNLSPS	FRVDRREDTFLSAEDLVLEGA	600
601	QY	GLRYSVPLIAQGNISYPSSET	VKVYFRLHEATDYPWRPAL	TPPEFQKLLNLTISKIRTY	660
601	Db	GLRYSVPLIAQGNISYPSSET	VKVYFRLHEATDYPWRPAL	TPPEFQKLLNLTISKIRTY	660
661	QY	SERAGYLDVDTLASAPPGVPA	TWVESCTCBVGYGQFCWCL	SGYVRETPNLGPYSP	720
661	Db	SERAGYLDVDTLASAPPGVPA	TWVESCTCBVGYGQFCWCL	SGYVRETPNLGPYSP	720
721	QY	CVLCAKNHSETCDPETGVNC	RDNTAGPHCEKCSDDYYG	SDTAGTSSDCQPCPCPGSSS	780
721	Db	CVLCAKNHSETCDPETGVNC	RDNTAGPHCEKCSDDYYG	SDTAGTSSDCQPCPCPGSSS	780
781	QY	CAVVPKTKHEVVTNCPGTGTT	GKCEICDDGYGDPGLGRNG	PVRLCRLCOCSDNIDPNAVG	840
781	Db	CAVVPKTKHEVVTNCPGTGTT	GKCEICDDGYGDPGLGRNG	PVRLCRLCOCSDNIDPNAVG	840
841	QY	NCNRLITGELCKCIYNTAGFY	CDRCCKDGFNGNPLAPNPAD	KCAKNCNPFYGGKKQOSSCNP	900

Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGFLAPNADKCKACNPNFYGTWKQSSCNP 900  
QY 901 VTGQCCECLPHVTGQDCGADPGFYNLQSGQGERCDCHALGSTNGQCDIRTCQCCQPGI 960  
Db 901 VTGQCCECLPHVTGQDCGADPGFYNLQSGQGERCDCHALGSTNGQCDIRTCQCCQPGI 960  
QY 961 TGHCECCEVNHFGPGECKPCDCHPEGSLSLQCKDGCCECRGFGVGNRCDCQCEENYF 1020  
Db 961 TGHCECCEVNHFGPGECKPCDCHPEGSLSLQCKDGCCECRGFGVGNRCDCQCEENYF 1020  
QY 1021 YNRSWPGCCECPACYLELVKDVADHRVKLQELLESILANLGTDEMVTQAFEDRLKEAER 1080  
Db 1021 YNRSWPGCCECPACYLELVKDVADHRVKLQELLESILANLGTDEMVTQAFEDRLKEAER 1080  
QY 1081 EVMDLLEAQQVDQVQDNLMDLQVNNLTSSQISRLQNRITIBETGNLAEOARHVEN 1140  
Db 1081 EVMDLLEAQQVDQVQDNLMDLQVNNLTSSQISRLQNRITIBETGNLAEOARHVEN 1140  
QY 1141 TERLIEIASRELEKAKVAANVSVTQPESTGPNMNTLLAEARKLAERHKEADDIVRV 1200  
Db 1141 TERLIEIASRELEKAKVAANVSVTQPESTGPNMNTLLAEARKLAERHKEADDIVRV 1200  
QY 1201 AKTANDTSTEAVNLLRTLAGENQTAFFEIEELNRKYEQAQNTSODLEKQAAVHVEAKRA 1260  
Db 1201 AKTANDTSTEAVNLLRTLAGENQTAFFEIEELNRKYEQAQNTSODLEKQAAVHVEAKRA 1260  
QY 1261 GDKAVIYASVAQLSPLDSETLENEANNIKMGAENLEQLIDQKLKDYEDLREDMRGKLE 1320  
Db 1261 GDKAVIYASVAQLSPLDSETLENEANNIKMGAENLEQLIDQKLKDYEDLREDMRGKLE 1320  
QY 1321 VKNLLEKGTQEQADQLARADAALAEAAKGRDQLQANDILNNLKDQFDRVNDN 1380  
Db 1321 VKNLLEKGTQEQADQLARADAALAEAAKGRDQLQANDILNNLKDQFDRVNDN 1380  
QY 1381 KTAABEALRKIPAINOTITTEANEKTRAEQAQALGSAADATEAKNKAHEAERTASAVQKNA 1440  
Db 1381 KTAABEALRKIPAINOTITTEANEKTRAEQAQALGSAADATEAKNKAHEAERTASAVQKNA 1440  
QY 1441 TSTKAEARTFAEVTDLNREVNMLKQLOEAEKELKRKQDDADQDMAGMASQAQAE 1500  
Db 1441 TSTKAEARTFAEVTDLNREVNMLKQLOEAEKELKRKQDDADQDMAGMASQAQAE 1500  
QY 1501 INARKAKNSTVLSLIIINDLEQLGQDVTDLNKLNEIEGTINKAKDEMKVSDLRKYSD 1560  
Db 1501 INARKAKNSTVLSLIIINDLEQLGQDVTDLNKLNEIEGTINKAKDEMKVSDLRKYSD 1560  
QY 1561 LENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
Db 1561 LENEAKKQEAAMIDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
RESULT 5  
AAB19803  
ID AAB19803 standard; protein; 1617 AA.  
AC AAB19803;  
XX  
XX 05-MAR-2001 (first entry)  
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.  
XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Peptide 1..33 /label= signal\_peptide  
XX Protein 34..1609 /label= Mature\_protein  
XX Peptide 1610..1617

FT XX /label= FLAG  
FN WO200066730-A2.  
XX  
XX PD 09-NOV-2000.  
XX  
XX PF 28-APR-2000; 2000WO-US011378.  
XX  
XX PR 30-APR-1999; 99US-0131720P.  
XX PR 15-JUN-1999; 99US-0139198P.  
XX PR 12-JUL-1999; 99US-0143289P.  
XX PR 24-SEP-1999; 99US-0155945P.  
XX  
XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
XX PI Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88903.  
XX  
XX PT Purified laminin 2 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
XX PS Claim 5; Page 263-268; 305pp; English.  
XX  
XX CC The present sequence is that of the gamma-1 chain of human laminin 2,  
CC with an additional C-terminal FLAG epitope, resulting from expression in  
CC transfected cells from mammalian expression vectors. Laminin 2 is  
CC composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)  
CC chains. It is thought to be specifically required for stabilizing  
CC myotubes during skeletal muscle development, and for preventing  
CC apoptosis. Genetic defects in its structure or expression are associated  
CC with a major type of congenital muscular dystrophy. Laminin 2 is also  
CC thought to be important in Schwann cell/basal lamina interactions. The  
CC invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain  
CC polypeptides (see AAB19791-806) and the polynucleotides encoding them  
CC (see AAB8891-936), methods for making recombinant laminin 2, cells that  
CC express recombinant laminin 2, and methods for using purified laminin 2  
CC for research and therapeutic purposes including peripheral nerve  
CC regeneration, treatment of degenerative muscle disorders, angiogenesis  
CC regulation, promoting cell attachment and migration, ex vivo cell  
CC therapy, improving the take of grafts, improving the biocompatibility of  
CC medical devices and preparing improved culture devices and media  
XX  
XX SQ Sequence 1617 AA;

Query Match 100.0%; Score 8713; DB 3; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAMDECTDEGRRPQRCMPFVNAAFN 60  
Db 1 MEGSHRAAPALRPRGLWPVLAVLAAAAAGCAQAAMDECTDEGRRPQRCMPFVNAAFN 60  
QY 61 VTVVATNTCGTPPEEYCVQGTGVTNKSCHLDCAGOPHLQHGAAFLTDYNNQADTTWQOS 120  
Db 61 VTVVATNTCGTPPEEYCVQGTGVTNKSCHLDCAGOPHLQHGAAFLTDYNNQADTTWQOS 120  
QY 121 QTMLAGVQYPSINLTLLHCKAFDITVRLKFTSRPESFAIKRTRDGPMPYQVYSG 180  
Db 121 QTMLAGVQYPSINLTLLHCKAFDITVRLKFTSRPESFAIKRTRDGPMPYQVYSG 180  
QY 181 SCENTYSKANRGFIRTCGDEQQAALCTDEFSDISPLTGGNVAFSTLEGSRPSAYNFDNSPVL 240  
Db 181 SCENTYSKANRGFIRTCGDEQQAALCTDEFSDISPLTGGNVAFSTLEGSRPSAYNFDNSPVL 240  
QY 241 QEWATATDIRVTNLNLTNLTFCGDEVNPKVLKSYVYALSDFAVGRCCKNGHASECKMNEF 300  
Db 241 QEWATATDIRVTNLNLTNLTFCGDEVNPKVLKSYVYALSDFAVGRCCKNGHASECKMNEF 300  
QY 301 DKLVCNCKHNTYGVDCCKCLPFFNDRPWRRTAESASECLPCDCNCGRSQSCYFDPPELYRS 360

301 DKLVNCKHNTYGVDCCKLPPFNDRPWRRTATASASECLPCDCNCGRSQBQCYFPFELYRS 360  
361 TGHGHCNTCNDTGDGHCRCRENFRLGNNEACSSCHCSFVGLSLTQCDSDYGRCSCKP 420  
361 TGHGHCNTCNDTGDGHCRCRENFRLGNNEACSSCHCSFVGLSLTQCDSDYGRCSCKP 420  
421 GVMGKDCRCQPGFHSLEAGRCPCSDPSIDECNVETGRCVKONVEGFNCERCKPG 480  
421 GVMGKDCRCQPGFHSLEAGRCPCSDPSIDECNVETGRCVKONVEGFNCERCKPG 480  
481 PFNLESSNPRGCTPCFCFHSVCTNAVGVSYISSTFQIDEDGWRAEQDGSSEASLEW 540  
481 PFNLESSNPRGCTPCFCFHSVCTNAVGVSYISSTFQIDEDGWRAEQDGSSEASLEW 540  
541 SSERODIAVISDSYPPRFIAPAKELGKQVLSYQNLVSFRVDRDRTRLSAEDLVLEGA 600  
541 SSERODIAVISDSYPPRFIAPAKELGKQVLSYQNLVSFRVDRDRTRLSAEDLVLEGA 600  
601 GLRVSVPLIAQNSVPSETTVKYVERLHEADYPMRPALTPFEFQKLNLTLSIKIRGTY 660  
601 GLRVSVPLIAQNSVPSETTVKYVERLHEADYPMRPALTPFEFQKLNLTLSIKIRGTY 660  
661 SERSAGYLDVTLASARPGVPATWVBSCTCPVYGGQPCMEMCLSGYRRRTPLNGPYSP 720  
661 SERSAGYLDVTLASARPGVPATWVBSCTCPVYGGQPCMEMCLSGYRRRTPLNGPYSP 720  
721 CVLCAACNGHSETCDPBTGVNCRDNTAGPHCKSDGYGSDTAGTSSDCQPCPCPGSS 780  
721 CVLCAACNGHSETCDPBTGVNCRDNTAGPHCKSDGYGSDTAGTSSDCQPCPCPGSS 780  
781 CAVPPTKEVCTNCTGTGKRCCLDDGYGDFPLGRNGPVRLCRLCQCSNDIDPNNAV 840  
781 CAVPPTKEVCTNCTGTGKRCCLDDGYGDFPLGRNGPVRLCRLCQCSNDIDPNNAV 840  
841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGPNLAENPADKCKACNCPYGTMKQSSCNP 900  
841 NCNRLTGECLKCIYNTAGFYCDRCXGDFGPNLAENPADKCKACNCPYGTMKQSSCNP 900  
901 VTGQCECLPHVTGQDGCACDPGFYNLQSGQGCERCDCHALGSTNGCQDRTGQCECQPGI 960  
901 VTGQCECLPHVTGQDGCACDPGFYNLQSGQGCERCDCHALGSTNGCQDRTGQCECQPGI 960  
961 TQHCERCERNHFGPGECKPCDCHPEGLSLQCKDGRCEGFGVGNRCQCEENYF 1020  
961 TQHCERCERNHFGPGECKPCDCHPEGLSLQCKDGRCEGFGVGNRCQCEENYF 1020  
1021 YNRSWPGQCECPACVRLVKVADHRVKLOELESILANLGTDEMVTDOAFEDRLKEAER 1080  
1021 YNRSWPGQCECPACVRLVKVADHRVKLOELESILANLGTDEMVTDOAFEDRLKEAER 1080  
1081 EYMDLLREAQDVKDQNLMDRLQRVNNTLSQISRLQNRNTIBETGNLAEQARAHVEN 1140  
1081 EYMDLLREAQDVKDQNLMDRLQRVNNTLSQISRLQNRNTIBETGNLAEQARAHVEN 1140  
1141 TERLIEIASRELEKAKVAANYSVTQPESTGDPNNWTLLEAEARKLAERHKOEDDVRV 1200  
1141 TERLIEIASRELEKAKVAANYSVTQPESTGDPNNWTLLEAEARKLAERHKOEDDVRV 1200  
1201 AKTANDTSTEAYNLLRTLAGENQTAFAFEELNRYEQAQNTISQLEKQAARVHEAKRA 1260  
1201 AKTANDTSTEAYNLLRTLAGENQTAFAFEELNRYEQAQNTISQLEKQAARVHEAKRA 1260  
1261 GKAVEIYASVLAQLSPDSETTLEANNIKMAENLEQLIDOKLYEDLEADMEGKELE 1320  
1261 GKAVEIYASVLAQLSPDSETTLEANNIKMAENLEQLIDOKLYEDLEADMEGKELE 1320  
1321 VKNLLEKGTQOOTADOLLARADAALAEAAKKGRTDLOEANDILNNLKDFFORVNDN 1380  
1321 VKNLLEKGTQOOTADOLLARADAALAEAAKKGRTDLOEANDILNNLKDFFORVNDN 1380  
1381 KTAABEALRKIPAINQITITEANEKTRAQOALGSAADATEAKNKAHEAERIASAVQKNA 1440  
1381 KTAABEALRKIPAINQITITEANEKTRAQOALGSAADATEAKNKAHEAERIASAVQKNA 1440

1441 TSTKABERTFAEVTDLNVEVNNMLKQLOEAEKELKRCODDADQDMVMAGMASQAQAEAE 1500  
1441 TSTKABERTFAEVTDLNVEVNNMLKQLOEAEKELKRCODDADQDMVMAGMASQAQAEAE 1500  
1501 INARKAKNSVTSLSLSIINDLLLEQLGQDLTVDLNKLNEIEGTILNKAKDEMKVSDLRKVSD 1560  
1501 INARKAKNSVTSLSLSIINDLLLEQLGQDLTVDLNKLNEIEGTILNKAKDEMKVSDLRKVSD 1560  
1561 LENEAKKQEAAMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
1561 LENEAKKQEAAMDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 6  
AAW50898 standard; protein; 1609 AA.  
XX  
AC AAW50898;  
XX  
DT 07-DEC-1998 (first entry)  
XX  
DE Human laminin G1 chain.  
XX  
KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gartnerman-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO9815179-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 08-OCT-1997; 97MO-US018145.  
XX  
PR 08-OCT-1996; 96US-0027981P.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Castillo G, Snow AD;  
XX  
DR WPI; 1998-240534/21.  
XX  
PT Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CJD.  
XX  
PS Claim 15; Page 106-109; 132pp; English.  
XX  
CC This is the amino acid sequence of the human laminin G1 chain. The  
CC primary object of the invention is to use laminin, laminin-derived  
CC protein fragments and/or laminin-derived polypeptides as potent  
CC inhibitors of amyloid formation, deposition, accumulation and/or  
CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
CC products (see AAW5088-98) may include mouse or human laminin A or A1  
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
CC binding domain of the laminin A chain. A claimed method for treating an  
CC amyloid disease comprises administering a polypeptide having a  
CC conformational similarity to a fragment of a laminin protein. A method  
CC for diagnosing an amyloid disease involves determining levels of laminin  
CC in a sample. Production of laminin or its fourth globular repeat in vivo  
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
CC products and methods can be used for the diagnosis, prognosis, monitoring  
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis



CC associated with chronic inflammation, various forms of malignancy and  
CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
CC prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler  
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis  
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or  
CC transthyretin amyloid), and the amyloidosis associated with endocrine  
CC tumours such as medullary carcinoma of the thyroid (variant of  
CC procalcitonin)  
XX  
SQ  
Query Match 100.0%; Score 8709; DB 2; Length 1609;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MRSHRAAPALPRGRLPVLAVALAAAGCAQAAMDECTDEGRPQRCMPEFVNAAFN 60  
DB 1 MRSHRAAPALPRGRLPVLAVALAAAGCAQAAMDECTDEGRPQRCMPEFVNAAFN 60  
QY 61 VTVAATNTCTPPEEYCVQGVGVTKSCHLDCAGOPHLQHGAAFLTDVNNQADITWQOS 120  
DB 61 VTVAATNTCTPPEEYCVQGVGVTKSCHLDCAGOPHLQHGAAFLTDVNNQADITWQOS 120  
QY 121 QTMLAGVQYPSINLTLHLKAFDITVRLKFTSRPESFAIYKRTREDGPIYQYISG 180  
DB 121 QTMLAGVQYPSINLTLHLKAFDITVRLKFTSRPESFAIYKRTREDGPIYQYISG 180  
QY 181 SCENTYSKANRGFTRTGGDQQAALCTDEFSDISPLTGNVAFSTLGRPSAYNFNSPVL 240  
DB 181 SCENTYSKANRGFTRTGGDQQAALCTDEFSDISPLTGNVAFSTLGRPSAYNFNSPVL 240  
QY 241 QEWYATDITRTLNLNTFGDEVNDPKVLKSYIYAIISDPVAGGRCKNGHASECMKNEF 300  
DB 241 QEWYATDITRTLNLNTFGDEVNDPKVLKSYIYAIISDPVAGGRCKNGHASECMKNEF 300  
QY 301 DKLVCNKHNTYGVDCCKLPFNDRPWRATASASECLPCDCNGRSQECYFDPBLYRS 360  
DB 301 DKLVCNKHNTYGVDCCKLPFNDRPWRATASASECLPCDCNGRSQECYFDPBLYRS 360  
QY 361 TGHGHCNTCQNDTDGAHCRCRENPFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420  
DB 361 TGHGHCNTCQNDTDGAHCRCRENPFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420  
QY 421 GVMGDKCDRCQPGFHSITEAGCRPCSDPSGSDENCVETGRVCVKDNTVEGNCERCKPG 480  
DB 421 GVMGDKCDRCQPGFHSITEAGCRPCSDPSGSDENCVETGRVCVKDNTVEGNCERCKPG 480  
QY 481 PFNLESNPRGCTPCFCFCHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLEW 540  
DB 481 PFNLESNPRGCTPCFCFCHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQRDGSEASLEW 540  
QY 541 SSERQDIAVSDSYFPRYFIAPAKFLGKQVLSYQNLSPSFVRDRDRLSABDLVLEGA 600  
DB 541 SSERQDIAVSDSYFPRYFIAPAKFLGKQVLSYQNLSPSFVRDRDRLSABDLVLEGA 600  
QY 601 GLRYSVPLIAQNSYPSSETTVKYVRLHEATDYPWRPALTPFFBQKLLNLTISKIRGY 660  
DB 601 GLRYSVPLIAQNSYPSSETTVKYVRLHEATDYPWRPALTPFFBQKLLNLTISKIRGY 660  
QY 661 SERAGYLDVTLASAPGPGVPATWVESCTCPVYGQGCENCLSGYRRETNLGYPSP 720  
DB 661 SERAGYLDVTLASAPGPGVPATWVESCTCPVYGQGCENCLSGYRRETNLGYPSP 720  
QY 721 CVLCAKNGHSTCDPETGVGNCRNTAGPHCEKSDGYGDSYTAGTSSDCQPCFCGGSS 780  
DB 721 CVLCAKNGHSTCDPETGVGNCRNTAGPHCEKSDGYGDSYTAGTSSDCQPCFCGGSS 780  
QY 781 CAVVPKTEVYVCTNCTPTGKRCCELDGDFGDPGLGRNGFVRLCRLCQCSNDIDPNAVG 840

DB 781 CAVVPKTEVYVCTNCTPTGKRCCELDGDFGDPGLGRNGFVRLCRLCQCSNDIDPNAVG 840  
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPLAPNADKCKACNCPYGTMTQSSCNP 900  
DB 841 NCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPLAPNADKCKACNCPYGTMTQSSCNP 900  
QY 901 VTGQCECLPHVTGQDCGACDPGFNVLQSGQRCRCDCHALGSTNGQCDITGQCECQPGI 960  
DB 901 VTGQCECLPHVTGQDCGACDPGFNVLQSGQRCRCDCHALGSTNGQCDITGQCECQPGI 960  
QY 961 TGOHCECEVNVHFGFPGCKPCDCHPEGSLSLQCKDDGRCEGREGFVGNRCDCQCENYF 1020  
DB 961 TGOHCECEVNVHFGFPGCKPCDCHPEGSLSLQCKDDGRCEGREGFVGNRCDCQCENYF 1020  
QY 1021 YRNSWPGQCEPCACRYLVKQVADHRVVKLOELBSLIANLTGDEMVTDOAFEDLKEAER 1080  
DB 1021 YRNSWPGQCEPCACRYLVKQVADHRVVKLOELBSLIANLTGDEMVTDOAFEDLKEAER 1080  
QY 1081 EVMOLLREAAQDVQDVQNLMDRLORVNTLSSQISRLQNIQNTIETGNLAQARAHVEN 1140  
DB 1081 EVMOLLREAAQDVQDVQNLMDRLORVNTLSSQISRLQNIQNTIETGNLAQARAHVEN 1140  
QY 1141 TERLIEIASRELEKAKVAAANVSVTQESTGDPNNMTLLAEBAKLAERHKQAEADDIVRV 1200  
DB 1141 TERLIEIASRELEKAKVAAANVSVTQESTGDPNNMTLLAEBAKLAERHKQAEADDIVRV 1200  
QY 1201 AKTANDTSTEAYNLLRTLAGENCTAFEIBELNRYEOKAKNISQLEKQAAHVHEEAKRA 1260  
DB 1201 AKTANDTSTEAYNLLRTLAGENCTAFEIBELNRYEOKAKNISQLEKQAAHVHEEAKRA 1260  
QY 1261 GDKAVEIYASVAQSPLDSETLENEANNIKWEAENLEQLIDQKLKQYEDLREDMRGKELE 1320  
DB 1261 GDKAVEIYASVAQSPLDSETLENEANNIKWEAENLEQLIDQKLKQYEDLREDMRGKELE 1320  
QY 1321 VKNLLEKGTQCOOTADOLLAADAAKALAEBAKKGRTDLOEANDILNNLKDPDRVNDN 1380  
DB 1321 VKNLLEKGTQCOOTADOLLAADAAKALAEBAKKGRTDLOEANDILNNLKDPDRVNDN 1380  
QY 1381 KTAABEALRKIPALNQITTEANETKTRAQALGSAADAATAEAKNKAHEAERIASAVOKNA 1440  
DB 1381 KTAABEALRKIPALNQITTEANETKTRAQALGSAADAATAEAKNKAHEAERIASAVOKNA 1440  
QY 1441 TSTKABAEARTFAEVTDLNENNNMLKQLEAEKELKQDADODMMAGWASQAQAE 1500  
DB 1441 TSTKABAEARTFAEVTDLNENNNMLKQLEAEKELKQDADODMMAGWASQAQAE 1500  
QY 1501 INARKAKNSVTSLSIINDLLEQLGQDVTDLNKLNEIEGTTLNKAKDBMKVSDLDKRVSD 1560  
DB 1501 INARKAKNSVTSLSIINDLLEQLGQDVTDLNKLNEIEGTTLNKAKDBMKVSDLDKRVSD 1560  
QY 1561 LENEAKKQEAAMIDYNRDIEIMKDINLEDIRKTLPSGCCNTTPIEKP 1609  
DB 1561 LENEAKKQEAAMIDYNRDIEIMKDINLEDIRKTLPSGCCNTTPIEKP 1609  
RESULT 7  
AAB19802  
ID AAB19802 standard; protein; 1576 AA.  
XX  
AC AAB19802;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Human laminin 2 mature gamma-1 chain.  
XX  
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
XX degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2000066730-A2.  
XX

PD 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011378.  
PF 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
PA Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88902.  
DR Purified laminin 2 protein, useful for research and therapeutic purposes  
DR including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 251-256; 305pp; English.  
PS The present sequence is that of human laminin 2 gamma-1 chain mature  
CC protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and  
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for  
CC stabilizing myotubes during skeletal muscle development, and for  
CC preventing apoptosis. Genetic defects in its structure or expression are  
CC associated with a major type of congenital muscular dystrophy. Laminin 2  
CC is also thought to be important in Schwann cell/basal lamina  
CC interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-  
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding  
CC them (see AAA8891-906), methods for making recombinant laminin 2, cells  
CC that express recombinant laminin 2, and methods for using purified  
CC laminin 2 for research and therapeutic purposes including peripheral  
CC nerve regeneration, treatment of degenerative muscle disorders,  
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo  
CC cell therapy, improving the take of grafts, improving the  
CC biocompatibility of medical devices and preparing improved culture  
CC devices and media  
XX SQ Sequence 1576 AA;  
Query Match 98.1%; Score 8544; DB 3; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 QAAMDECTDEGRPORCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTWSCHLCD 93  
DB 1 QAAMDECTDEGRPORCMPEFVNAAFNVTVATNTCGTPPEYCVQGTGVTWSCHLCD 60  
QY 94 AQPHLOHGAALFDYNNQADTTWQSOOTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 153  
DB 61 AQPHLOHGAALFDYNNQADTTWQSOOTMLAGVQYPSINLTLHLGKAFDITYVRLKFH 120  
QY 154 TSPRSFAYIKRTREDGPMIPYQYSGSCENTYKANKRGFRTGGDEQALCTDEFSDIS 213  
DB 121 TSPRSFAYIKRTREDGPMIPYQYSGSCENTYKANKRGFRTGGDEQALCTDEFSDIS 180  
QY 214 PUTGNNVAFSTLEGRPSAYNPNDSVPLOSWTATDIRVTLNRLNTFGDEVNDPKVLKSY 273  
DB 181 PUTGNNVAFSTLEGRPSAYNPNDSVPLOSWTATDIRVTLNRLNTFGDEVNDPKVLKSY 240  
QY 274 YYAISDFAVGGCKNGHASECMKNEFDKLVNCKHNTYVGDCEKCLPFNDPWRRATA 333  
DB 241 YYAISDFAVGGCKNGHASECMKNEFDKLVNCKHNTYVGDCEKCLPFNDPWRRATA 300  
QY 334 ESASECLPCDCCNGRSQECYFDELYRSTGHGCHCTNCQDNTDGAHCERENFFRLGNNE 393  
DB 301 ESASECLPCDCCNGRSQECYFDELYRSTGHGCHCTNCQDNTDGAHCERENFFRLGNNE 360  
QY 394 ACSSCHSPVGLSTQCDISYGRCSCKPGVMGDKDCRQCPGFHSLTEAGCRPCSDPSGSI 453  
DB 361 ACSSCHSPVGLSTQCDISYGRCSCKPGVMGDKDCRQCPGFHSLTEAGCRPCSDPSGSI 420

QY 454 DECNVETGRVCVKDNVEGFNCERCKPGFFNLSNPRGCTPCFCFSGHSVCTNAVGSYVY 513  
DB 421 DECNVETGRVCVKDNVEGFNCERCKPGFFNLSNPRGCTPCFCFSGHSVCTNAVGSYVY 480  
QY 514 SISSTFOIDEDGWRARQDGSSEASLEWSSERODIAVISDSYPRYFIAPAKLGKQVLSY 573  
DB 481 SISSTFOIDEDGWRARQDGSSEASLEWSSERODIAVISDSYPRYFIAPAKLGKQVLSY 540  
QY 574 GQNLSPSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 633  
DB 541 GQNLSPSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYVFLRHEATDY 600  
QY 634 PWRPALTPPEFQKLLANLTSIKIRGYTSERSAGYLDVTLASARPGPGVPATWVESCTCP 693  
DB 601 PWRPALTPPEFQKLLANLTSIKIRGYTSERSAGYLDVTLASARPGPGVPATWVESCTCP 660  
QY 694 VVGGGQFCMCCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPETGYCNCRDNTAGPHCEK 753  
DB 661 VVGGGQFCMCCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPETGYCNCRDNTAGPHCEK 720  
QY 754 CSDGYVGDSTAGTSSDCQPCPGSSCAVVPKTKVVCNTCTGTTGKRCELCDGDFYF 813  
DB 721 CSDGYVGDSTAGTSSDCQPCPGSSCAVVPKTKVVCNTCTGTTGKRCELCDGDFYF 780  
QY 814 DPLGRNGPVLRLCCLCOCSNIDNPNVNCNRLTGECLKCIYNTAGFYCDRCCKDGGFNGPL 873  
DB 781 DPLGRNGPVLRLCCLCOCSNIDNPNVNCNRLTGECLKCIYNTAGFYCDRCCKDGGFNGPL 840  
QY 874 APNADKCKACNCPYGTWKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSQGCE 933  
DB 841 APNADKCKACNCPYGTWKQSSCNFVTGQCECLPHVTGQDCGACDPGFYNLQSQGCE 900  
QY 934 RCDHALGNSGQDRTGCECPGIGTGOHCERCEVNHFGFPGCEKPCDCHPEGSLSL 993  
DB 901 RCDHALGNSGQDRTGCECPGIGTGOHCERCEVNHFGFPGCEKPCDCHPEGSLSL 960  
QY 994 QCKDDRCCEGREGVGNRCDCQCEENFYNRSPGQCECPACVRLVKDKVADHRVRLKQLE 1053  
DB 961 QCKDDRCCEGREGVGNRCDCQCEENFYNRSPGQCECPACVRLVKDKVADHRVRLKQLE 1020  
QY 1054 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREADVQDVQDQVNDLMDRLQVNNLTSSQ 1113  
DB 1021 SLIANLTGDEMVTDOAFEDRLKEAREVMDLLREADVQDVQDQVNDLMDRLQVNNLTSSQ 1080  
QY 1114 ISRLQNRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTPESTGDP 1173  
DB 1081 ISRLQNRNTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTPESTGDP 1140  
QY 1174 NNMTLLAEAEARKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTAGENQTAFAIEELN 1233  
DB 1141 NNMTLLAEAEARKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTAGENQTAFAIEELN 1200  
QY 1234 RYEQAKNIISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1293  
DB 1201 RYEQAKNIISODLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPLDSETLENEANNIKMEA 1260  
QY 1294 ENLEQLIDQKLDYEDLREDMRGKELEVNKLEKGTKEQOTADQLLARADAAKALAEAEA 1353  
DB 1261 ENLEQLIDQKLDYEDLREDMRGKELEVNKLEKGTKEQOTADQLLARADAAKALAEAEA 1320  
QY 1354 KXGRDTLOEANDILNNLKDFDRVNDNKTAAEBALRKIPAINOTITEANEKTEAQAALG 1413  
DB 1321 KXGRDTLOEANDILNNLKDFDRVNDNKTAAEBALRKIPAINOTITEANEKTEAQAALG 1380  
QY 1414 SAAADATEAKNKAHAERIASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLEAEK 1473  
DB 1381 SAAADATEAKNKAHAERIASAVQKNATSTKAEARTFAEVTDLDNVNNMLKQLEAEK 1440  
QY 1474 ELKRXQDDADODMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLBOLGOLDTVDLN 1533  
DB 1441 ELKRXQDDADODMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLBOLGOLDTVDLN 1500

QY	1534	KLNEIEGTLINKAKDEMKSVDLDRKVS	DLNEAKQEAAMVDYNRDIEBIMKD	IRNLEDIR	1593
DB	1501	KLNEIEGTLINKAKDEMKSVDLDRKVS	DLNEAKQEAAMVDYNRDIEBIMKD	IRNLEDIR	1560
QY	1594	KTLPSGCFNTPSIEKP	1569		
DB	1561	KTLPSGCFNTPSIEKP	1576		
RESULT 8					
ID	AAB48453	AAB48453 standard; protein; 1576 AA.			
XX	AAB48453;				
AC	XX				
XX	DT	02-MAR-2001 (first entry)			
XX	DE	Human laminin 8 polypeptide, SEQ ID NO: 24.			
XX	XX	Human; laminin 8; neuroprotective; angiogenic; osteopathic; antiarteriosclerotic; glycoprotein; mesenchymal tissue injury; vascular tissue injury; neural injury; angiogenesis regulation.			
XX	OS	Homo sapiens.			
XX	XX	WO200066732-A2.			
XX	PN	09-NOV-2000.			
XX	PD				
XX	XX	28-APR-2000; 2000WO-US011543.			
XX	PF	30-APR-1999; 99US-0131720P.			
XX	PR	21-AUG-1999; 99US-0149738P.			
XX	PR	24-SEP-1999; 99US-0155945P.			
XX	PR	11-FEB-2000; 2000US-0182012P.			
XX	XX	(BIOS-) BIOSTRATUM INC.			
PA	XX	Kortesmaa J, Tryggvason K;			
PI	XX	WPI: 2000-697539/67.			
XX	XX	N-PSDB; AAC83714.			
DR	XX	Purified laminin 8 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.			
PT	XX	Claim 5; Page 214-218; 245pp; English.			
PS	XX	The present sequence is a laminin 8 polypeptide chain. Laminins are a family of heterotrimeric glycoproteins that function via binding interactions with neighbouring cell receptors and by forming laminin networks. They are signalling molecules which influence cellular function. Laminin 8 is useful for treating injuries to tissue of mesenchymal origin, such as bone, cartilage, tendon, and ligament, treating injuries to vascular tissue, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, and preparing improved cell culture devices and media. Laminin 8 is also useful for promoting re-endothelialisation at the site of vascular injuries, improving the take of grafts, improving the biocompatibility of medical devices, treating neural injuries (neural regeneration), regulating angiogenesis, and promoting cell attachment and migration			
XX	XX	Sequence 1576 AA;			
XX	XX	Query Match 98.1%; Score 8544; DB 3; Length 1576;			
XX	XX	Best Local Similarity 100.0%; Pred. No. 0;			
XX	XX	Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	34	QAAMDECTDGGPQRCMPFVNAAFNVV	TAINTCGTPPEYCVQGTGVTK	CHLCD	93
DB	1	QAAMDECTDGGPQRCMPFVNAAFNVV	TAINTCGTPPEYCVQGTGVTK	CHLCD	60

QY	94	AGPHLQHGAAFLTDYNNQADTTWWSQ	OTMLAGVQYPPSSINLT	HLGKAFDITTVRLKEH	153		
DB	61	AGPHLQHGAAFLTDYNNQADTTWWSQ	OTMLAGVQYPPSSINLT	HLGKAFDITTVRLKEH	120		
QY	154	TSRPESFAIYKRTREDGPWIPYQY	SGSCENTYSKANRGFIR	TGGDEQOALCTDEFS	213		
DB	121	TSRPESFAIYKRTREDGPWIPYQY	SGSCENTYSKANRGFIR	TGGDEQOALCTDEFS	180		
QY	214	PLTGGNVAFSTLEGRPSAYNFNS	PVYLQEWVATDIRVTLNRLNTFGDEV	NDPKVLSY	273		
DB	181	PLTGGNVAFSTLEGRPSAYNFNS	PVYLQEWVATDIRVTLNRLNTFGDEV	NDPKVLSY	240		
QY	274	YYAISDFAVGGRCKNGHASECM	KNFDFKLVNCNKHNTY	GVDCCKLPFENDR	PWRATA 333		
DB	241	YYAISDFAVGGRCKNGHASECM	KNFDFKLVNCNKHNTY	GVDCCKLPFENDR	PWRATA 300		
QY	334	ESASECLPCDCNGRSQECYFDP	PELYRSTGHGHCTNCQDNTDGAHCERC	RENFRIGNNE	393		
DB	301	ESASECLPCDCNGRSQECYFDP	PELYRSTGHGHCTNCQDNTDGAHCERC	RENFRIGNNE	360		
QY	394	ACSSCHSPVGSLS	TQCDSDYGRCSCKPGV	MGDKDCRCQFPHSL	TEAGRCPCSDPSGSI 453		
DB	361	ACSSCHSPVGSLS	TQCDSDYGRCSCKPGV	MGDKDCRCQFPHSL	TEAGRCPCSDPSGSI 420		
QY	454	DECNVETGRVCVKDNVEGFNC	ERCCKPGFNFLESSN	PRGCTPCFCF	GHSSVCTNAVGYSYV 513		
DB	421	DECNVETGRVCVKDNVEGFNC	ERCCKPGFNFLESSN	PRGCTPCFCF	GHSSVCTNAVGYSYV 480		
QY	514	SISSTFOIDEDGWRABORD	SGSEASLESWSERQDIAVISDSY	PPRYFIAPAKELGKOVLSY	573		
DB	481	SISSTFOIDEDGWRABORD	SGSEASLESWSERQDIAVISDSY	PPRYFIAPAKELGKOVLSY	540		
QY	574	GQNLSPFRVDRDRTL	LSAEDLVLEGAGLR	VSVPVLI	AQNSYPSSETTVKYVRLHEATDY 633		
DB	541	GQNLSPFRVDRDRTL	LSAEDLVLEGAGLR	VSVPVLI	AQNSYPSSETTVKYVRLHEATDY 600		
QY	634	PWRPALTPEFQKLLNNL	TSIKIRGYTSERSAGYLDVTLASAR	POPGVPATWVESCTCP	693		
DB	601	PWRPALTPEFQKLLNNL	TSIKIRGYTSERSAGYLDVTLASAR	POPGVPATWVESCTCP	660		
QY	694	VGYGGQFCMCLSGYRRET	NLGPYSPVLCA	CNCHSETCDPET	GVNCNCRDNTAGPHCEK 753		
DB	661	VGYGGQFCMCLSGYRRET	NLGPYSPVLCA	CNCHSETCDPET	GVNCNCRDNTAGPHCEK 720		
QY	754	CSDGYGDS	TAGTSSDQCPCPGSSCAVVPKTK	KEVCTNCPTGTTGKRC	ELCDDGYFG 813		
DB	721	CSDGYGDS	TAGTSSDQCPCPGSSCAVVPKTK	KEVCTNCPTGTTGKRC	ELCDDGYFG 780		
QY	814	DPLGRNGPVLRLCRLCCSDNIDP	NAGNRLTGECLKCIYNTAGV	CDCKDGFGNPL	873		
DB	781	DPLGRNGPVLRLCRLCCSDNIDP	NAGNRLTGECLKCIYNTAGV	CDCKDGFGNPL	840		
QY	874	APNPADKCKAC	CNPNYGTMMQSSCN	PVTGQCECLPHVTGQDCG	ADPGFYNLQSGQGE 933		
DB	841	APNPADKCKAC	CNPNYGTMMQSSCN	PVTGQCECLPHVTGQDCG	ADPGFYNLQSGQGE 900		
QY	934	RCDCHALGSTNGQDIR	TGQCECPGTGQHCERCEVNH	FGPEGCKPCDCH	PEGSLSL 993		
DB	901	RCDCHALGSTNGQDIR	TGQCECPGTGQHCERCEVNH	FGPEGCKPCDCH	PEGSLSL 960		
QY	994	QCKDDGRC	CEGREGVGNRCQDCEENFYNNR	SFPGQCECPAC	YRLVKDKVADHRV	LQGELE 1053	
DB	961	QCKDDGRC	CEGREGVGNRCQDCEENFYNNR	SFPGQCECPAC	YRLVKDKVADHRV	LQGELE 1020	
QY	1054	SLIANLTG	DEMVTDOAFEDRLKEAREVMD	LAREADVKDQNLMD	RLQRVN	NLTSSQ 1113	
DB	1021	SLIANLTG	DEMVTDOAFEDRLKEAREVMD	LAREADVKDQNLMD	RLQRVN	NLTSSQ 1080	
QY	1114	ISRLQNT	RNTIETGNLAEQAR	AVENTERLILIASRELE	KAKVAA	ANVS	VTPESTGDP 1173
DB	1081	ISRLQNT	RNTIETGNLAEQAR	AVENTERLILIASRELE	KAKVAA	ANVS	VTPESTGDP 1140

QY 1174 NMNTLLAEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRLTAGENOTAFIEBELN 1233  
Db 1141 NMNTLLAEARKLAERHKEADDDIVRVAKTANDTSTAYNLLRLTAGENOTAFIEBELN 1200  
QY 1234 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLNEANNIKWEA 1293  
Db 1201 RYEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLNEANNIKWEA 1260  
QY 1294 ENLEQIDOKLQVDELDREDMRGKELEVKNLLEKGTQOOTADOLLAADAKALAEAA 1353  
Db 1261 ENLEQIDOKLQVDELDREDMRGKELEVKNLLEKGTQOOTADOLLAADAKALAEAA 1320  
QY 1354 KKGRTDQEAANDILNNLKDFRRVNDNKTAAAEALRKIPAINOTITEANEXTREAAQALG 1413  
Db 1321 KKGRTDQEAANDILNNLKDFRRVNDNKTAAAEALRKIPAINOTITEANEXTREAAQALG 1380  
QY 1414 SAAADATEAKNAKHAERIASVQKNATSTYAEAEETFAEVTDDLDNEVNNMLKQLEAEK 1473  
Db 1381 SAAADATEAKNAKHAERIASVQKNATSTYAEAEETFAEVTDDLDNEVNNMLKQLEAEK 1440  
QY 1474 ELKRQDDADODMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLEQLGQDQTDVDLN 1533  
Db 1441 ELKRQDDADODMMAGMASQAAQAEAEINARKAKNSVTSLSIINDLLEQLGQDQTDVDLN 1500  
QY 1534 KLNIEGTLNKAKDMKVSDDLDRKVSQDLENAKQAEAAIMDYNRDIBIEMKDINLEDIR 1593  
Db 1501 KLNIEGTLNKAKDMKVSDDLDRKVSQDLENAKQAEAAIMDYNRDIBIEMKDINLEDIR 1560  
QY 1594 KTLPSGCFNTPSIEKP 1609  
Db 1561 KTLPSGCFNTPSIEKP 1576  
RESULT 9  
ABB81595  
ID ABB81595 standard; protein; 1576 AA.  
AC ABB81595;  
XX  
DT 19-SEP-2002 (first entry)  
XX  
DE Human laminin 10 third chain protein sequence SEQ ID NO:16.  
XX  
KW Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX  
OS Homo sapiens.  
XX  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PF 21-DEC-2001; 2001WO-US051035.  
PR 21-DEC-2000; 2000US-0257449P.  
PR 28-MAR-2001; 2001US-0279282P.  
PR 13-NOV-2001; 2001US-00279282.  
XX  
PA (BIOS-) BIOTRATUM INC.  
XX  
XX Tryggvason K, Doi M, Thyboll J;  
XX  
XX WPI; 2002-557650/59.  
XX N-PSDB; ABQ72913.  
XX  
XX New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX  
PS Claim 9; Page 177-182; 231pp; English.  
XX

CC The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a third chain protein of laminin 10, from the present  
CC invention  
XX  
SQ Sequence 1576 AA;  
Query Match 98.1%; Score 8544; DB 5; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 QAAMDSECTDEGRPQRCMPFVNAAPNVTVVATNTCGTPPEEYCVQTVGTGTSKCHLCD 93  
Db 1 QAAMDSECTDEGRPQRCMPFVNAAPNVTVVATNTCGTPPEEYCVQTVGTGTSKCHLCD 60  
QY 94 AGOPHLOHGAFLTDYNNQADTTWQSQMLAGVYPPSSINLTLLHKGAFDITYVRLKPH 153  
Db 61 AGOPHLOHGAFLTDYNNQADTTWQSQMLAGVYPPSSINLTLLHKGAFDITYVRLKPH 120  
QY 154 TSPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFINTGDEQOALCTDFSQIS 213  
Db 121 TSPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFINTGDEQOALCTDFSQIS 180  
QY 214 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNFTGDEVNDPKVLSY 273  
Db 181 PLTGGNVAFSTLEGRPSAYNFNSPVLQEWVTATDIRVTLNRLNFTGDEVNDPKVLSY 240  
QY 274 YYAISDFAVGGRCKNGHASECMQNEFDKLVNCKNHTYGVDCCKLPFFNDRPMRRATA 333  
Db 241 YYAISDFAVGGRCKNGHASECMQNEFDKLVNCKNHTYGVDCCKLPFFNDRPMRRATA 300  
QY 334 ESASECLPCDCNGRQSOBCYFDPFLYRSTGHGCHTNCQDNTDGAHCERCERENFFLGNNE 393  
Db 301 ESASECLPCDCNGRQSOBCYFDPFLYRSTGHGCHTNCQDNTDGAHCERCERENFFLGNNE 360  
QY 394 ACSSCHCSFVGSLSITOCDSYGRCSCKPGWGMGKDCRCOPGFHSLTEAGRCPCSCDPSGSI 453  
Db 361 ACSSCHCSFVGSLSITOCDSYGRCSCKPGWGMGKDCRCOPGFHSLTEAGRCPCSCDPSGSI 420  
QY 454 DECNVETGRVCVKDNVEGFCNBERCKPFPNLESSNPRGCTPCFCGHSVCTNAVGVSY 513  
Db 421 DECNVETGRVCVKDNVEGFCNBERCKPFPNLESSNPRGCTPCFCGHSVCTNAVGVSY 480  
QY 514 SISSTFQIDEDGWABORDGSEASLEWSSERQDIAVISDSYPRYFIAPAKELGQVLSY 573  
Db 481 SISSTFQIDEDGWABORDGSEASLEWSSERQDIAVISDSYPRYFIAPAKELGQVLSY 540  
QY 574 GQNLSPSFVRDRDRTRLSAEDLVLEGAGLURVSVPLIAQNSYSPSETTVKYVFRLEHATDY 633  
Db 541 GQNLSPSFVRDRDRTRLSAEDLVLEGAGLURVSVPLIAQNSYSPSETTVKYVFRLEHATDY 600  
QY 634 PWRPALTPPEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPGVPATWVESCCTCP 693  
Db 601 PWRPALTPPEFQKLLNNLTSLIKIRGTYSERSAGYLDVTLASARPGVPATWVESCCTCP 660  
QY 694 VGYGQFCMCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPBTGVNCRDNTAGPHCEK 753  
Db 661 VGYGQFCMCLSGYRRETPNLGYPSPCVLCAACNGHSETCDPBTGVNCRDNTAGPHCEK 720  
QY 754 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGRCLCDDGVFG 813  
Db 721 CSDGYGDSSTAGTSSDCQPCPCPGSSCAVVPKTKVCTNCTPTGTTGRCLCDDGVFG 780  
QY 814 DPLGRNGPVRLCRLCQCSNDIDPNVAGNCNRLTGELCKIYNTAGFYCDRCCKDGFGNPL 873  
Db 781 DPLGRNGPVRLCRLCQCSNDIDPNVAGNCNRLTGELCKIYNTAGFYCDRCCKDGFGNPL 840

QY 874 APNADKCKACNCPYGTMTKQSSNCPVITGQCECLPHVTGQCGADPGFYNLQSGQCE 933  
Db  
QY 841 APNADKCKACNCPYGTMTKQSSNCPVITGQCECLPHVTGQCGADPGFYNLQSGQCE 900  
Db  
QY 934 RCDHALGSTNGQCDITRTGQCECPQGITGHCERCENHFGPGCKPCDCHPGSL 993  
Db  
QY 901 RCDHALGSTNGQCDITRTGQCECPQGITGHCERCENHFGPGCKPCDCHPGSL 960  
QY 994 QCKDGRCEGCEGFGVNRCDQCEENFYNRSPGCECPACVRLVKDKVADHRVKLQELE 1053  
Db  
QY 961 QCKDGRCEGCEGFGVNRCDQCEENFYNRSPGCECPACVRLVKDKVADHRVKLQELE 1020  
QY 1054 SLIANLGTGDEMVTDAFEDRLKEAREVMDLLREAOQVQKVDQNDLQVNTLSQ 1113  
Db  
QY 1021 SLIANLGTGDEMVTDAFEDRLKEAREVMDLLREAOQVQKVDQNDLQVNTLSQ 1080  
QY 1114 ISRLQIRNTIETGNLAEGARAHVENTERLIEIASRELEKAKVAANVSVPSTGDP 1173  
Db  
QY 1081 ISRLQIRNTIETGNLAEGARAHVENTERLIEIASRELEKAKVAANVSVPSTGDP 1140  
QY 1174 NNMTLAEARKLAERHKOADDIVRVAKTANDTSTAYNLLRLTAGENQTAPEIELN 1233  
Db  
QY 1141 NNMTLAEARKLAERHKOADDIVRVAKTANDTSTAYNLLRLTAGENQTAPEIELN 1200  
QY 1234 RKYEQAKNISODLEKQAAKVHEBAKRGADKAVEIYASVAQLSPDSELTENANNIKMA 1293  
Db  
QY 1201 RKYEQAKNISODLEKQAAKVHEBAKRGADKAVEIYASVAQLSPDSELTENANNIKMA 1260  
QY 1294 ENLEQLIDQKDYEDLREDMRGKELEVKVNLKKGTEQQTADQLLARADAKALAEAA 1353  
Db  
QY 1261 ENLEQLIDQKDYEDLREDMRGKELEVKVNLKKGTEQQTADQLLARADAKALAEAA 1320  
QY 1354 KKGRTLOEANDILNLLKQDFRVNOKTAAEALAKI PAINTITEANEKTRAQOALG 1413  
Db  
QY 1321 KKGRTLOEANDILNLLKQDFRVNOKTAAEALAKI PAINTITEANEKTRAQOALG 1380  
QY 1414 SAAADATEAKNKAHEARIASAVQKNATSTKAEAEFTFAEVDLDNEVNNMLKQLEAK 1473  
Db  
QY 1381 SAAADATEAKNKAHEARIASAVQKNATSTKAEAEFTFAEVDLDNEVNNMLKQLEAK 1440  
QY 1474 ELKRGQDDADQDMWAGMASQAQAEIENARKAKNSVTSLLSIINDLLEQLQDVTDLN 1533  
Db  
QY 1441 ELKRGQDDADQDMWAGMASQAQAEIENARKAKNSVTSLLSIINDLLEQLQDVTDLN 1500  
QY 1534 KLANEIEGTLNKAKDEMKSVDLRKVDLENAKQEAAMDVNRDYEIMKDIRNLEDIR 1593  
Db  
QY 1501 KLANEIEGTLNKAKDEMKSVDLRKVDLENAKQEAAMDVNRDYEIMKDIRNLEDIR 1560  
QY 1594 KTLPSGCFNTPSIEKP 1609  
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 10  
AAB19804  
ID AAB19804 standard; protein; 1584 AA.

AC AAB19804;  
XX  
DT 05-MAR-2001 (first entry)  
XX Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.  
DE  
XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
KW  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 1. .33  
FT Peptide /label= Signal\_peptide  
FT 34. .1609  
FT Protein

FT Peptide /label= Mature\_protein  
FT 1610. .1617  
XX /label= FLAG  
PN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PP 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
XX Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88904.  
XX  
XX Purified laminin 2 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
XX Claim 5; Page 275-280; 305pp; English.  
XX  
XX The present sequence is that of the mature gamma-1 chain of human laminin  
XX 2, with an additional C-terminal FLAG epitope, resulting from expression  
XX in transfected cells from mammalian expression vectors. Laminin 2 is  
XX composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa)  
XX chains. It is thought to be specifically required for stabilizing  
XX myotubes during skeletal muscle development, and for preventing  
XX apoptosis. Genetic defects in its structure or expression are associated  
XX with a major type of congenital muscular dystrophy. Laminin 2 is also  
XX thought to be important in Schwann cell/basal lamina interactions. The  
XX invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain  
XX polypeptides (see AAB19791-806) and the polynucleotides encoding them  
XX (see AAA8891-906), methods for making recombinant laminin 2, cells that  
XX express recombinant laminin 2, and methods for using purified laminin 2  
XX for research and therapeutic purposes including peripheral nerve  
XX regeneration, treatment of degenerative muscle disorders, angiogenesis  
XX regulation, promoting cell attachment and migration, ex vivo cell  
XX therapy, improving the take of grafts, improving the biocompatibility of  
XX medical devices and preparing improved culture devices and media  
XX  
XX Sequence 1584 AA;

Query Match 98.1%; Score 8544; DB 3; Length 1584;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAMDECTDEGRPQRCMPPEFVNAAFNVTVVATNCTGTPPEYCVQTVGTGKSLCLD 93  
Db 1 QAAMDECTDEGRPQRCMPPEFVNAAFNVTVVATNCTGTPPEYCVQTVGTGKSLCLD 60  
QY 94 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVOYESSINLTLHLGKAFDITVRLKPH 153  
Db 61 AGQPHLQHGAAFLTDYNNQADTTWQSQOTMLAGVOYESSINLTLHLGKAFDITVRLKPH 120  
QY 154 TSRPESFAIYKRTREDGWPWPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDFSDIS 213  
Db 121 TSRPESFAIYKRTREDGWPWPYQYSGSCENTYSKANRGFIRTGDEQQAALCTDFSDIS 180  
QY 214 PLTGCVNAFSTLEGRPSAYNFDNSPVLQEWVTATDIRTLNRLNTFGDEVNDPKVLSKY 273  
Db 181 PLTGCVNAFSTLEGRPSAYNFDNSPVLQEWVTATDIRTLNRLNTFGDEVNDPKVLSKY 240  
QY 274 YYAISDFAVGRCCKNGHASECMKNFEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA 333  
Db 241 YYAISDFAVGRCCKNGHASECMKNFEFDKLVNCNKHNTYGVDCCKLPFFNDRPWRATA 300

334 ESASECLPCDNGRSQECYFDPFLYRSTGHGHCTNQDNTDGAHCRCRENFFRLGNNE 393  
301 ESASECLPCDNGRSQECYFDPFLYRSTGHGHCTNQDNTDGAHCRCRENFFRLGNNE 360  
394 ACSCHCSFVSGSLSTQCDSDYGRCSCKPGVGMGDKDRCPQPHSLTEAGCPCSCDPSGSI 453  
361 ACSCHCSFVSGSLSTQCDSDYGRCSCKPGVGMGDKDRCPQPHSLTEAGCPCSCDPSGSI 420  
454 DECNVETGRGVCKDNVEGFNCERCKPGFPNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 513  
421 DECNVETGRGVCKDNVEGFNCERCKPGFPNLESSNPRGCTPCFCFGHSSVCTNAVGYSVY 480  
514 SISSTFQIDEGWRAEQRDGEASLEWSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 573  
481 SISSTFQIDEGWRAEQRDGEASLEWSERQDIAVISDSYFFRYFIAPAKFLGKQVLSY 540  
574 GONLSFSPVRDRTRLSAEDLVLEAGLRVSVPLIAQNSYPSSETTKVFRLEHATDY 633  
541 GONLSFSPVRDRTRLSAEDLVLEAGLRVSVPLIAQNSYPSSETTKVFRLEHATDY 600  
634 PWRPALTPEFKLNNLTISKIRGTYSERAGYLDVDTLASRPPGPGVPATWVSECTCP 693  
601 PWRPALTPEFKLNNLTISKIRGTYSERAGYLDVDTLASRPPGPGVPATWVSECTCP 660  
694 VYGGQFCFCEMCLSGVRRRTPNLGPVPCVLCACNGHSETCDPETGVCNCRDNTAGPCHCK 753  
661 VYGGQFCFCEMCLSGVRRRTPNLGPVPCVLCACNGHSETCDPETGVCNCRDNTAGPCHCK 720  
754 CSDGYGDSGTAGTSSDCQPCPCGSSCAVVPKTEVVCNTPCTGTTGKCELCDDGYFG 813  
721 CSDGYGDSGTAGTSSDCQPCPCGSSCAVVPKTEVVCNTPCTGTTGKCELCDDGYFG 780  
814 DPLGNGPVRCLRCQCSNIDPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 873  
781 DPLGNGPVRCLRCQCSNIDPNAGVNCNRLTGECLKCIYNTAGFYCDRCCKGFFGNPL 840  
874 APNPADKCKACNCPYGTWKQSSCNPTVGOCECLPHVTGQDCGACDPGFYNLQSGQCE 933  
841 APNPADKCKACNCPYGTWKQSSCNPTVGOCECLPHVTGQDCGACDPGFYNLQSGQCE 900  
934 RCDCHALSTNGQCDIRTGQCECQPIITGQCECEVNHFGFEGCKPCDCHPEGSLSL 993  
901 RCDCHALSTNGQCDIRTGQCECQPIITGQCECEVNHFGFEGCKPCDCHPEGSLSL 960  
994 QCKDDGRCEGFGVGNRCQCEENYFYNRSPGQCECPACVRLVKQVADHRVVKLQJLE 1053  
961 QCKDDGRCEGFGVGNRCQCEENYFYNRSPGQCECPACVRLVKQVADHRVVKLQJLE 1020  
1054 SLIANLGTGDEMVTDOAFEDRLKEAREVMOLLREAOQVQDVQDQNLMDRLQRVNNTLSQ 1113  
1021 SLIANLGTGDEMVTDOAFEDRLKEAREVMOLLREAOQVQDVQDQNLMDRLQRVNNTLSQ 1080  
1114 ISRLQNIINTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173  
1081 ISRLQNIINTIETGNLAEOARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140  
1174 NNMTLLAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRLTAGENOTAFEIBELN 1233  
1141 NNMTLLAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRLTAGENOTAFEIBELN 1200  
1234 RYEQAKNISOLEKQARVHEEAKRAGDKAVIYASVAQSPSLDSELEANNIKMEA 1293  
1201 RYEQAKNISOLEKQARVHEEAKRAGDKAVIYASVAQSPSLDSELEANNIKMEA 1260  
1294 ENLEQLIDQKDYEDLREDMRGKEVKNLLEKGTQEQATDQQLARADAALAEPA 1353  
1261 ENLEQLIDQKDYEDLREDMRGKEVKNLLEKGTQEQATDQQLARADAALAEPA 1320  
1354 KKGRTLOEANDILNNLKDFDRVNDNTAAEALRKIPALNOTTEANETREAAQALG 1413  
1321 KKGRTLOEANDILNNLKDFDRVNDNTAAEALRKIPALNOTTEANETREAAQALG 1380  
1414 SAAADATEAKKAHEAERIASAVQKNTATSKAEERTFAEVTDLDDNEVNNMLKQJQAEK 1473

1381 SAAADATEAKKAHEAERIASAVQKNTATSKAEERTFAEVTDLDDNEVNNMLKQJQAEK 1440  
1474 ELKRRQDDADQDMWAGMASQAQAQAEINARKAKNSVTSLLSIINDLLEQLGQDVTDLN 1533  
1441 ELKRRQDDADQDMWAGMASQAQAQAEINARKAKNSVTSLLSIINDLLEQLGQDVTDLN 1500  
1534 KUNEIEGTINKAKDEMKVSDLDKRVSDIENAKKQEAAMDYNRDIEEIMKDINLEDIR 1593  
1501 KUNEIEGTINKAKDEMKVSDLDKRVSDIENAKKQEAAMDYNRDIEEIMKDINLEDIR 1560  
1594 KTLPSGCFNTPSIEKP 1609  
1561 KTLPSGCFNTPSIEKP 1576  
RESULT 11  
AAB19805  
ID AAB19805 standard; protein; 1605 AA.  
XX  
AC AAB19805;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Mouse laminin 2 gamma-1 chain.  
XX  
KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
XX degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..33  
FT Protein /label= Signal\_peptide  
FT /label= Mature\_protein  
XX  
XX WO200066730-A2.  
XX  
XX 09-NOV-2000.  
XX  
XX 28-APR-2000; 2000WO-USO11378.  
XX  
XX 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
XX 12-JUL-1999; 99US-0143289P.  
XX 24-SEP-1999; 99US-0155945P.  
XX  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
XX Yurchenco P;  
XX  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88905.  
XX  
XX Purified laminin 2 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
XX Claim 5; Page 288-294; 305pp; English.  
XX  
XX The present sequence is that of the gamma-1 chain of mouse laminin 2.  
XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
XX (100 kDa) chains. It is thought to be specifically required for  
XX stabilizing myotubes during skeletal muscle development, and for  
XX preventing apoptosis. Genetic defects in human laminin 2 structure or  
XX expression are associated with a major type of congenital muscular  
XX dystrophy. Laminin 2 is also thought to be important in Schwann  
XX cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
XX beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
XX polynucleotides encoding them (see AAA88991-906), methods for making  
XX recombinant laminin 2, cells that express recombinant laminin 2, and  
XX methods for using purified laminin 2 for research and therapeutic

CC	purposes including peripheral nerve regeneration, treatment of									
CC	degenerative muscle disorders, angiogenesis regulation, promoting cell									
CC	attachment and migration, ex vivo cell therapy, improving the take of									
CC	grafts, improving the biocompatibility of medical devices and preparing									
CC	improved culture devices and media									
XX										
XX										
XX										
QY	Sequence 1605 AA;									
QY	Query Match	93.5%;	Score 8148;	DB 3;	Length 1605;					
QY	Best Local Similarity	92.8%;	Pred. No. 0;							
QY	Mismatches 1493;	Conservative 59;	Mismatches 53;	Indels 4;	Gaps 3;					
QY	1	MRGSHRAAPALRGRGLWFLVLA	AAAAAGCAQAAMDECTDEGGRPQRCMEFVNAAFN	60						
QY	1	MTGGRAALALQPRGLWFLAVL	-AAVAGCVRAAMDECADEGGPQRCMEFVNAAFN	58						
QY	61	VTVVATNTCGTPPEEYCVGTGVT	SKCHLDAGQPHLOHGAFLTYVNNQADTTWQS	120						
QY	59	VTVVATNTCGTPPEEYCVGTGVT	SKCHLDAGQPHLOHGAFLTYVNNQADTTWQS	118						
QY	121	QTMAGVQVPSSNLTGKAFDITVRL	KHTSPESFALYKRTREDGPMIPQYYSG	180						
QY	119	QTMAGVQVPSSNLTGKAFDITVRL	KHTSPESFALYKRTREDGPMIPQYYSG	178						
QY	181	SCNTYSKANRGFIRTGDEBQALCT	DEFSDISPLTGNVAFSTLEGPSAYNFNSPVL	240						
QY	179	SCNTYSKANRGFIRTGDEBQALCT	DEFSDISPLTGNVAFSTLEGPSAYNFNSPVL	238						
QY	241	QEWVATDITVTLNRLNTGDEVNDP	KVLSYVIAISDFAVGRCCKNGHASECKWNEF	300						
QY	239	QEWVATDITVTLNRLNTGDEVNDP	KVLSYVIAISDFAVGRCCKNGHASECKWNEF	298						
QY	301	DKLVCKNHTYGVCEKCLPFNDP	WRRAATASASECLPCDCNGRSQECYFDPFLYRS	360						
QY	299	DKLVCKNHTYGVCEKCLPFNDP	WRRAATASASECLPCDCNGRSQECYFDPFLYRS	358						
QY	361	TGHGGHCTNCDNTDGAHCBRCRE	NFRIGNNEACSSCHSPVGSLSUQDYSYGRCSCKP	420						
QY	359	TGHGGHCTNCDNTDGAHCBRCRE	NFRIGNNEACSSCHSPVGSLSUQDYSYGRCSCKP	418						
QY	421	GVMDKCDRCQPFHSLTEAGRCPC	SDPSGSDENCVETGRVCNDVGEFNCRCCKP	480						
QY	419	GVMDKCDRCQPFHSLTEAGRCPC	SDPSGSDENCVETGRVCNDVGEFNCRCCKP	478						
QY	481	FFNLESNPRGCTPCFCFHSSVCT	NAVGSYVTSISSTQIDBDGWRAEQRDGSASLEW	540						
QY	479	FFNLESNPRGCTPCFCFHSSVCT	NAVGSYVTSISSTQIDBDGWRAEQRDGSASLEW	538						
QY	541	SSERQDIATVSDSYFRYFIAPAK	ELGKQVLSYQNLSPSFRVDRDRLSAEDLVLEGA	600						
QY	539	SSERQDIATVSDSYFRYFIAPAK	ELGKQVLSYQNLSPSFRVDRDRLSAEDLVLEGA	598						
QY	601	GLRVSVPLIAQGNISYPSSETTV	KYVRLHEATDYPWRPALTPPEFQKLLNLT	660						
QY	599	GLRVSVPLIAQGNISYPSSETTV	KYVRLHEATDYPWRPALTPPEFQKLLNLT	658						
QY	661	SERSAGVLDVTLASARPGVPAT	WVESCTCPVGGGFCMCLSGYRETENLGPYSP	720						
QY	659	SERSAGVLDVTLASARPGVPAT	WVESCTCPVGGGFCMCLSGYRETENLGPYSP	718						
QY	721	CVLCACNGHSETCDPETGVNCN	DRNTAGPHCEKCSGTYGDSSTAGTSSDCQPCPCGSS	780						
QY	719	CVLCACNGHSETCDPETGVNCN	DRNTAGPHCEKCSGTYGDSSTAGTSSDCQPCPCGSS	778						
QY	781	CAVVPKTKVVTNCPFTGTTGK	RCCLDDGYFGDPLGRNGPVLRLCCLCCSNDIDNNAV	840						
QY	779	CAVVPKTKVVTNCPFTGTTGK	RCCLDDGYFGDPLGRNGPVLRLCCLCCSNDIDNNAV	838						
QY	841	NCNRLTGECLKCIYNTAGFY	CDRCCKGFFGNPLAPNADKCKACNPNYGTWKQSSCNP	900						
QY	839	NCNRLTGECLKCIYNTAGFY	CDRCCKGFFGNPLAPNADKCKACNPNYGTWKQSSCNP	897						
QY	901	VTGQCECLPHVTGQDCGACD	PGFNYLQSGGRCRCDHALGSTNGQCDINTGQCECQPGI	960						

Db	898	VTGQCECLPHVTGQDCGACD	PGFNYLQSGGRCRCDHALGSTNGQCDINTGQCECQPGI	957
Qy	961	TGQCECEVNHFGFEGCKPCD	CHPEGSLSLQCKDDGRCCECEGFGVGNRCQCEENYF	1020
Db	958	TGQCECEVNHFGFEGCKPCD	CHPEGSLSLQCKDDGRCCECEGFGVGNRCQCEENYF	1017
Qy	1021	YNRSWPCQCPACRYLVKDKV	ADHRVKLOELSLANLTGDMVTDQAFEDRLKEAER	1080
Db	1018	YNRSWPCQCPACRYLVKDKV	ADHRVKLOELSLANLTGDMVTDQAFEDRLKEAER	1077
Qy	1081	EVMDLLREAOQVXDQONLMD	RILQRVNNTLSSQISRLQNTIRNTIETGNIARAHVEN	1140
Db	1078	EVMDLLREAOQVXDQONLMD	RILQRVNNTLSSQISRLQNTIRNTIETGNIARAHVEN	1137
Qy	1141	TERLIETASRELEKAKVAA	ANVSUTQESTGDPNNMTLLAEBAERKQADDDIVRV	1200
Db	1138	TEQIETASRELEKAKVAA	ANVSUTQESTGDPNNMTLLAEBAERKQADDDIVRV	1196
Qy	1201	AKTANDTSTAYNLLRLTLAG	ENQTAFEI BELNRKYEQAKNI SODLEKQAARVHEEAKRA	1260
Db	1197	AKTANETSAYNLLRLTLAG	ENQTALEI BELNRKYEQAKNI SODLEKQAARVHEEAKRA	1256
Qy	1261	GDKAVEIYASVAQLSPDSE	TLENEANNI KWEAENLEQLIDOKLKOVEDREDMRGKELE	1320
Db	1257	GDKAVEIYASVAQLTPVD	SEALENEANKI KKEAADLRLIDOKLKOVEDREDMRGKEHE	1316
Qy	1321	VKNLLEKGTQEQOTADQ	LARADAALAEBAEAKKGRDTLQEAANDILNLLKDFDRVNDN	1380
Db	1317	VKNLLEKGTQEQOTADQ	LARADAALAEBAEAKKGRDTLQEAANDILNLLKDFDRVNDN	1376
Qy	1381	KTAAEELRKIPAINQIT	TEANEKTRQAQALGSAADATEAKNAHEAERIASAQKNA	1440
Db	1377	KTAAEELRKIPAINRTIA	EANEKTRQAQALGSAADATEAKNAHEAERIASAQKNA	1436
Qy	1441	TSTKAEAEERTPAEVT	LDNEVNNMLKQLEAEKELKRRKQDDADQDMMAGVSAQAQAE	1500
Db	1437	TSTKAEAEERTPAEVT	LDNEVNNMLKQLEAEKELKRRKQDDADQDMMAGVSAQAQAE	1496
Qy	1501	INAKKAKNSVTSLLSI	INDLLEQLGQDITVDLKNLNEIGTLNKADEMVKSDLDKRVSD	1560
Db	1497	INAKKAKNSVTSLLSI	INDLLEQLGQDITVDLKNLNEIGTLNKADEMVKSDLDKRVSD	1556
Qy	1561	LENKAKQEAAMNDYND	IEEIMKDIEINLEDIRKTLPSGCFNTPSIEKP	1609
Db	1557	LESEARKQEAAMNDYND	IEEIMKDIEINLEDIRKTLPSGCFNTPSIEKP	1605
RESULT 12				
AAB48454				
ID	AAB48454	standard; protein; 1605 AA.		
XX	AAB48454;			
AC	AAB48454;			
DT	02-MAR-2001	(first entry)		
XX	Mouse laminin 8 polypeptide, SEQ ID NO: 26.			
DE	Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;			
KW	antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;			
KW	vascular tissue injury; neural injury; angiogenesis regulation.			
XX	Mus musculus.			
XX	WO200066732-A2.			
PN	09-NOV-2000.			
PD	28-APR-2000; 2000MO-US011543.			
XX	30-APR-1999; 99US-0131720P.			
PR	21-AUG-1999; 99US-0149738P.			
PR	24-SEP-1999; 99US-0155945P.			





ABB81596  
ID ABB81596 standard; protein; 1605 AA.  
XX AC ABB81596;  
XX DT 19-SEP-2002 (first entry)  
XX DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.  
XX KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
XX KW tissue repair development; laminin; healing; vascular tissue;  
XX KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
XX KW proliferation; migration.  
XX OS Mus musculus.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..33  
XX FT /label= signal  
XX FT Protein 34..1605  
XX FT /label= laminin\_10\_third\_chain  
XX WO200250111-A2.  
XX PN 27-JUN-2002.  
XX PD 21-DEC-2001; 2001WO-US051035.  
XX PF 21-DEC-2000; 2000US-0257449P.  
XX PR 28-MAR-2001; 2001US-0279282P.  
XX PR 13-NOV-2001; 2001US-00279282.  
XX XX (BIOS-) BIOSTRATUM INC.  
XX PI Tryggvason K, Doi M, Thyboil J;  
XX XX WPI: 2002-557650/59.  
XX XX N-PSDS; ABQ72914.  
XX XX New human laminin-10 proteins, useful for accelerating the healing of  
XX FT vascular tissue, improving the biocompatibility of grafts, or for  
XX FT promoting re-endothelialization at the site of vascular injuries.  
XX PS Claim 9; Page 191-195; 231pp; English.  
XX CC The present invention describes human laminin alpha 5. Also described is  
XX CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
XX CC useful in maintaining cell/tissue phenotype as well as promoting cell  
XX CC growth and differentiation in tissue repair development. Specifically,  
XX CC laminin 10 can be used for accelerating the healing injuries of vascular  
XX CC tissue, improving the biocompatibility of grafts useful for treating such  
XX CC injuries, for promoting re-endothelialisation at the site of vascular  
XX CC injuries, and promote cell attachment and subsequent cell stasis.  
XX CC proliferation, differentiation, and/or migration. The present sequence  
XX CC represents a third chain protein of laminin 10, from the present  
XX CC invention  
XX SQ Sequence 1605 AA;  
Query Match 93.5%; Score 8148; DB 5; Length 1605;  
Best Local Similarity 92.8%; Pred. No. 0;  
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;  
QY 1 MRGSHRAAPALRPRGRWPVLAVLAAAAAGCAQAAVDECTDEGGRPQRCMPFVNAFN 60  
DB 1 MTGGRAALALQPRGLWPLAVL--AAVAGCVRAAMDECADEGGRPQRCMPFVNAFN 58  
QY 61 VTVVATNTCTPPREYCVQGVTKSCHLADAGPHLOHGAFLTDYNNQADTTWQS 120  
DB 59 VTVVATNTCTPPREYCVQGVTKSCHLADAGPHLOHGAFLTDYNNQADTTWQS 118  
QY 121 QTMLAGVQYPSINLTLHLGKAFDITYVRLKFTSPESFAIYKRTREDGFWIPYQYSG 180

DB 119 QTMLAGVQYPSINLTLHLGKAFDITYVRLKFTSPESFAIYKRTREDGFWIPYQYSG 178  
QY 181 SCENTYSKANRGFIRTCGDSQOALCTDEPSDIPLTGCNVAFSTLEGRPSAYNFDNSPVL 240  
DB 179 SCENTYSKANRGFIRTCGDSQOALCTDEPSDIPLTGCNVAFSTLEGRPSAYNFDNSPVL 238  
QY 241 QEWYATDIDRVTLNRLNTFGDEVFNDPKVLSYIYAIISDFAVGRCCKNGHASECKNEF 300  
DB 239 QEWYATDIDRVTLNRLNTFGDEVFNDPKVLSYIYAIISDFAVGRCCKNGHASECKNEF 298  
QY 301 DKLVCNCKHTYGVDCCKLCPFFNDRPWRATASASECLPCDCNGRSQBCYFDPPELYRS 360  
DB 299 DKLVCNCKHTYGVDCCKLCPFFNDRPWRATASASECLPCDCNGRSQBCYFDPPELYRS 358  
QY 361 TGHGCHTNCODNTDGAHCRCRCRENFRLGNACSSCHCSPVGSLSQCDSTYGRCSCKP 420  
DB 359 TGHGCHTNCODNTDGAHCRCRCRENFRLGNACSSCHCSPVGSLSQCDSTYGRCSCKP 418  
QY 421 GVMGDKDRCPQPGFHSILTEAGRCPCSDPSGSDIDECNVETGRCVCKDNVGFNCERCKPG 480  
DB 419 GVMGDKDRCPQPGFHSILTEAGRCPCSDPSGSDIDECNVETGRCVCKDNVGFNCERCKPG 478  
QY 481 FFNLESSNPRGCTPCFCFHSSVCTNAVGYSVISISTFOIDEDGWRABORDGSEASLEW 540  
DB 479 FFNLESSNPRGCTPCFCFHSSVCTNAVGYSVISISTFOIDEDGWRABORDGSEASLEW 538  
QY 541 SSERQDIAVISDSYFPFYFTAPAKFLGKOVLSYQNLSPSFRVDRDRTRLSAEDLVLEGA 600  
DB 539 SSDQYIAVISDSYFPFYFTAPAKFLGKOVLSYQNLSPSFRVDRDRTRLSAEDLVLEGA 598  
QY 601 GLRVSVPLIAQNSYPSSETTVKYVRLHEATDYPWRPALTPFFQKLLNLTISIKIRGTY 660  
DB 599 GLRVSVPLIAQNSYPSSETTVKYVRLHEATDYPWRPALTPFFQKLLNLTISIKIRGTY 658  
QY 661 SERAGYLDVTLASARPGVPATWVETCTCPVYGQFCFCEMLSCSYRETNLGYSYP 720  
DB 659 SERAGYLDVTLASARPGVPATWVETCTCPVYGQFCFCEMLSCSYRETNLGYSYP 718  
QY 721 CVLCAKNGHSETCDPETGVNCRDNTAGPCHCKSDGYGDDSTAGTSSDCQPCPCPGSS 780  
DB 719 CVLCAKNGHSETCDPETGVNCRDNTAGPCHCKSDGYGDDSTAGTSSDCQPCPCPGSS 778  
QY 781 CAVVPKIVVCTNCPGTGKRCCELDGVDGFGDGLGNGPVRCLRCQCDNDIDPNAVG 840  
DB 779 CAVVPKIVVCTNCPGTGKRCCELDGVDGFGDGLGNGPVRCLRCQCDNDIDPNAVG 838  
QY 841 NCNLTGECLEKIYNTAGFYCDRCCKDGFNGLAPNADKCKACNCPYGTMTKQSSCNP 900  
DB 839 NCNLTGECLEKIYNTAGFYCDRCCKDGFNGLAPNADKCKACNCPYGTMTKQSSCNP 897  
QY 901 VTGQCECLPHVTGDCGACDGPVNLQSGQCCERCDCHALGSTNGQCDIRTGQCECQPGI 960  
DB 898 VTGQCECLPHVTGDCGACDGPVNLQSGQCCERCDCHALGSTNGQCDIRTGQCECQPGI 957  
QY 961 TGQHCERCEVNHFGPGECKPCDCHPEGSLSLQCKDDGRCCEGFGVGNRCDCQENYF 1020  
DB 958 TGQHCERCEVNHFGPGECKPCDCHPEGSLSLQCKDDGRCCEGFGVGNRCDCQENYF 1017  
QY 1021 YNRNWPQCECPACVRLVKDVAHVRVKLQELSLIANLGTGDEMVTDOAFEDLKEAR 1080  
DB 1018 YNRNWPQCECPACVRLVKDVAHVRVKLQELSLIANLGTGDEMVTDOAFEDLKEAR 1077  
QY 1081 EVMDLREAOQVDQNDQMLORVANTLSSQISRLQNIINTIETCNLAEQARAHVEN 1140  
DB 1078 EVMDLREAOQVDQNDQMLORVANTLSSQISRLQNIINTIETCNLAEQARAHVEN 1137  
QY 1141 TERLTIASRELEKAKAAANVSVTPQESTGDPNNMTLLAEAKLARHKKQAEADDIVR 1200  
DB 1138 TERLTIASRELEKAKAAANVSVTPQESTGDPNNMTLLAEAKLARHKKQAEADDIVR 1196  
QY 1201 AKTANDTSTAYNLLLTLAGENQTAFEIELNKKYQAKNISQDLEKQAAARVHEEAKRA 1260  
DB 1197 AKTANDTSTAYNLLLTLAGENQTAFEIELNKKYQAKNISQDLEKQAAARVHEEAKRA 1256

QY 1261 GDKAVEIYASVAQLSPDSELTLENNANNIKMEAEENLEOLIDOKLYEDLREDMRGKLE 1320  
 DB 1257 GDKAVEIYASVAQLTPVDSLENNANKIKERADLDRLIDOKLYEDLREDMRGKHE 1316  
 QY 1321 VKNLEKTEQQTADQLARADAAKALAEAAKGRDTLQEAANDILNNLKDFRRVNDN 1380  
 DB 1317 VKNLEKGAEQQTADQLARADAAKALAEAAKGRSTLQEAANDILNNLKDFRRVNDN 1376  
 QY 1381 KTAABEALRKIPAINCTITEANEKTRQAQALGSAADATAEAKNAHEABRIASAVOKNA 1440  
 DB 1377 KTAABEALRRIPAINRTTAEANEKTRQAQALGNAADATAEAKNAHEABRIASAAQNA 1436  
 QY 1441 TSTKAEABRTFAEVTLDNEVNNMLKQLEAEKELKRRQDDADQDMMAGMASAAQAE 1500  
 DB 1437 TSTKADAERTFGEVTDLDNEVNGMLRQLEAEENELKRRQDDADQDMMAGMASAAQAE 1496  
 QY 1501 INARKAKSVTSLSIINDLLEQLQDLDVLDKLNIEGTINKAKDEMKVSDIDRKYSD 1560  
 DB 1497 INARKAKSVSLLSOLANLLDQLQDLDVLDKLNIEGTINKAKDEMKASDIDRKYSD 1556  
 QY 1561 LENEAKQEAAMIDYNDIEEIMKDIRNLEIRKTLPSGCFNTPTSEKP 1609  
 DB 1557 LSEARKQEAAMIDYNDIABIIDKHLEIDIKKTLPTGCFNTPTSEKP 1605

## RESULT 14

AAW50897  
 ID AAW50897 standard; protein; 1607 AA.

XX AC AAW50897;

DT 07-DEC-1998 (first entry)

DE Mouse laminin G1 chain.

XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;  
 KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
 KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
 KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
 KW Gerstmann-Strausler syndrome; kuru; scrapie; haemodialysis;  
 KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
 KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
 KW therapy.

XX Mus sp.

XX WO9815179-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.

XX (UNIW ) UNIV WASHINGTON.

XX Castillo G, Snow AD;

XX WPI; 1998-240534/21.

XX Use of laminin and fragments - for developing products for use in the  
 PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
 PT CJD.

PS Claim 15; Page 102-105; 132pp; English.

XX This is the amino acid sequence of the mouse laminin G1 chain. The  
 CC primary object of the invention is to use laminin, laminin-derived  
 CC protein fragments and/or laminin-derived polypeptides as potent  
 CC inhibitors of amyloid formation, deposition, accumulation and/or  
 CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
 CC products (see AAW50888-98) may include mouse or human laminin A or A1

CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
 CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
 CC binding domain of the laminin A chain. A claimed method for treating an  
 CC amyloid disease comprises administering a polypeptide having a  
 CC conformational similarity to a fragment of a laminin protein. A method  
 CC for diagnosing an amyloid disease involves determining levels of laminin  
 CC in a sample. Production of laminin or its fourth globular repeat in vivo  
 CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
 CC products and methods can be used for the diagnosis, prognosis, monitoring  
 CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
 CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
 CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
 CC associated with chronic inflammation, various forms of malignancy and  
 CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
 CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
 CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
 CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
 CC prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler  
 CC syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis  
 CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
 CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
 CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
 CC transthyretin amyloid), and the amyloidosis associated with endocrine  
 CC tumours such as medullary carcinoma of the thyroid (variant of  
 CC procalcitonin)

XX SQ Sequence 1607 AA;

Query Match 93.5%; Score 8147; DB 2; Length 1607;  
 Best Local Similarity 92.6%; Pred. No. 0;  
 Matches 1490; Conservative 61; Mismatches 56; Indels 2; Gaps 1;  
 QY 1 MRGSHRAAPALRPRGLWPVLAVLAAAGCAQAAAMDECTDEGGRPQRCMPEFVNAAFN 60  
 DB 1 MTGGGAALALQPRGLWPLLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58  
 QY 61 VTVVATNTCGTPPEEYCVQTVGTGVTKSCHLDCAGQPHLQHGAAFLTDYNNQADTTWOS 120  
 DB 59 VTVVATNTCGTPPEEYCVQTVGTGVTKSCHLDCAGQPHLQHGAAFLTDYNNQADTTWOS 118  
 QY 121 QTLVAGVQVPSINLTLHLGKAFDIYVRLKHTSPESFAIYKRTREGDPITPYQYSG 180  
 DB 119 QTLVAGVQVPSINLTLHLGKAFDIYVRLKHTSPESFAIYKRTREGDPITPYQYSG 178  
 QY 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNSPVL 240  
 DB 179 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFNSPVL 238  
 QY 241 QEWVATDIRVTLNRLNTFGDEVNDPKVLKSYIYAIISDFAVGGRCKCKNGHASECMKNEF 300  
 DB 239 QEWVATDIRVTLNRLNTFGDEVNDPKVLKSYIYAIISDFAVGGRCKCKNGHASECMKNEF 298  
 QY 301 DKLVCNCKNTYGVDCCKLPPFNDPRPRAATAESASECLPCDCNGRSQBCYFDPPELYRS 360  
 DB 299 DKLVCNCKNTYGVDCCKLPPFNDPRPRAATAESASECLPCDCNGRSQBCYFDPPELYRS 358  
 QY 361 TGHGGHCTNQDNTDGAHCERENFFRLGNNEACSSCHSPVGSLSSTQCDYSGRCSCKP 420  
 DB 359 TGHGGHCTNQDNTDGAHCERENFFRLGNNEACSPCHSPVGSLSSTQCDYSGRCSCKP 418  
 QY 421 GVMGDKCDRCQCFHSLTEAGRCPCSDPSGSDICNVETGRVCCKDNYGENCECKPG 480  
 DB 419 GVMGDKCDRCQCFHSLTEAGRCPCSDLRGSTDICNVETGRVCCKDNYGENCECKPG 478  
 QY 481 FPNLESNPRGCTPCFCFGHSSVCTTNAVGVSYVSISSFTQIDEDGWRAEQRDGSEASLEW 540  
 DB 479 FPNLESNPKGCTPCFCFGHSSVCTTNAVGVSYVSISSFTQIDEDGWRAEQRDGSEASLEW 538  
 QY 541 SSRQDIIVISDYFPRYIAPAKFLGKQVLSYGQNLSPSFVRDREDTSLAEDLLVEGA 600  
 DB 539 SSRQDIIVISDYFPRYIAPAKFLGKQVLSYGQNLSPSFVRDREDTSLAEDLLVEGA 598  
 QY 601 GLRVSVELIAQGNYSYPTTIVKVFRLHEATDYPWRPALTPPEFQKLLNLTISIKIRGY 660

599 GLRVSVELIAQNSVPSSETTVKVIIFRLHEATDYPWRPALSPFEQKLLNLTSTIKRTY 658  
661 SRSAGYLDVLTASAPGPGVPATWVESCTCPVGGQFCBMLSGYRRETPNLGPSP 720  
659 SRTAGYLDVLTQSLAPGPGVPATWVESCTCPVGGQFCETCLPGYRRETPSLGPSP 718  
721 CVLCACNHSETCDPTGVCNCRDNTAGPHCKSCSDGYYGDSGTAGTSSDCQPCPCPGSS 780  
719 CVLCTCNHSETCDPTGVCNCRDNTAGPHCKSCSDGYYGDSGTAGTSSDCQPCPCPGSS 778  
781 CAWPKTKVCTNCPGTGKCELCDDGFGDPLGRNGPVRLCLQCSNIDPNNAV 840  
779 CAIVPKTKVCTNCPGTGKCELCDDGFGDPLGRNGPVRLCLQCSNIDPNNAV 838  
841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNADKCKACNPNYGTWKQSSCNP 900  
839 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNPLAPNADKCKACNPNYGTWKQSSCNP 898  
901 VTQCCECLPHVTQDGCAGCPGYNLQSGQGCRCCHALGTNGOCIRTQCCQCPGI 960  
899 VTQCCECLPHVTQDGCAGCPGYNLQSGQGCRCCHALGTNGOCIRTQCCQCPGI 958  
961 TGQHCERCEVNHFGFPEGCKPCDCHPEGSLSQCKDGRCEGFGVGNRCDCQCEENYF 1020  
959 TGQHCERCEVNHFGFPEGCKPCDCHPEGSLSQCKDGRCEGFGVGNRCDCQCEENYF 1018  
1021 YNRSWPCQCPACRYLVKDVADHRVKLOELSLIANLTGDMVTDQAFEDRLKEAR 1080  
1019 YNRSWPCQCPACRYLVKDVADHRVKLOELSLIANLTGDMVTDQAFEDRLKEAR 1078  
1081 EVMDLLAEADVDKVDQNLMDRLQRVNNTLSSOISRLQINRTIETGNLAQAARHVEN 1140  
1079 EVMDLLAEADVDKVDQNLMDRLQRVNNTLSSOISRLQINRTIETGNLAQAARHVEN 1138  
1141 TERLIEIASRELEKAKVAANVSVOPESTGDDNNMTLAEARKLAERHKGAEADIVRV 1200  
1139 TEQLIEIASRELEKAKVAANVSVOPESTGDDNNMTLAEARKLAERHKGAEADIVRV 1198  
1201 AKTANDTSTAYNLLTLAGENQTAPEIEELNRKYEQAQNSQDLEKQAARVHEAKKA 1260  
1199 AKTANDTSTAYNLLTLAGENQTAPEIEELNRKYEQAQNSQDLEKQAARVHEAKKA 1258  
1261 GDKAVEIYASVAQLSPDSTLENEANNIKVEAENLEQLIDQKLKDYEDLREDMRGKELE 1320  
1259 GDKAVEIYASVAQLSPDSTLENEANNIKVEAENLEQLIDQKLKDYEDLREDMRGKELE 1318  
1321 VKNLLEKKEQQTADQLARADAALAEBAKKGEDTLOEANDILNLLKOPDRRVNDN 1380  
1319 VKNLLEKKEQQTADQLARADAALAEBAKKGEDTLOEANDILNLLKOPDRRVNDN 1378  
1381 KTAAREALRKIPAINQITTEANETREAOQALGSAADATEAKNKAHEARERIASAVQKNA 1440  
1379 KTAAREALRKIPAINQITTEANETREAOQALGSAADATEAKNKAHEARERIASAVQKNA 1438  
1441 TSTKAERTEPAETVTDLDNEVNNMLKQIQAELKEXKODADODMMWAGMASQAQAE 1500  
1439 TSTKAERTEPAETVTDLDNEVNNMLKQIQAELKEXKODADODMMWAGMASQAQAE 1498  
1501 INARKAKNSVTSLLSIINDLEQLGQDQTDVLDNKLNEIEGTLNKAKDEMKVSDLRKVS 1560  
1499 INARKAKNSVTSLLSIINDLEQLGQDQTDVLDNKLNEIEGTLNKAKDEMKVSDLRKVS 1558  
1561 LENAKKQBAIMYNDRIEIMKQIDNLEIDIKTLPSGCFNTPSIEKP 1609  
1559 LESBARKQBAIMYNDRIEIMKQIDNLEIDIKTLPSGCFNTPSIEKP 1607

RESULT 15  
AAB19806  
ID AAB19806 standard; protein; 1572 AA.  
XX  
AC AAB19806;

05-MAR-2001 (first entry)  
Mouse laminin 2 mature gamma-1 chain.  
Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
degenerative muscle disorder; muscular dystrophy; cell therapy.  
Mus musculus.  
W0200066730-A2.  
09-NOV-2000.  
28-APR-2000; 2000WO-US011378.  
30-APR-1999; 99US-0131720P.  
15-JUN-1999; 99US-0139198P.  
12-JUL-1999; 99US-0143289P.  
24-SEP-1999; 99US-0155945P.  
(UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Yurchenco P;  
WPI; 2000-687537/67.  
N-PSDB; AAA88906.  
Purified laminin 2 protein, useful for research and therapeutic purposes  
including peripheral nerve regeneration, treatment of degenerative muscle  
disorders, angiogenesis regulation, and ex vivo cell therapy.  
Claim 5; Page 302-306; 305pp; English.  
The present sequence is that of mouse laminin 2 gamma-1 chain mature  
protein. Laminin-2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and  
gamma-1 (100 kDa) chains. It is thought to be specifically required for  
stabilizing myotubes during skeletal muscle development, and for  
preventing apoptosis. Genetic defects in human laminin 2 structure or  
expression are associated with a major type of congenital muscular  
dystrophy. Laminin 2 is also thought to be important in Schwann  
cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
polynucleotides encoding them (see AAA8891-906), methods for making  
recombinant laminin 2, cells that express recombinant laminin 2, and  
methods for using purified laminin 2 for research and therapeutic  
purposes including peripheral nerve regeneration, treatment of  
degenerative muscle disorders, angiogenesis regulation, promoting cell  
attachment and migration, ex vivo cell therapy, improving the take of  
grafts, improving the biocompatibility of medical devices and preparing  
improved culture devices and media

Query Match 92.3%; Score 8038; DB 3; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;  
QY 36 AMDECTDEGGPQRCMPFVNAAFNVVATNTCGTPPEYCVQTVGTGVTKSHCLCDAG 95  
DB 1 AMDECADEGGPQRCMPFVNAAFNVVATNTCGTPPEYCVQTVGTGVTKSHCLCDAG 60  
QY 96 QPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSSINLTLLHKGAFDITYVRLKFTS 155  
DB 61 QQLHQAFLTDYNNQADTTWQSQTMLAGVQVPNSINLTLLHKGAFDITYVRLKFTS 120  
QY 156 RPESFAIKYRREDGFWIPYQYSGSCENTYSKANRGFIRGTGDBEQQALCTDEFSDISPL 215  
DB 121 RPESFAIKYRREDGFWIPYQYSGSCENTYSKANRGFIRGTGDBEQQALCTDEFSDISPL 180  
QY 216 TGGNVAFTSLGRPSAYNFDNSPVLQEWVATDTRVTLNRLNTFGDEVNDPKVLKSY 275  
DB 181 TGGNVAFTSLGRPSAYNFDNSPVLQEWVATDTRVTLNRLNTFGDEVNDPKVLKSY 240

QY 1356 GRDTLQEAANDILNNLKDFDRRVNDNKTAAEEALRKIPAINOTITEANEKTRQAQALGSA 1415  
Db 1319 GRSTLQEAANDILNNLKDFDRRVNDNKTAAEEALRRIPAINRTIAEANEKTRQAQALGNA 1378  
QY 1416 AADATEAKNAKHAERIASAVQKNATSTKAEABERTFAEVTDLDNVNNMLKOLQEAKEKL 1475  
Db 1379 AADATEAKNAKHAERIASAAQKNATSTKADABERTTGEVTDLDNEVNGMLRQLEEAENEL 1438  
QY 1476 KRQDDADODMMWAGMASQAQAEAINARKAKNSVTSLLSIINDLLEQLGQLDVTVDLNLK 1535  
Db 1439 KRQDDADODMMWAGMASQAQAEAINARKAKNSVTSLLSQNNLLDQLGQLDVTVDLNLK 1498  
QY 1536 NEIEGTLINKAKDEMVSDDLDRKVSDDLNEAKQKQAAIMDYNDRDIEIMKDIRNLEDIRKT 1595  
Db 1499 NEIEGSLINKAKDEMVSDDLDRKVSDDLSEARKQKQAAIMDYNDRDIAEIIKDIHNLEDIRKKT 1558  
QY 1596 LPSGCENFTPSIEKP 1609  
Db 1559 LPTGCFNFTPSIEKP 1572

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Job time : 50.7478 secs

QY 276 AISDFAVGRCKNGHASECMNNEFDKLVNCGKHTNYGVDCEKCLPFNDPWRBATAES 335  
Db 241 AISDFAVGRCKNGHASECVNEFDKLMCNCKHTNYGVDCEKCLPFNDPWRBATAES 300  
QY 336 ASECLPCDCNGRSQCYFDPPELYRSTGHGGCTNCODNTDGAHCRCRENFRLGNNEAC 395  
Db 301 ASECLPCDCNGRSQCYFDPPELYRSTGHGGCTNCODNTDGAHCRCRENFRLGNNEAC 360  
QY 396 SSCHCSPVGLSTQCDSSYGRCSCKPGVMDKDCRCQPGFHSLSITEAGCRPCSCDPSGSIDE 455  
Db 361 SPCHCSPVGLSTQCDSSYGRCSCKPGVMDKDCRCQPGFHSLSITEAGCRPCSCDPSGSIDE 420  
QY 456 CNVETGRVCCKDNVGFNCRCCKPGFNLSSNPRGCTPCFCFHHSSVCTNAVGSVYSI 515  
Db 421 CNVETGRVCCKDNVGFNCRCCKPGFNLSSNPRGCTPCFCFHHSSVCTNAVGSVYSI 480  
QY 516 SSTFOIDEDGMRAEQDGSSEASLEWSSERQDIAVISDYFPRFYIAPAKFLGKQVLSYGQ 575  
Db 481 SSTFOIDEDGMRVQDGSSEASLEWSSDRQYIAVISDSYFPRFYIAPVKFLGNQVLSYGQ 540  
QY 576 NLSFSPFRVDRRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYVFLRHEATDYPW 635  
Db 541 NLSFSPFRVDRRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYIPLRHEATDYPW 600  
QY 636 RPALTPFEFQKLLNNLTSIKIRGTYSERSAGYLDDVTLASARPFGVPATWVESCCTCPVG 695  
Db 601 RPALSPFEFQKLLNNLTSIKIRGTYSERSAGYLDVTLQASRPFGVPATWVESCCTCPVG 660  
QY 696 YGQFCPEMCLSGVRRTPNLGYPSPVLCACNGHSETCDPETGVNCRDNTAGPCEKCS 755  
Db 661 YGQFCETCLPGYRRETPLSGYPSPVLCVCTCNHSETCDPETGVNCRDNTAGPCEKCS 720  
QY 756 DGYGDSGTAGTSDQCPGSSCAVVPKKEVVCTNCTPTGTTGKRCCLCDDGYFGDP 815  
Db 721 DGYGDSGTAGTSDQCPGSSCAI1VPKKEVVCTNCTPTGTTGKRCCLCDDGYFGDP 780  
QY 816 LGRNGPVRICRLQCSNDIPNAGVNCNRLTGECLKIYNTAGFYCDRCCKDGFNGNPLAP 875  
Db 781 LGSNGPVRICRQCCNDIPNAGVNCNRLTGECLKIYNTAGFYCDRCCKDGFNGNPLAP 840  
QY 876 NPADKCKACNCPYGMKQSSCNPTGOCBCLPHVTGDCGACDPGFYNLQSGGQCERC 935  
Db 841 NPADKCKACACN-YGTVQOQSSCNPTGOCQCLPHVSGRDCGTCDPGYVNLQSGGQCERC 899  
QY 936 DCHALGSTNGQCDIRTGQCECQPGITGQHCECEVNHFGFPGCKPCDCHPEGSLSLQC 995  
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCECETNHFPGFPGCKPCDCHPEGSLSLQC 959  
QY 996 KDDGRCEGREGFVGNRCDCQCEENYFNRSPGCOECPACVRLVKDVAADHVRVKLQLESL 1055  
Db 960 KDDGRCEGREGFVGNRCDCQCEENYFNRSPGCOECPACVRLVKDVAADHVRVKLQLESL 1019  
QY 1056 IANLGTGDEMVTQAFEDRLKEAREVMOLLREAOVDKVDQNLMDRLQRVNNTLSSQIS 1115  
Db 1020 IANLGTGDEMVTQAFEDRLKEAREVTDLLREAOVDKVDQNLMDRLQRVNNTLSSQIS 1079  
QY 1116 RLQNIWNTIBETGNLAEQAPAHVENTERLIEIASRELEKAKVAANVSUTOPESTCDPNN 1175  
Db 1080 RLQNIWNTIBETGILAEARFVSVESTQIEIASRELEKAKM-AANVSITQPESTGEPPNN 1138  
QY 1176 MTLLEAEARLAEHRKQEAADDIVRVAKTANDTSTEAYNLLRLTAGENQTAPEIEBELNK 1235  
Db 1139 MTLLEAEARLAEHRKQEAADDIVRVAKTANETSAAEAYNLLRLTAGENQTAPEIEBELNK 1198  
QY 1236 YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIKMEAN 1295  
Db 1199 YEQAKNISQLEKQAAARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258  
QY 1296 LEOI1DQKLDYEDLREDMRGKELEVKNLEKGTQOOTADQLARADAALABEAAKK 1355  
Db 1259 LDR1IDQKLDYEDLREDMRGKEHEVKNLEKGAEQOOTADQLARADAALABEAAKK 1318

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OM protein - protein search, using sw model  
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Gapop 10.0 , Gapext 0.5  
Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 389414  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A-COMB.pdp:\*  
2: /cgn2\_6/prodata/2/iaa/5B-COMB.pdp:\*  
3: /cgn2\_6/prodata/2/iaa/6A-COMB.pdp:\*  
4: /cgn2\_6/prodata/2/iaa/6B-COMB.pdp:\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS-COMB.pdp:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
SUMMARIES  
Result No. Score Query Match Length DB ID Description  
1 8713 100.0 1609 4 US-09-562-702A-22 Sequence 22, Appl  
2 8713 100.0 1609 4 US-09-561-818A-22 Sequence 22, Appl  
3 8713 100.0 1617 4 US-09-562-702A-26 Sequence 26, Appl  
4 8544 98.1 1576 4 US-09-562-702A-24 Sequence 24, Appl  
5 8544 98.1 1576 4 US-09-561-818A-24 Sequence 24, Appl  
6 8544 98.1 1584 4 US-09-562-702A-28 Sequence 28, Appl  
7 8148 93.5 1805 4 US-09-562-702A-30 Sequence 30, Appl  
8 8148 93.5 1805 4 US-09-561-818A-26 Sequence 26, Appl  
9 8038 92.3 1572 4 US-09-562-702A-32 Sequence 32, Appl  
10 8038 92.3 1572 4 US-09-561-818A-28 Sequence 28, Appl  
11 3611 41.4 1587 4 US-09-845-583A-10 Sequence 10, Appl  
12 3611 41.4 1587 4 US-09-561-709B-3 Sequence 3, Appl  
13 2637 30.3 1193 1 US-08-317-450B-13 Sequence 13, Appl  
14 2637 30.3 1193 3 US-08-800-593-13 Sequence 13, Appl  
15 2516.5 28.9 1111 1 US-08-317-450B-15 Sequence 15, Appl  
16 2516.5 28.9 1111 3 US-08-800-593-15 Sequence 15, Appl  
17 2355.5 27.0 1171 1 US-08-445-135-1 Sequence 1, Appl  
18 1782.5 20.5 3110 4 US-09-562-702A-2 Sequence 2, Appl  
19 1782.5 20.5 3110 4 US-09-562-702A-6 Sequence 6, Appl  
20 1782.5 20.5 3110 4 US-09-561-709B-7 Sequence 7, Appl  
21 1782 20.5 3111 2 US-09-561-709B-7 Sequence 7, Appl  
22 1782 20.5 3111 2 US-08-125-077-4 Sequence 4, Appl  
23 1776 20.4 3088 4 US-09-562-702A-8 Sequence 8, Appl  
24 1776 20.4 3088 4 US-09-562-702A-4 Sequence 4, Appl  
25 1774.5 20.4 3106 4 US-09-562-702A-10 Sequence 10, Appl  
26 1768.5 20.3 3084 4 US-09-562-702A-12 Sequence 12, Appl  
27 1717.5 19.7 3075 2 US-08-460-309-5 Sequence 5, Appl

Sequence 5, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 9, Appl  
Sequence 1, Appl  
Sequence 18, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 6, Appl  
Sequence 11, Appl  
Sequence 8, Appl  
Sequence 12, Appl  
Sequence 38, Appl  
Sequence 37, Appl  
Sequence 22, Application US/09562702A  
Patent No. 6632790  
GENERAL INFORMATION:  
APPLICANT: Yurchenco, Peter  
TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
CURRENT APPLICATION NUMBER: US/09/562,702A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/155,945  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: 60/143,289  
PRIOR FILING DATE: 1999-07-12  
PRIOR APPLICATION NUMBER: 60/139,198  
PRIOR FILING DATE: 1999-06-15  
PRIOR APPLICATION NUMBER: 60/131,720  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 22  
LENGTH: 1609  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-562-702A-22

Query Match 100.0%; Score 8713; DB 4; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEGSHRAAPALRPRGRLWPVLAIAAAAGCAQAAMDECTDEGGPQRCMPEFVNAAFN 60  
Db 1 MRGSHRAAPALRPRGRLWPVLAIAAAAGCAQAAMDECTDEGGPQRCMPEFVNAAFN 60  
Qy 61 VTVAINTCGTPPEEYCVQGTGVTGKSCHELDAGQPHLOHGAFLTDYNNQADTTWQS 120  
Db 61 VTVAINTCGTPPEEYCVQGTGVTGKSCHELDAGQPHLOHGAFLTDYNNQADTTWQS 120  
Qy 121 QTMLAGVOYESSNLTILHLKAFDITVRLKHTSPESFAIKRTREGDPMIPYOYSG 180  
Db 121 QTMLAGVOYESSNLTILHLKAFDITVRLKHTSPESFAIKRTREGDPMIPYOYSG 180  
Qy 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240  
Db 181 SCENTYSKANRGFIRTTGGDEQQALCTDEFSDISPLTGGNVAFSTLEGRPSAYNFDNSPVL 240  
Qy 241 QEWWTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGCRCKCKGHASECMKNEF 300  
Db 241 QEWWTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGCRCKCKGHASECMKNEF 300

ALIGNMENTS

301 QY DKLVNCKHNTYGVDEKCLPFNDPWRARATASBCLPCDNGRQOEYFDPBLYRS 360  
301 Db DKLVNCKHNTYGVDEKCLPFNDPWRARATASBCLPCDNGRQOEYFDPBLYRS 360  
361 QY TGHGCHTNCQDNTDGAHCERCFRFLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP 420  
361 Db TGHGCHTNCQDNTDGAHCERCFRFLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP 420  
421 QY GWGDKDCRCQGFHSLTAGRCPCSDSGSIDCNVETGRCVCKDNVEGNCRCRCPG 480  
421 Db GWGDKDCRCQGFHSLTAGRCPCSDSGSIDCNVETGRCVCKDNVEGNCRCRCPG 480  
481 QY FNLSSNPRGCTPCFCFHSVSVCTNAVGSYVSISSTFQIDEDGWRARQDGSASLEW 540  
481 Db FNLSSNPRGCTPCFCFHSVSVCTNAVGSYVSISSTFQIDEDGWRARQDGSASLEW 540  
541 QY SSEQDIAVSISSYFPRYFIAPAKFLGKQVLGYQNLSPFSFRVDRDRTRLSNEDLVLEGA 600  
541 Db SSEQDIAVSISSYFPRYFIAPAKFLGKQVLGYQNLSPFSFRVDRDRTRLSNEDLVLEGA 600  
601 QY GLRVSVPLIAQNSYSESTTKVFRLEHATYPWRPALTPPEFQKLNLTISIKIRGT 660  
601 Db GLRVSVPLIAQNSYSESTTKVFRLEHATYPWRPALTPPEFQKLNLTISIKIRGT 660  
661 QY SERSAGYLDVTLASARPGPGVATWVSECTCPVGYGGQFCMCLSGYRRETPNLGPYSP 720  
661 Db SERSAGYLDVTLASARPGPGVATWVSECTCPVGYGGQFCMCLSGYRRETPNLGPYSP 720  
721 QY CVLCACNHSETCDPTGVCNCRDNTAGPHCKSDGYGDTAGTSSDCQPCPCPGSS 780  
721 Db CVLCACNHSETCDPTGVCNCRDNTAGPHCKSDGYGDTAGTSSDCQPCPCPGSS 780  
781 QY CAVVPKTKVVCNCTGTTGKRCCLDGDYFGDPLGRNGPVRLCRLCQCSNIDPNNAV 840  
781 Db CAVVPKTKVVCNCTGTTGKRCCLDGDYFGDPLGRNGPVRLCRLCQCSNIDPNNAV 840  
841 QY NCNRLTGECLKCIYNTAGFYCDCKDGFNGPLAPNADCKKACNCPVGTWKQSSCNP 900  
841 Db NCNRLTGECLKCIYNTAGFYCDCKDGFNGPLAPNADCKKACNCPVGTWKQSSCNP 900  
901 QY VTQCECLPHVTQDGCACDPGFYNLQSGQGERCDCHALGSTNGQDRTQCCBQPGI 960  
901 Db VTQCECLPHVTQDGCACDPGFYNLQSGQGERCDCHALGSTNGQDRTQCCBQPGI 960  
961 QY TGHQRCERCEVNHFGFEGEGKPCDCHPEGSLSLQCKDDGRCERGFVGNRCQCEENYF 1020  
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1021 Db YNRSWPCQCPACRYLVKQVADHVKLQELSLIANLTGDEMVTDOAFEDRLKEAER 1080  
1081 QY EVMDDLREAQDVKDQNDLMDRLQRVNNTLSQISRLQINRTIETGNLAGOARAHVEN 1140  
1081 Db EVMDDLREAQDVKDQNDLMDRLQRVNNTLSQISRLQINRTIETGNLAGOARAHVEN 1140  
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1141 Db TERLIEIASBELEKAKVAANVSVTQESTGDPNNMTLLAEARKLAERHKEADDIRV 1200  
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1261 Db GDKAVEIYASVAQLSPDSETLEANNIKWEAENLEQLIDQKDYEDLREDMRKELE 1320  
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1321 Db VKNLLKKGTEQQQTADQLLARADAALAEAAKGRDRTLOEANDILNLLKOPDRVNDN 1380  
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1381 Db KTAABEALRKIPAINQITTEANEKTRQAQALGSAADATEAKNKAHEARIASAVOKNA 1440  
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1501 Db INARKAKNSVTSLLSIINDLLLEQLGQDVTDLNKLNEIEGTNLNKADEMKSVDLDRKVS 1560  
1561 QY LENEAKKQEAAMINDYNDRIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609  
1561 Db LENEAKKQEAAMINDYNDRIEIMKDINLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 2  
US-09-561-818A-22  
; Sequence 22, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-22

Query Match 100.0%; Score 8713; DB 4; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALRPRGRLLWPLVLAIAAAAGCAQAAMDECTDGGRRQRCMPPEFVNAFN 60  
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Db 181 SCENTYSKANRGFTRTGGDEQOALCTDFSDISPLTGNVAFSTLEGRPSAYNFDNSPVL 240  
QY 241 QEWVATDITRTLRLNTFGDEVNDPKVLKSYIYALSDPVGRCCKNGHASECMKNEF 300  
Db 241 QEWVATDITRTLRLNTFGDEVNDPKVLKSYIYALSDPVGRCCKNGHASECMKNEF 300  
QY 301 DKLVCNCKHNTYGVDEKCLPFNDPWRARATASBCLPCDNGRQOEYFDPBLYRS 360  
Db 301 DKLVCNCKHNTYGVDEKCLPFNDPWRARATASBCLPCDNGRQOEYFDPBLYRS 360  
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Db 361 TGHGCHTNCQDNTDGAHCERCFRFLGNNEACSSCHSPVGSLSLTCDSYGRCSCKP 420  
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Db 481 PFNLESSNPRGCTPCFCGHSSVCTNAVGVSYVSISSSTFQIDEDGWRAEQRDGSEASLEW 540  
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Db 541 SSERODIAVINDSYPRFPIAPAKFLGKOVLSYGNLSFSFRVDRDRLSADRLVLEGA 600  
Qy 601 GLRVSVPLIAQNSYPSSTTKVYVFLHEATDYPWRPALTPFEFQKLLNLTISKIRGT 660  
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Qy 961 TQHCERCEVNHFGPGEGKPCDCHPEGSLSLOCKDDGRCCEGFGVGNRCDCOENYF 1020  
Db 961 TQHCERCEVNHFGPGEGKPCDCHPEGSLSLOCKDDGRCCEGFGVGNRCDCOENYF 1020  
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Qy 1081 EYMDLLEAQQVQVDQNLMBLQVNNLTSSQISRLQNIINTLEETGNLAEQARHVEN 1140  
Db 1081 EYMDLLEAQQVQVDQNLMBLQVNNLTSSQISRLQNIINTLEETGNLAEQARHVEN 1140  
Qy 1141 TERLLEIASRELEKAKVAAANVSVPQESTGDPNNMTLLAEARHHEAERHHEAER 1200  
Db 1141 TERLLEIASRELEKAKVAAANVSVPQESTGDPNNMTLLAEARHHEAERHHEAER 1200  
Qy 1201 AKTANDTSEAYNLLRLTAGENQTAPEIEBLNRKYEQAKNISOLEKQAAHVHEAKRA 1260  
Db 1201 AKTANDTSEAYNLLRLTAGENQTAPEIEBLNRKYEQAKNISOLEKQAAHVHEAKRA 1260  
Qy 1261 GDKAVEIIVASVAQLSPLDSETLEENANNIKMAEENLEQIDQKLKDYEDLREDMRGKELE 1320  
Db 1261 GDKAVEIIVASVAQLSPLDSETLEENANNIKMAEENLEQIDQKLKDYEDLREDMRGKELE 1320  
Qy 1321 VKNLLEKGTQOOTADQALLARADAKALAEBAKKGRTLOEANDILNLLKDFRRVNDN 1380  
Db 1321 VKNLLEKGTQOOTADQALLARADAKALAEBAKKGRTLOEANDILNLLKDFRRVNDN 1380  
Qy 1381 KTAABEALRKIPAINQTTTEANEKTRAQALGSAADATAEAKNAHEAERIAVAKQNA 1440  
Db 1381 KTAABEALRKIPAINQTTTEANEKTRAQALGSAADATAEAKNAHEAERIAVAKQNA 1440  
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Db 1441 TSTKABERTFAEVTDLNEVNNMLKQLEAKELKRQDDADQDMMAGMASAAQAEAE 1500  
Qy 1501 INARAKSVTSLLSIINDLLBOLGQDLDVNLKLINEIEGTNKAEDMKYSDLDKRVSD 1560  
Db 1501 INARAKSVTSLLSIINDLLBOLGQDLDVNLKLINEIEGTNKAEDMKYSDLDKRVSD 1560  
Qy 1561 LENEAKQEAAIMDYNDRIEIMKDRLNLEDIRKTLPGSCFNTPSIEKP 1609  
Db 1561 LENEAKQEAAIMDYNDRIEIMKDRLNLEDIRKTLPGSCFNTPSIEKP 1609

## RESULT 3

US-09-562-702A-26  
; Sequence 26, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 1617  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-26

Query Match 100.0%; Score 8713; DB 4; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSHRAAALPRGRRLPWLAVLAAAGCAQAAMDECTDEGGPQRCMPEFVNAAFN 60  
Db 1 MRGSHRAAALPRGRRLPWLAVLAAAGCAQAAMDECTDEGGPQRCMPEFVNAAFN 60  
Qy 61 VTVVATNTCGTPEEYCVQGTGVTGKSLCHDAGOPHLQHGAFFLTDYNNQADTTWQOS 120  
Db 61 VTVVATNTCGTPEEYCVQGTGVTGKSLCHDAGOPHLQHGAFFLTDYNNQADTTWQOS 120  
Qy 121 QTMVAGVQVPESSINLTLHLGKAPDITVYVLEKHTSRPESFALYKRTREDGPMIPQYISG 180  
Db 121 QTMVAGVQVPESSINLTLHLGKAPDITVYVLEKHTSRPESFALYKRTREDGPMIPQYISG 180  
Qy 181 SCENTYSKANRGFIRITGGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFNDNSPVL 240  
Db 181 SCENTYSKANRGFIRITGGDEQALCTDEFSDISPLTGGNVAFSTLEGPSAYNFNDNSPVL 240  
Qy 241 QEWVTATDTRVTLNRLNTFGDEVNDPKVLKSYIYAIISDFAYGGRCKCKNGHASECMKNEF 300  
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Qy 301 DKLVCNCKNTYGVDCCKLPPFNDRPWRRAATAESASECLPCDCNCRSGOECYFDPELYRS 360  
Db 301 DKLVCNCKNTYGVDCCKLPPFNDRPWRRAATAESASECLPCDCNCRSGOECYFDPELYRS 360  
Qy 361 TGHGHCTNCQDNTDGAHCERENPFRLGNNEACSSCHCSVPGSLSTOCDYGRCSCKP 420  
Db 361 TGHGHCTNCQDNTDGAHCERENPFRLGNNEACSSCHCSVPGSLSTOCDYGRCSCKP 420  
Qy 421 GVWMDKCDRCQCPGFHSLTEAGCRPCSDPGSISDECNVETGRVCVKNVGEVNCERCKP 480  
Db 421 GVWMDKCDRCQCPGFHSLTEAGCRPCSDPGSISDECNVETGRVCVKNVGEVNCERCKP 480  
Qy 481 FPNLESSNPRGCTPCFCFGHSSVCTNAVGVSYVSISSSTFQIDEDGWRAEQRDGSEASLEW 540  
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Db 541 SSERODIAVINDSYPRFPIAPAKFLGKOVLSYGNLSFSFRVDRDRLSADRLVLEGA 600  
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601	Db		GLRVSPLIAQGNSPSETTKYVFRFLHEATDYWRPALTPFFQKLLNLTISKIRGT	660
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661	Db		SERSAGYLDVTLASARPGPGVPATWBSCTCPVGYGGQFCMCLSGYRRETPNLGPXP	720
721	Qy		CVLCACNHSETCDPETHVCNCRDNTAGPCHCKSDGYIGDSTAGTSSDQCPCPCPGSS	780
721	Db		CVLCACNHSETCDPETHVCNCRDNTAGPCHCKSDGYIGDSTAGTSSDQCPCPCPGSS	780
781	Qy		CAVVPKTEWVCTNCTGTTGKRCBELCDGDFGDPGLGRNGPVRCLRCLQCSDNIDPNAVG	840
781	Db		CAVVPKTEWVCTNCTGTTGKRCBELCDGDFGDPGLGRNGPVRCLRCLQCSDNIDPNAVG	840
841	Qy		NCNRLTGECLKCIYNTAGFYCDRCXDFGPNLAPADPKCKACACNPVGTWKQOSSCNP	900
841	Db		NCNRLTGECLKCIYNTAGFYCDRCXDFGPNLAPADPKCKACACNPVGTWKQOSSCNP	900
901	Qy		VTQGCBELPHVTGQDCGADPFGFYNLQSGQCCERCDCHALGSTNGQCDTIRTCQCCPGI	960
901	Db		VTQGCBELPHVTGQDCGADPFGFYNLQSGQCCERCDCHALGSTNGQCDTIRTCQCCPGI	960
961	Qy		TGQHCERCEVNHFGPBGSKPCDCHPEGSLSLQCKDGCRCBGFGVGNRCDCOEENYF	1020
961	Db		TGQHCERCEVNHFGPBGSKPCDCHPEGSLSLQCKDGCRCBGFGVGNRCDCOEENYF	1020
1021	Qy		YNSWPGQCEPCACVRLVKDVAHRVKLQBELSLIANLGTGDMVTOAPEDRLKEABR	1080
1021	Db		YNSWPGQCEPCACVRLVKDVAHRVKLQBELSLIANLGTGDMVTOAPEDRLKEABR	1080
1081	Qy		EYMDLLREAQDVKDQNDMLRQVRNNTLSSQISRLQNI RN TIBETGNLAEQARAHVEN	1140
1081	Db		EYMDLLREAQDVKDQNDMLRQVRNNTLSSQISRLQNI RN TIBETGNLAEQARAHVEN	1140
1141	Qy		TERLIEIASRELEKAKVAAANVSUTQESTGDPNNMTLAEARKLAERHQBADDIVRV	1200
1141	Db		TERLIEIASRELEKAKVAAANVSUTQESTGDPNNMTLAEARKLAERHQBADDIVRV	1200
1201	Qy		AKTANDTSTEAYNLLRRTLAGEHOTAFIEBELNRKTEQAKNISQDLEKQARVHSEAKRA	1260
1201	Db		AKTANDTSTEAYNLLRRTLAGEHOTAFIEBELNRKTEQAKNISQDLEKQARVHSEAKRA	1260
1261	Qy		GDKAVEIYASVAQSLPDSLSELTENEANNIKWEAENLEQI DO KLDYEDIEDRWGRKELE	1320
1261	Db		GDKAVEIYASVAQSLPDSLSELTENEANNIKWEAENLEQI DO KLDYEDIEDRWGRKELE	1320
1321	Qy		VGNLLEKGTQEOTADQLLAAADAAKALAEAAKGRDTLQEANDILNNLKDFDRRVNDN	1380
1321	Db		VGNLLEKGTQEOTADQLLAAADAAKALAEAAKGRDTLQEANDILNNLKDFDRRVNDN	1380
1381	Qy		KTAASEALRKPIPNQTTTEANEXTRAQALGSAADATEAKNKAHEARIASAVQKNA	1440
1381	Db		KTAASEALRKPIPNQTTTEANEXTRAQALGSAADATEAKNKAHEARIASAVQKNA	1440
1441	Qy		TSTKAEBERTFAEVTDLDNEVNNMLKQLEBAEKELRKQDDADQDMWAGMASQAQEAEE	1500
1441	Db		TSTKAEBERTFAEVTDLDNEVNNMLKQLEBAEKELRKQDDADQDMWAGMASQAQEAEE	1500
1501	Qy		INARAKNSVTSLSIINDLLEQI GQDVTVDANKLNEIEGTLINKAKDEWKVSDLDLRKUSD	1560
1501	Db		INARAKNSVTSLSIINDLLEQI GQDVTVDANKLNEIEGTLINKAKDEWKVSDLDLRKUSD	1560
1561	Qy		LENEAKQEAALIMDVNRDIEBIMKOTRNLEDIKTLPSCGFNTPSIEKP	1609
1561	Db		LENEAKQEAALIMDVNRDIEBIMKOTRNLEDIKTLPSCGFNTPSIEKP	1609

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; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 93-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-24

Query Match      98.1%; Score 8544; DB 4; Length 1576;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAADECTDEGRPQRCMEEFVNAAFNVTVATNTCGTPPEBYCVOTGVTGVTKSCHLCD 93
DB 1 QAADECTDEGRPQRCMEEFVNAAFNVTVATNTCGTPPEBYCVOTGVTGVTKSCHLCD 60

QY 94 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTHLGKAFDITYVRLKXF 153
DB 61 AGPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSSINLTHLGKAFDITYVRLKXF 120

QY 154 TSPSPFAYIKKTREDGPNIPQYYSGSCENTYSKANRGFIETGDEQOALCTDFSDIS 213
DB 121 TSPSPFAYIKKTREDGPNIPQYYSGSCENTYSKANRGFIETGDEQOALCTDFSDIS 180

QY 214 PLTGGNVAFTLEGRPSAYNFNSPVLQBWVTATDIRVTNLRLNTFGDEVFNDPKVLSY 273
DB 181 PLTGGNVAFTLEGRPSAYNFNSPVLQBWVTATDIRVTNLRLNTFGDEVFNDPKVLSY 240

QY 274 YVAISDFAYGGRCKNGHASECMKNEFDKLVNCCKHNTYGVDCCKLFFNDRPWRATA 333
DB 241 YVAISDFAYGGRCKNGHASECMKNEFDKLVNCCKHNTYGVDCCKLFFNDRPWRATA 300

QY 334 ESASECLPCDCNGRSGEQCYFDPDELYRSTGHGGHCTNCQDNTDGAHCERCENFFRLGNNE 393
DB 301 ESASECLPCDCNGRSGEQCYFDPDELYRSTGHGGHCTNCQDNTDGAHCERCENFFRLGNNE 360

QY 394 ACSSCHCSVPVGLSTQCDISYGRCSCKPGVMGDKDRCPGPHSHLITEACRCPSCDPGSGI 453
DB 361 ACSSCHCSVPVGLSTQCDISYGRCSCKPGVMGDKDRCPGPHSHLITEACRCPSCDPGSGI 420

QY 454 DECNVETGRCVKQNDVYGNPCNRCRKPGEFNLSSNPRGCTPCFCFGHSVCTNAVGSYVY 513

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RESULT 4  
US-09-562-702A-24  
; Sequence 24, Application US/09562702A  
; Patent No. 6832790  
; GENERAL INFORMATION:

QY 754 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVCTNCPTGTTGKRCBCLCDGDFG 813  
DB 721 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVCTNCPTGTTGKRCBCLCDGDFG 780  
QY 814 DPLGRNGPVRRLCRLCCSDNIDPNAVGNCRNLITGELCKICINVTAGFYCDRCXKDGFFGNPL 873  
DB 781 DPLGRNGPVRRLCRLCCSDNIDPNAVGNCRNLITGELCKICINVTAGFYCDRCXKDGFFGNPL 840  
QY 874 APNPADKCAKNCNPGYTMKQSSCNPVTVGOCECLPHVTGQDCGACDGFYNLQSGQCE 933  
DB 841 APNPADKCAKNCNPGYTMKQSSCNPVTVGOCECLPHVTGQDCGACDGFYNLQSGQCE 900  
QY 934 RCDCHALGSTNGQCDIRTGQCEQPGITGQHCECEVNHFGPBGCKPCDCHPEGSLSL 993  
DB 901 RCDCHALGSTNGQCDIRTGQCEQPGITGQHCECEVNHFGPBGCKPCDCHPEGSLSL 960  
QY 994 QCKDDGRCCEGFGVNRCDQCEENFYNRSPGQCEACVRLVKDKVADHRVKLOLE 1053  
DB 961 QCKDDGRCCEGFGVNRCDQCEENFYNRSPGQCEACVRLVKDKVADHRVKLOLE 1020  
QY 1054 SLTANLGTGDMVTDQAFEDRLKEAREVNDLLREAQDVKDQNDLMDRLQVNNLTSSQ 1113  
DB 1021 SLTANLGTGDMVTDQAFEDRLKEAREVNDLLREAQDVKDQNDLMDRLQVNNLTSSQ 1080  
QY 1114 ISRLQIRNTIETGNLABQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1173  
DB 1081 ISRLQIRNTIETGNLABQARAHVENTERLIEIASRELEKAKVAAANVSVTQPESTGDP 1140  
QY 1174 NNMTLAEARKLAERHKQADDI VRVAKTANDTSTEAYNLLRLTLAGEQTAFIEELN 1233  
DB 1141 NNMTLAEARKLAERHKQADDI VRVAKTANDTSTEAYNLLRLTLAGEQTAFIEELN 1200  
QY 1234 RYEOAKNI SODLEKQAAARVHEBAKAGDKAVEIYASVQSLPDSSETLENBANNIKMEA 1293  
DB 1201 RYEOAKNI SODLEKQAAARVHEBAKAGDKAVEIYASVQSLPDSSETLENBANNIKMEA 1260  
QY 1294 ENLEQIDQKDYEDLREDMRKELVKNLLKKGTEQQTADOLLARADAKALAEBA 1353  
DB 1261 ENLEQIDQKDYEDLREDMRKELVKNLLKKGTEQQTADOLLARADAKALAEBA 1320  
QY 1354 KKGRTLQEAANDILNLLKQDPRVNDNKTAAEALRKIPAINQITTEANEKTRAQOALG 1413  
DB 1321 KKGRTLQEAANDILNLLKQDPRVNDNKTAAEALRKIPAINQITTEANEKTRAQOALG 1380  
QY 1414 SAAADATEAKNAHEABRIASAVQKNATSKAEARTFAEVTDLDEVNMLKQLOEAK 1473  
DB 1381 SAAADATEAKNAHEABRIASAVQKNATSKAEARTFAEVTDLDEVNMLKQLOEAK 1440  
QY 1474 ELKEKQDADQDMMAGMASQAAQAEINARKAKNSVTSLSIINDLLEQLGQDLDVDLN 1533  
DB 1441 ELKEKQDADQDMMAGMASQAAQAEINARKAKNSVTSLSIINDLLEQLGQDLDVDLN 1500  
QY 1534 KLNIEGTLNKAKDEMVSOLDKRVSDLENEAKKQBAAMIDYNRDIEEIMKDIRNLEDIR 1593  
DB 1501 KLNIEGTLNKAKDEMVSOLDKRVSDLENEAKKQBAAMIDYNRDIEEIMKDIRNLEDIR 1560  
QY 1594 KTLPSGCFNTPSIEKP 1609  
DB 1561 KTLPSGCFNTPSIEKP 1576

RESULT 5

US-09-561-818A-24  
; Sequence 24. Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1576

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-561-818A-24

Query Match 98.1%; Score 8544; DB 4; Length 1576;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 QAAWDECTDGGRPORCMPEFVNAAFNVTVVANTTCGTPPEEYCVQGTGVTKSKHCLCD 93  
DB 1 QAAWDECTDGGRPORCMPEFVNAAFNVTVVANTTCGTPPEEYCVQGTGVTKSKHCLCD 60  
QY 94 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLKAKADITTVRLKHF 153  
DB 61 AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQVPSINLTLHLKAKADITTVRLKHF 120  
QY 154 TSRPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDQQAALCTDFFSDIS 213  
DB 121 TSRPESAIYKRTREDGFWIPYQYSGSCENTYSKANRGFIRTGDDQQAALCTDFFSDIS 180  
QY 214 PLTGNVAFSTLEGRPSAYNFDSNVPVLOEWWTATDIRVTNLRLNTFGDEVNDFPKVLKSY 273  
DB 181 PLTGNVAFSTLEGRPSAYNFDSNVPVLOEWWTATDIRVTNLRLNTFGDEVNDFPKVLKSY 240  
QY 274 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCHNTYGVDCCKCLPFFNDRPWRDATA 333  
DB 241 YYAISDFAVGRCCKNGHASECMKNEFDKLVCKNCHNTYGVDCCKCLPFFNDRPWRDATA 300  
QY 334 ESASECLPCDCNMGSOECYDPPELYRSTGHGCHTNCQDNTDGAHCERCENPRLGNE 393  
DB 301 ESASECLPCDCNMGSOECYDPPELYRSTGHGCHTNCQDNTDGAHCERCENPRLGNE 360  
QY 394 ACSSCHSPVSGSLSTQCDSDYGRCKPVGMDKCDRCQOPGFSHLSLEAGCRPCSDPSSGI 453  
DB 361 ACSSCHSPVSGSLSTQCDSDYGRCKPVGMDKCDRCQOPGFSHLSLEAGCRPCSDPSSGI 420  
QY 454 DECNVETGRVCYKONVGFNCERCKPGFNLESNPRGCTPCPCFCHSSVCTNAGVSVY 513  
DB 421 DECNVETGRVCYKONVGFNCERCKPGFNLESNPRGCTPCPCFCHSSVCTNAGVSVY 480  
QY 514 SISSTFQIDEDGWAERQDGSSEASLEWSSERQDIASVDSYFPRFYIAPAKFLGKQVLSY 573  
DB 481 SISSTFQIDEDGWAERQDGSSEASLEWSSERQDIASVDSYFPRFYIAPAKFLGKQVLSY 540  
QY 574 GONLSFSFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQGNPSYSETTKVYVRLHEATDY 633  
DB 541 GONLSFSFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQGNPSYSETTKVYVRLHEATDY 600  
QY 634 PWRPALTFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVPGVATWYESCTCP 693  
DB 601 PWRPALTFEFQKLLNLTISKIRGTYSERSAGYLDVTLASARPGVPGVATWYESCTCP 660  
QY 694 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 753  
DB 661 VYGGQFCMCLSGYRRRTPNLGYPSPCVLCACNGHSETCDPETGVCNCRDNTAGPHCEK 720  
QY 754 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVCTNCPTGTTGKRCBCLCDGDFG 813  
DB 721 CSDGYGDSSTAGTSSDCQPCPGSSCAVVPKTKVCTNCPTGTTGKRCBCLCDGDFG 780  
QY 814 DPLGNGPVRRLCRLCCQSDNIDPNAVGNCRNLITGELCKICINVTAGFYCDRCXKDGFFGNPL 873  
DB 781 DPLGNGPVRRLCRLCCQSDNIDPNAVGNCRNLITGELCKICINVTAGFYCDRCXKDGFFGNPL 840  
QY 874 APNPADKCAKNCNPGYTMKQSSCNPVTVGOCECLPHVTGQDCGACDGFYNLQSGQCE 933  
DB 841 APNPADKCAKNCNPGYTMKQSSCNPVTVGOCECLPHVTGQDCGACDGFYNLQSGQCE 900  
QY 934 RCDCHALGSTNGQCDIRTGQCEQPGITGQHCECEVNHFGPBGCKPCDCHPEGSLSL 993

Db	901	RCCHALGSTNGQDRTGQCEQPGITGQHCERCEVNHFGFGECKPCDCHPEGSLSL	960
Qy	994	QCKDDGRCCEGFGVGNRCQCEENFYNRSWFGCOECPACVRLVKVADHRVKLOBLE	1053
Db	961	QCKDDGRCCEGFGVGNRCQCEENFYNRSWFGCOECPACVRLVKVADHRVKLOBLE	1020
Qy	1054	SLIANLGTGDEWYTDQAFEDRLKEAREVMDLREAZQDVKDQVNDQNLMDRLQRVNTLSQ	1113
Db	1021	SLIANLGTGDEWYTDQAFEDRLKEAREVMDLREAZQDVKDQVNDQNLMDRLQRVNTLSQ	1080
Qy	1114	ISLQNIIRNTIBETGNLAQARAHVENTERLIIASRELEKAKVAANUSVTPGESTGP	1173
Db	1081	ISLQNIIRNTIBETGNLAQARAHVENTERLIIASRELEKAKVAANUSVTPGESTGP	1140
Qy	1174	NNMTLLAEAREKLAERKHQADDIRVAKTANDTSTEAYNLLRTLAGENOTAFETEELN	1233
Db	1141	NNMTLLAEAREKLAERKHQADDIRVAKTANDTSTEAYNLLRTLAGENOTAFETEELN	1200
Qy	1234	KRYEQAKNISQDLBKQARVHEBAKAGDKAVIYASVAQLSPDSETTENEANNIKMEA	1293
Db	1201	KRYEQAKNISQDLBKQARVHEBAKAGDKAVIYASVAQLSPDSETTENEANNIKMEA	1260
Qy	1294	ENLEQDIDQKLYEDREDWRGKELEVNKLEKGTQEQDQADQALLARADAALAEAAA	1353
Db	1261	ENLEQDIDQKLYEDREDWRGKELEVNKLEKGTQEQDQADQALLARADAALAEAAA	1320
Qy	1354	KKGRDITLOEANDILNLUKDFDRVNDNKTAAEALRKPAINOTITTEANEKTRAQOALG	1413
Db	1321	KKGRDITLOEANDILNLUKDFDRVNDNKTAAEALRKPAINOTITTEANEKTRAQOALG	1380
Qy	1414	SAAADATEAKNAHEAREIASAVOKNATSKAAERTEFAEVTDLNNEVNNMLKQLOEAK	1473
Db	1381	SAAADATEAKNAHEAREIASAVOKNATSKAAERTEFAEVTDLNNEVNNMLKQLOEAK	1440
Qy	1474	ELKFKQDDADQMMWAGWAGQAEABINARKAKNSVTSLLSIINDLLBOLGOLDTVDLN	1533
Db	1441	ELKFKQDDADQMMWAGWAGQAEABINARKAKNSVTSLLSIINDLLBOLGOLDTVDLN	1500
Qy	1534	KLNEIEGTLNKAKDEKMSDLDKRVSDLENEAKKQEAAMNDYNDRIEIMKDIRNLEDIR	1593
Db	1501	KLNEIEGTLNKAKDEKMSDLDKRVSDLENEAKKQEAAMNDYNDRIEIMKDIRNLEDIR	1560
Qy	1594	KTLPSGCFNTPSIEKP	1609
Db	1561	KTLPSGCFNTPSIEKP	1576

RESULT 6  
US-09-562-702A-28  
; Sequence 28, Application us/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 1584  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-28

Query Match	98.1%;	Score 8544;	DB 4;	Length 1584;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1576;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	34	QAAMDECTDEGRPQRCMPFVNAAFNVTVATNTCGTPBEEYCVQGVGTGKSKCHLCD	93	
Db	1	QAAMDECTDEGRPQRCMPFVNAAFNVTVATNTCGTPBEEYCVQGVGTGKSKCHLCD	60	
Qy	94	AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLKAKFDTIVYRLKFH	153	
Db	61	AGQPHLQHGAAFLTDYNNQADTTWQSQTMLAGVQYPSINLTLHLKAKFDTIVYRLKFH	120	
Qy	154	TSRPESFAIYKRTREDGFWPIYQYSGSCENTYSKANRGFIRTDGDEQOALCTDEBDSIS	213	
Db	121	TSRPESFAIYKRTREDGFWPIYQYSGSCENTYSKANRGFIRTDGDEQOALCTDEBDSIS	180	
Qy	214	PLTGNVAFSTLEGRPSAYNFDNSFVLQEWWTATDIRVTNLNRLNTFGDEVNDPKVLKSY	273	
Db	181	PLTGNVAFSTLEGRPSAYNFDNSFVLQEWWTATDIRVTNLNRLNTFGDEVNDPKVLKSY	240	
Qy	274	YIATSDFAVGRCKNGHSHASECMKNEFDKLVCKNCHNTYGVDCCKLPFFNDRPWRATA	333	
Db	241	YIATSDFAVGRCKNGHSHASECMKNEFDKLVCKNCHNTYGVDCCKLPFFNDRPWRATA	300	
Qy	334	ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNQCNDTDGAHCRCRENFRLGNNE	393	
Db	301	ESASECLPCDCNGRSQECYFDPPELYRSTGHGCHCTNQCNDTDGAHCRCRENFRLGNNE	360	
Qy	394	ACSSCHCSPVSGSLTQCDSDYGRCKPQGMGDKDRCPQPHSLTEAGRCPCSDPGSGI	453	
Db	361	ACSSCHCSPVSGSLTQCDSDYGRCKPQGMGDKDRCPQPHSLTEAGRCPCSDPGSGI	420	
Qy	454	DECNVETGRCKVCKNVEGFNCERCKPGFFNLESNPRGCTPCFCFHSSSVCTNAGVSVY	513	
Db	421	DECNVETGRCKVCKNVEGFNCERCKPGFFNLESNPRGCTPCFCFHSSSVCTNAGVSVY	480	
Qy	514	SISSTFQIDEDGWRARQDGEASELWSSERQDIAVSDSYFPRYFIAPAKFLKQVLSY	573	
Db	481	SISSTFQIDEDGWRARQDGEASELWSSERQDIAVSDSYFPRYFIAPAKFLKQVLSY	540	
Qy	574	GNLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYVFLHEATDY	633	
Db	541	GNLSFSFRVDRDRTRLSAEDLVLEGAGLRVSVPLIAGNSYPSSETTVKYVFLHEATDY	600	
Qy	634	PWRPALTPFEFQKLIINLTISIKIRGTYSERSAGYLDVTLASAPRGQVPATWVESCCTP	693	
Db	601	PWRPALTPFEFQKLIINLTISIKIRGTYSERSAGYLDVTLASAPRGQVPATWVESCCTP	660	
Qy	694	VGYGQFCCEMCLSGYRRTPNLGPYSPVLCACNGHSETCDPETGVCNCRDNTAGPHCEK	753	
Db	661	VGYGQFCCEMCLSGYRRTPNLGPYSPVLCACNGHSETCDPETGVCNCRDNTAGPHCEK	720	
Qy	754	CSDGYIGDSTAGTSSDCQFCPCPGSSCAVVPKTKVWVCTNCTPTGTTGKRCCELDDGYFG	813	
Db	721	CSDGYIGDSTAGTSSDCQFCPCPGSSCAVVPKTKVWVCTNCTPTGTTGKRCCELDDGYFG	780	
Qy	814	DPLGRNGPRLCRLCQCSNDTDPNAGVNCNLTGCECLKCIYNTAGFYCDRCCKDGFNGNPL	873	
Db	781	DPLGRNGPRLCRLCQCSNDTDPNAGVNCNLTGCECLKCIYNTAGFYCDRCCKDGFNGNPL	840	
Qy	874	APNPADKCKACNCPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQCE	933	
Db	841	APNPADKCKACNCPYGTMKQSSCNPTVGTQCECLPHVTGQDCGACDPGFYNLQSGQCE	900	
Qy	934	RCDCHALGSTNGQDRTGQCEQPGITGQHCERCEVNHFGFGECKPCDCHPEGSLSL	993	
Db	901	RCDCHALGSTNGQDRTGQCEQPGITGQHCERCEVNHFGFGECKPCDCHPEGSLSL	960	
Qy	994	QCKDDGRCCEGFGVGNRCQCEENFYNRSWFGCOECPACVRLVKVADHRVKLOBLE	1053	
Db	961	QCKDDGRCCEGFGVGNRCQCEENFYNRSWFGCOECPACVRLVKVADHRVKLOBLE	1020	
Qy	1054	SLIANLGTGDEWYTDQAFEDRLKEAREVMDLREAZQDVKDQVNDQNLMDRLQRVNTLSQ	1113	

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Db 1021 SLIANLGTGDMVTDQAFEDRLKEAREVMDLLREAOQVDVQNDQNDLRLQRVNNTLSSQ 1080
Qy 1114 ISRLQNRINTTEETCNLAEOQARAVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1173
Db 1081 ISRLQNRINTTEETCNLAEOQARAVENTERLIEIASRELEKAKVAAANVSVPSTGDP 1140
Qy 1174 NMWTLLEAKLAEKHQEDD1VRVAKTANDTSTAYNLLILRTLAGENQTAPEIEELN 1233
Db 1141 NMWTLLEAKLAEKHQEDD1VRVAKTANDTSTAYNLLILRTLAGENQTAPEIEELN 1200
Qy 1234 RKYEOAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIRKEA 1293
Db 1201 RKYEOAKNISODLEKQARVHEEAKRAGDKAVEIYASVAQLSPDSETLENEANNIRKEA 1260
Qy 1294 ENLSQIDQKLYEDLREDNRGKELEVNLLLEKGTQEQOTADOLLARADAALAEAA 1353
Db 1261 ENLSQIDQKLYEDLREDNRGKELEVNLLLEKGTQEQOTADOLLARADAALAEAA 1320
Qy 1354 KKGRTTQJEANDILNNLKDFRRVNDNKTAAEEALRKIPAINQITTEANEKTRAEQAALG 1413
Db 1321 KKGRTTQJEANDILNNLKDFRRVNDNKTAAEEALRKIPAINQITTEANEKTRAEQAALG 1380
Qy 1414 SAAADATSAKNAHEAERIA SAVQKNATSTKAEAEERTFAEVTDLJDNVNNMLKQLOBAEK 1473
Db 1381 SAAADATSAKNAHEAERIA SAVQKNATSTKAEAEERTFAEVTDLJDNVNNMLKQLOBAEK 1440
Qy 1474 ELKRQDDADODMMWAGASQAQAEAEINAKKANSVTSLSIINDLLEQLGQDITVDLN 1533
Db 1441 ELKRQDDADODMMWAGASQAQAEAEINAKKANSVTSLSIINDLLEQLGQDITVDLN 1500
Qy 1534 KLINEJGLNKAEMKQVSDLDKRVSDLENEAKKQEAAMINDYNDIRBEIMKDIRNLEDIR 1593
Db 1501 KLINEJGLNKAEMKQVSDLDKRVSDLENEAKKQEAAMINDYNDIRBEIMKDIRNLEDIR 1560
Qy 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576

RESULT 7
US-09-562-702A-30
; Sequence 30, Application US/09562702A
; Patent No.: 632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1605
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-30

Query Match 93.5%; Score 8148; DB 4; Length 1605;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

Qy 1 MEGSHRAAPALPRGRGLWFLVLAIAAAACAAQAMDECTDEGRPCORCMPEFVNAAFN 60
Db 1 MTGGRAALALQPRGLWFLVLAIVL--AAVAGCVRAAWECADEGRPCORCMPEFVNAAFN 58
```

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Qy 61 VTVVATNTCGTPEEYCVQTVGTGVTYKSHCLDAGOPHLOHGAFLTDYNNQADTTWQS 120
Db 59 VTVVATNTCGTPEEYCVQTVGTGVTYKSHCLDAGOPHLOHGAFLTDYNNQADTTWQS 118
Qy 121 QTMLAGVQVPSSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKTRDEGPMPIQYYSG 180
Db 119 QTMLAGVQVPSSINLTLLHKGAFDITYVRLKFHTSRPESFAIYKTRDEGPMPIQYYSG 178
Qy 181 SCENTYSKANRQFIPTGGDEOQALCTDEFSDISPLTGGNVAFSTLEGPSAVNPDSVPL 240
Db 179 SCENTYSKANRQFIPTGGDEOQALCTDEFSDISPLTGGNVAFSTLEGPSAVNPDSVPL 238
Qy 241 QEWMTATDIRVTLNRLNTPGDEVFNDPKVLKSYVYVAISDFAVGGRCCKNGHASECKNEF 300
Db 239 QEWMTATDIRVTLNRLNTPGDEVFNDPKVLKSYVYVAISDFAVGGRCCKNGHASECKNEF 298
Qy 301 DKLVNCKNTYGVDCCKLPFNDRPWRRTAESASECLPCDCNCRGQECYFDPBELYRS 360
Db 299 DKLMCNCKNTYGVDCCKLPFNDRPWRRTAESASECLPCDCNCRGQECYFDPBELYRS 358
Qy 361 TGHGHCTMCOQNTDGAHCERENFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 420
Db 359 TGHGHCTMCOQNTDGAHCERENFRLGNNEACSSCHSPVGSLSLTCQDSYGRCSCKP 418
Qy 421 GVMGDKCDRCQPGFHSLETAGCRPCSDPSGSDIDCNVETGRVCYCKDNVEGFNCRCRKP 480
Db 419 GVMGDKCDRCQPGFHSLETAGCRPCSDPSGSDIDCNVETGRVCYCKDNVEGFNCRCRKP 478
Qy 481 FFLNLESSNPRGCTPCFCFHSVSVCTNAVGSYVYSISSTFQIDEDGWRAEQRDGSASLEW 540
Db 479 FFLNLESSNPRGCTPCFCFHSVSVCTNAVGSYVYSISSTFQIDEDGWRAEQRDGSASLEW 538
Qy 541 SSERQDIAVISDSYPPRYPIAPAKFLGKQVLSYGNQLSFSFVDRDRDRLSADLVLEGA 600
Db 539 SSERQDIAVISDSYPPRYPIAPAKFLGKQVLSYGNQLSFSFVDRDRDRLSADLVLEGA 598
Qy 601 GURVSVPLIAQNSYPSSETTVKYVFLHEATDYPWRPALTPPEFQKLNLLNTSIKIRGY 660
Db 599 GURVSVPLIAQNSYPSSETTVKYVFLHEATDYPWRPALTPPEFQKLNLLNTSIKIRGY 658
Qy 661 SERSAGYLDVTLASARPQGVPAVWESCTCPVGYGGQFCMCLSGYRRRETNLGPVSP 720
Db 659 SERSAGYLDVTLASARPQGVPAVWESCTCPVGYGGQFCMCLSGYRRRETNLGPVSP 718
Qy 721 CVLTCNGHSETCDPBTGVCNEDNTAGPHCEKSDGYGSDTAGTSSDCQPCPCPGSS 780
Db 719 CVLTCNGHSETCDPBTGVCNEDNTAGPHCEKSDGYGSDTAGTSSDCQPCPCPGSS 778
Qy 781 CAVPKTKEVVCTNCTPTGTTGKRCBCLDDGYGDFPLGRNGPVRLCRLCQCSNIDPNNAV 840
Db 779 CAVPKTKEVVCTNCTPTGTTGKRCBCLDDGYGDFPLGRNGPVRLCRLCQCSNIDPNNAV 838
Qy 841 NCNRLTGECLKIYNTAGFYCDRCXDGPFNPLANPADKCKACNCPYGMKQSSCNP 900
Db 839 NCNRLTGECLKIYNTAGFYCDRCXDGPFNPLANPADKCKACNCPYGMKQSSCNP 897
Qy 901 VTGQCECLPHVTGDCGACDPGYNLQSGQGERCDCHALGSTNGCQDITRTQCCEQPGI 960
Db 898 VTGQCECLPHVTGDCGACDPGYNLQSGQGERCDCHALGSTNGCQDITRTQCCEQPGI 957
Qy 961 TGOHCERCERNHFGPECEKPCDCHPEGSLQCKDGRCECRGFGVGNRCQCEENYF 1020
Db 958 TGOHCERCERNHFGPECEKPCDCHPEGSLQCKDGRCECRGFGVGNRCQCEENYF 1017
Qy 1021 YNRSWPGCOECPACVRLVKDVADHRVLOELSLIANLGTGDMVTDQAFEDRLKEAR 1080
Db 1018 YNRSWPGCOECPACVRLVKDVADHRVLOELSLIANLGTGDMVTDQAFEDRLKEAR 1077
Qy 1081 EYMDLLREAAQYKVDQNDQNDLRLQRVNNTLSSQISRLQNRINTTIEETGNLAEQASAHVN 1140
Db 1078 EYMDLLREAAQYKVDQNDQNDLRLQRVNNTLSSQISRLQNRINTTIEETGNLAEQASAHVN 1137
```

QY 1141 TELIIEASBELEKAKVAANVSUPTOSTGDPNNNTLLAEBAKLAERHKEADIVRV 1200  
Db 1138 TEQLIEIASBELEKAKW-AAANVSITOPSTGEPNNNTLLAEBAARRLAERHKEADIVRV 1196  
QY 1201 AKTANDTSTAYNLLRTLAGENQTAFAIEBELNRYEQAKNISQDLEKQAAARVHEBAKKA 1260  
Db 1197 AKTANETSAAAYNLLRTLAGENQTALEIEELNRYEQAKNISQDLEKQAAARVHEBAKKA 1256  
QY 1261 GDKAVEIYASVAQISPLDSTLENEANNIKWBAENLEQIDOKLXDYEDLREDMRGKELE 1320  
Db 1257 GDKAVEIYASVAQITPVDSSEALENEANKIKKEAADLDRIDOKLXDYEDLREDMRGKEHE 1316  
QY 1321 VKNLLKGTKEQOTADOLLARADAALAEBAKGRDITLQEAANDILNLLKDFDRRVNDN 1380  
Db 1317 VKNLLKGAEQOTADOLLARADAALAEBAKGRSTLQEAANDILNLLKDFDRRVNDN 1376  
QY 1381 KTAABEARLKI PAINTITIBANKTREAOALGSAADATEAKNKAHEARTASAVQKVA 1440  
Db 1377 KTAABEARLKI PAINTITIAENKTRTREAQALGNAADATEAKNKAHEARTASAAQKVA 1436  
QY 1441 TSTKABAEERTFAEVTDLNENWMLKQLEAEKELKRKODDADQDMMWAGMASQAQAQEA 1500  
Db 1437 TSTKADAEERTFGEVTDLDNEVGMRLQLEAEKELKRKODDADQDMMWAGMASQAQAQEA 1496  
QY 1501 INARKAKNSVTSLSIINDLLEQLGQDVTVDLANKLNEIEGTLLNKADEMKVSDLRKVS 1560  
Db 1497 LNARKAKNSVSSLSQLNLLDQLGQDVTVDLANKLNEIEGTLLNKADEMKASDLRKVS 1556  
QY 1561 LENFAKQEAALNDYNDIEEIMKODIENLEDIRKTLPSGCFNTPSIEKP 1609  
Db 1557 LESEARKQEAALNDYNDIEEIMKODIENLEDIRKTLPSGCFNTPSIEKP 1605

RESULT 8  
US-09-561-818A-26  
; Sequence 26, Application US/09561818A  
; Patent No. 6638307  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-26

Query Match 93.5%; Score 8148; DB 4; Length 1605;  
Best Local Similarity 92.8%; Pred. No. 0;  
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;

QY 1 MRGSHRAPALPRGRWPLVLAALAAAGCAQAAMDECTDEGRPQRCMPFVNAAFN 60  
Db 1 MTGGRAALALQPRGLWPLVLAAL--AAAGCVRAANDECADEGRPQRCMPFVNAAFN 58  
QY 61 VTVATNTCGTPPEYCVQTVGTWKSCHLQDAGPHLOHGAFLTDYNNQADTTWQS 120  
Db 59 VTVATNTCGTPPEYCVQTVGTWKSCHLQDAGPHLOHGAFLTDYNNQADTTWQS 118  
QY 121 QTMLAGVQPSINILTLHLGKAFDITVYRLKFHTSRPESPAIYKRTEDGFWIPYQYSG 180  
Db 119 QTMLAGVQPSINILTLHLGKAFDITVYRLKFHTSRPESPAIYKRTEDGFWIPYQYSG 178  
QY 181 SCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPLTGCNVAFSTLEGRPSAYNFDSN 240  
Db 179 SCENTYSKANRGFIRTTGGDEQQAALCTDFSDISPLTGCNVAFSTLEGRPSAYNFDSN 238  
QY 241 QEWWTATDIRVTLNRLNTFGDEVNDPKVLSYYIALSDFAVGRCCKNGHASECMKNEF 300

Db 239 QEWWTATDIRVTLNRLNTFGDEVNDPKVLSYYIALSDFAVGRCCKNGHASECMKNEF 298  
QY 301 DXLVNCKNHTYGVDCSKCLPPFNDRPWRATASASECLPCDCNGRSQCYCFDPPELYRS 360  
Db 299 DXLVNCKNHTYGVDCSKCLPPFNDRPWRATASASECLPCDCNGRSQCYCFDPPELYRS 358  
QY 361 TGHGCHTNCODNTDGAHCERCENFRLGNNEACSSCHGSPVGSLSQDSTQDCSYGRCSCKP 420  
Db 359 TGHGCHTNCODNTDGAHCERCENFRLGNNEACSSCHGSPVGSLSQDSTQDCSYGRCSCKP 418  
QY 421 GVMGDKDRCPGPHSLITEAGRCPCSDPGSDIECNVETGRVCYCKDNVGFNCFERCKPG 480  
Db 419 GVMGDKDRCPGPHSLITEAGRCPCSDPGSDIECNVETGRVCYCKDNVGFNCFERCKPG 478  
QY 481 PFNLESSNPRCTCFCFGHSSVCTNAGVSVYSISSTFOIDEDGWRAEORDGSEASLEW 540  
Db 479 PFNLESSNPRCTCFCFGHSSVCTNAGVSVYSISSTFOIDEDGWRAEORDGSEASLEW 538  
QY 541 SSERQDIATVSDSYPPRYFTAPAKFLQKVLQVLSYQNLSPFSDVDRDRDTRLSAEDLVLEGA 600  
Db 539 SSERQDIATVSDSYPPRYFTAPAKFLQKVLQVLSYQNLSPFSDVDRDRDTRLSAEDLVLEGA 598  
QY 601 GLRYSVPLIAOGNSVPSETTVKYVFLHEATDYWRPALTPFBFQKLLNLTLSIKIRGTY 660  
Db 599 GLRYSVPLIAOGNSVPSETTVKYVFLHEATDYWRPALTPFBFQKLLNLTLSIKIRGTY 658  
QY 661 SERAGYLDDVTLASAPGVPATWVESCTCPVGYGQFCMCLSGYRRTPLNGYSP 720  
Db 659 SERAGYLDDVTLASAPGVPATWVESCTCPVGYGQFCMCLSGYRRTPLNGYSP 718  
QY 721 CVLCAKNGHSETCPETGVCNCRDNTAGPHCEKSDGYVGDSTAGTSSDQPCPCPGSS 780  
Db 719 CVLCAKNGHSETCPETGVCNCRDNTAGPHCEKSDGYVGDSTAGTSSDQPCPCPGSS 778  
QY 781 CAVVPKTEVVCTNCTGTTGKRCCLDDGDFGDLGRNGPVRCLRCQCSDNIDPNNAV 840  
Db 779 CAVVPKTEVVCTNCTGTTGKRCCLDDGDFGDLGRNGPVRCLRCQCSDNIDPNNAV 838  
QY 841 NCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAPNADCKACNCPYGTMTQSSCNP 900  
Db 839 NCNRLTGECLKIYNTAGFYCDRCCKGFFGNPLAPNADCKACNCPYGTMTQSSCNP 897  
QY 901 VTGQCECLPHVTGDCGACDPFYNLQSGQCECDCHALGSTNGQCDIRFGQCECPGI 960  
Db 898 VTGQCECLPHVTGDCGACDPFYNLQSGQCECDCHALGSTNGQCDIRFGQCECPGI 957  
QY 961 TGQHCERCEVNHFGPGECKPCDCHPEGSLSLOCKDDGRCECEGFGVGNRCDOCEENYF 1020  
Db 958 TGQHCERCEVNHFGPGECKPCDCHPEGSLSLOCKDDGRCECEGFGVGNRCDOCEENYF 1017  
QY 1021 YNRSWPGCECPACVRLVKDQVADHRVKLQLESLIANLGTGDEMVTDDQAFEDRLKEAR 1080  
Db 1018 YNRSWPGCECPACVRLVKDQVADHRVKLQLESLIANLGTGDEMVTDDQAFEDRLKEAR 1077  
QY 1081 EYMDLLREAQDVQDQNLMDRLQVNNLTSSQISRLQNTINTTIEGTNLAEQARAHVEN 1140  
Db 1078 EYMDLLREAQDVQDQNLMDRLQVNNLTSSQISRLQNTINTTIEGTNLAEQARAHVEN 1137  
QY 1141 TEELIEIASBELEKAKVAANVSUPTOSTGDPNNNTLLAEBAKLAERHKEADIVRV 1200  
Db 1138 TEELIEIASBELEKAKW-AAANVSITOPSTGEPNNNTLLAEBAARRLAERHKEADIVRV 1196  
QY 1201 AKTANDTSTAYNLLRTLAGENQTAFAIEBELNRYEQAKNISQDLEKQAAARVHEBAKKA 1260  
Db 1197 AKTANETSAAAYNLLRTLAGENQTALEIEELNRYEQAKNISQDLEKQAAARVHEBAKKA 1256  
QY 1261 GDKAVEIYASVAQISPLDSTLENEANNIKWBAENLEQIDOKLXDYEDLREDMRGKELE 1320  
Db 1257 GDKAVEIYASVAQITPVDSSEALENEANKIKKEAADLDRIDOKLXDYEDLREDMRGKEHE 1316  
QY 1321 VKNLLKGTKEQOTADOLLARADAALAEBAKGRDITLQEAANDILNLLKDFDRRVNDN 1380

Db 1317 VKNLLEKGAEOQTADQLLARADAAKALAEAAKGRSTLQEQANDILNNLKDFFRRVNDN 1376  
Qy 1381 KTAABEALRKIPAINOTITEANEKTRAQOALGSAADATAEAKNKAHEAERIAASAVOKNA 1440  
Db 1377 KTAABEALRRIPAINKTITAEANEKTRAQOALGSAADATAEAKNKAHEAERIAASAKNA 1436  
Qy 1441 TSTKAEARTFAEVTDLONEVNNMLKQLOBAEKELKRQDDADQDMMAGMASQAQBAE 1500  
Db 1437 TSTKAEARTFGEVTDLONEVNNMLRQLBEAENELKRQDDADQDMMAGMASQAQBAE 1496  
Qy 1501 INARAKNSVTSLLSIINDLLEQLOLDTVDLKNLEIEGTINKAKDEMKVSDLDKRVSD 1560  
Db 1497 LNARAKNSVTSLLSQLNNLLDOLGQDVTVDLKNLEIEGSLINKAKDEMKASDLDKRVSD 1556  
Qy 1561 LENEAKKQBAATMDYNRDIEETMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
Db 1557 LSEARKQBAATMDYNRDIAEIIKDHNLEDIKKTLPTGCFNTPSIEKP 1605

RESULT 9

US-09-562-702A-32  
; Sequence 32, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-32

Query Match 92.3%; Score 8038; DB 4; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

Qy 36 AMDECTDEGRPQRCMPEFVNAAFNVVATNTCGTPPEEYCVQGVGVTKSCHLCDAG 95  
Db 1 AMDECADEGRPQRCMPEFVNAAFNVVATNTCGTPPEEYCVQGVGVTKSCHLCDAG 60  
Qy 96 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVOYPSINLTLHLGKAFDITVYRLKFTS 155  
Db 61 QPHLOHGAFLTDYNNQADTTWQSQTMLAGVOYPSINLTLHLGKAFDITVYRLKFTS 120  
Qy 156 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 215  
Db 121 RPESFAIYKRTREDGPWIPYQYSGSCENTYSKANRGFIRTGDEQQALCTDEFSDISPL 180  
Qy 216 TGNVAFSTLEGRPSAYNFDNPSVLQSWTATDIRVTLNRLNFTGDEVNDPKVLKSYYY 275  
Db 181 TGNVAFSTLEGRPSAYNFDNPSVLQSWTATDIRVTLNRLNFTGDEVNDPKVLKSYYY 240  
Qy 276 AISDPAVGRCCKNGHASCVMKNEFDKLVNCNKHNTYGVDCBKCLPFFNDRPWRATAES 335  
Db 241 AISDPAVGRCCKNGHASCVMKNEFDKLVNCNKHNTYGVDCBKCLPFFNDRPWRATAES 300  
Qy 336 ASECLPCDCNGRSQBCYFDPFLYRSTGHGCHTNCQDNTDGAHCRCRENPFRLGNNEAC 395  
Db 301 ASECLPCDCNGRSQBCYFDPFLYRSTGHGCHTNCQDNTDGAHCRCRENPFRLGNNEAC 360

Qy 396 SSCCHSPVSGSLSTQCDYSYQRCCKPQVMDGKCDRCQPGFHSLTEACRCPCSDPSSIDE 455  
Db 361 SPCHSPVSGSLSTQCDYSYQRCCKPQVMDGKCDRCQPGFHSLTEACRCPCSDPSSIDE 420  
Qy 456 CNVETGRCVKDNVEGFNCERCKGFFNLESSNPRCTPCFCFCHSSVCTNAGVSVYSI 515  
Db 421 CNVETGRCVKDNVEGFNCERCKGFFNLESSNPKGCTPCFCFCHSSVCTNAGVSVYDI 480  
Qy 516 SSTFQIDEDGWRAEQDGGSEASLEWSSERQIAVISDSYFPRYFIAPAKFLGKQVLSYGQ 575  
Db 481 SSTFQIDEDGWRYEQDGGSEASLEWSSDRQYIAVISDSYFPRYFIAPVFLGNQVLSYGQ 540  
Qy 576 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFRLEHEATDYPN 635  
Db 541 NLSFSFRVDRDRTRLAEDLVLEGAGLRVSVPLIAQNSYPSSETTKYVFRLEHEATDYPN 600  
Qy 636 RPALTPEFQFKLNNLTSIKIRGTYSERSAGYLDVTLASARPGVGPATWVESCPCPVG 695  
Db 601 RPALSPEFQFKLNNLTSIKIRGTYSERSAGYLDVTLQASARPGVGPATWVESCPCPVG 660  
Qy 696 YGGQFCMCLSGYRRRTPNLGPSPCVLCAACNHSSETCDPCTGVCNCRONTAGPHCEKCS 755  
Db 661 YGGQFCBTCLPGYRRRTPSLGYPSPCVLCTCNHSETCDPCTGVCNCRONTAGPHCEKCS 720  
Qy 756 DGYVGDSTAGTSDCOPCPGSGSSCAVVPKTKVVTNCTTGTGKRCCELCDGDFGDP 815  
Db 721 DGYVGDSTLGTSSDCOPCPGSGSSCAIYPTKKEVVTCHCTGTAGKRCCELCDGDFGDP 780  
Qy 816 LGNGPVLRLCQCSNDIDFNAGVNCNRLTGCLKCIYNTAGFYCDRCCKDGFPGNPLAP 875  
Db 781 LGNGPVLRLCRPCQCNNDIDFNAGVNCNRLTGCLKCIYNTAGFYCDRCCKEGFPGNPLAP 840  
Qy 876 NPADKCKACNCPVGTWKQSSCNVPTGOCCELPHTVGTGDCGACDPGFYNLQSGQCERC 935  
Db 841 NPADKCKACACN-YGTVQOQSSCNVPTGQOCLPHVSGRDCGTCDPOYVNLQSGQCERC 899  
Qy 936 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERNVHFGPEGKPCDCHPEGSLQ 995  
Db 900 DCHALGSTNGQCDIRTGQCECQPGITGQHCECERNVHFGPEGKPCDCHPEGSLQ 959  
Qy 996 KDDGRCEGREGVGNRCDCQCEENYFNRSWPGQCEPACVRLVKDVAHRVKLQLES 1055  
Db 960 KDDGRCEGREGVGNRCDCQCEENYFNRSWPGQCEPACVRLVKDVAHRVKLQLES 1019  
Qy 1056 IANLGTGDEMVTDOAFEDRLKEAREYMDLLREAQDVQDQNLMDRLQVNNLTSQS 1115  
Db 1020 IANLGTGDEMVTDOAFEDRLKEAREYMDLLREAQDVQDQNLMDRLQVNNLTSQS 1079  
Qy 1116 RLQNRITIEETGNLABQARAHVENTERLIEIASRELEKAKVAANVSVTQPESTGPN 1175  
Db 1080 RLQNRITIEETGILAEARSVESTEQLEIASRELEKAKM-AANVSVTQPESTGPN 1138  
Qy 1176 MTLLEAEARKLAERHKEADDIVRVAKTANDTSTEAYNLLRLTAGENOTAFIEELNRK 1235  
Db 1139 MTLLEAEARKLAERHKEADDIVRVAKTANETSAAEAYNLLRLTAGENOTAFIEELNRK 1198  
Qy 1236 YEQAKNISQLEKQAAARVHEEAKRAGDAVEIYASVAQJSPDSETELEANNIKWEAEN 1295  
Db 1199 YEQAKNISQLEKQAAARVHEEAKRAGDAVEIYASVAQJTPVDSEALEANEAKIKEAAD 1258  
Qy 1296 LEOLIDOKLXDYEDLREDMEGKELEVKNLLEKGTQOATDQLLADAKALAEBAAKK 1355  
Db 1259 LDRUIDOKLXDYEDLREDMEGKEHEVKNLEKAEQOATDQLLADAKALAEBAAKK 1318  
Qy 1356 GRDTLQEBANDILNNLKDFFRRVNDKTAABEALURKI PAINTITTEANEKTRAQOALGSA 1415  
Db 1319 GRSTLQEBANDILNNLKDFFRRVNDKTAABEALURRIPAINRTIAEANEKTRAQOALGSA 1378  
Qy 1416 AADATEAKNKAHEAERIAASAVOKNATSTKAEARTFAEVTDLONEVNNMLKQLOBAEKEL 1475  
Db 1379 AADATEAKNKAHEAERIAASAAQKATSTKADARTTGEVTDLONEVNNMLQLEBAENEL 1438  
Qy 1476 KRKQDDADQDMMAGMASQAQBAEINARKAKNSVTSLLSIINDLLEQLQGLDTPVNLKL 1535



Db 1439 KRQDDADQMMWAGNAGSQAQAEALNARKAKNSVSSLLSQNNLLDQQLGQDVTDLNKL 1498  
QY 1536 NEIEGTINAKDEMKVSDLDKRVSDLENEAKQAEAAIMDYNDRIEEMKDIRNLEDIRKT 1595  
Db 1499 NEIEGSANAKDEMKASDLDRKVSLESEAKQAEAAIMDYNDRIEEMKDIRNLEDIRKT 1558  
QY 1596 LPSGCFNTPSIEKP 1609  
Db 1559 LPTGCFNTPSIEKP 1572

RESULT 10  
US-09-561-818A-28  
; Sequence 28, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortemas, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 1572  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-28

Query Match 92.3%; Score 8038; DB 4; Length 1572;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 1469; Conservative 56; Mismatches 47; Indels 2; Gaps 2;

QY 36 ANDECTDEGRQRCMPFVNAFNVVAVNTCTPPEYCVQGTGVTGKSLCHLCDAG 95  
Db 1 AMDECADEGRQRCMPFVNAFNVVAVNTCTPPEYCVQGTGVTGKSLCHLCDAG 60  
QY 96 QPHLQGAFLDYNNQADTTWQSQTMLAGVQVPSINLTLLHKGAFDITYVRLKPHTS 155  
Db 61 QPHLQGAFLDYNNQADTTWQSQTMLAGVQVPSINLTLLHKGAFDITYVRLKPHTS 120  
QY 156 RPESAIYKRTREDGFWIPYQYISGSCENTYSKANRGPIRTGDEQALCTDFSDISPL 215  
Db 121 RPESAIYKRTREDGFWIPYQYISGSCENTYSKANRGPIRTGDEQALCTDFSDISPL 180  
QY 216 TSGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 275  
Db 181 TSGNVAFSTLEGRPSAYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVNDPKVLKSYYY 240  
QY 276 AISDFAVGGRCKNGHASECMWNEPDKLVCKNNTYGVDCCKLPFFNDRPWRRTAES 335  
Db 241 AISDFAVGGRCKNGHASECMWNEPDKLVCKNNTYGVDCCKLPFFNDRPWRRTAES 300  
QY 336 ASECLPCDCNGRSQCYDPPELYRSTGHGHTCQDNTDGAHCERCENRPFRLGNNEAC 395  
Db 301 ASECLPCDCNGRSQCYDPPELYRSTGHGHTCQDNTDGAHCERCENRPFRLGNTEAC 360  
QY 396 SSCGSPVGSLSLTCDSYGRCKPQVGMGDKCDRCQPGFHSLSLTBAGRPCSCDPSGSIDE 455  
Db 361 SPCHSPVGSLSLTCDSYGRCKPQVGMGDKCDRCQPGFHSLSLTBAGRPCSCDPSGSTDE 420  
QY 456 CNVETGRVCCKDNVGFNCERCKPGFFNLESNPRGCTPCPCFCHSSVCTNAVGYYSI 515  
Db 421 CNVETGRVCCKDNVGFNCERCKPGFFNLESNPRGCTPCPCFCHSSVCTNAVGYYSI 480  
QY 516 SSTFOIDEGWRAORDGSEASLESWSRQDIIVSISYPRPIAPAKFLGKQVLSYGQ 575  
Db 481 SSTFOIDEGWRAORDGSEASLESWSRQDIIVSISYPRPIAPAKFLGKQVLSYGQ 540  
QY 576 NLSFSFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 635

RESULT 11  
US-09-845-583A-10

Db 541 NLSFSFRVDRRTRLSAEDLVLEGAGLRVSVPLIAQNSYSPSETTVKYIFRLHEATDYPW 600  
QY 636 RPALPFFFOKLNNLNTSIRKITYSERSAGYLDVTLASARPQGPVATWVESCTCPVG 695  
Db 601 RPALPFFFOKLNNLNTSIRKITYSERSAGYLDVTLASARPQGPVATWVESCTCPVG 660  
QY 696 YGQFCCEMCLSGYRRETENLGPVSPCVLCACNGHSETCDPBTGVNCRDNTAGHCEKCS 755  
Db 661 YGQFCCEMCLSGYRRETENLGPVSPCVLCACNGHSETCDPBTGVNCRDNTAGHCEKCS 720  
QY 756 DGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWVTCNCTGTGTRKRCBLCDGYYGDP 815  
Db 721 DGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTKVWVTCNCTGTGTRKRCBLCDGYYGDP 780  
QY 816 LGRNGPVRLCRLCOCSDNIDPNAVGNCRNLTEGLCKCIYNTAGCYDCRCKDGFPGNPLAP 875  
Db 781 LGRNGPVRLCRLCOCSDNIDPNAVGNCRNLTEGLCKCIYNTAGCYDCRCKDGFPGNPLAP 840  
QY 876 NPADCKACNPNYGTMTKQSSCNPTVGTQCECLPHVTGQDCGACDPOFYNLQSGQGCERC 935  
Db 841 NPADCKACACN-YGTVQQSSCNPTVGTQCECLPHVTGQDCGACDPOFYNLQSGQGCERC 899  
QY 936 DCHALGSTNGOCIDRTGQCECQPGITGQHCEBCEVNHFGFPGCKPCDCHPESGSLQ 995  
Db 900 DCHALGSTNGOCIDRTGQCECQPGITGQHCEBCEVNHFGFPGCKPCDCHPESGSLQ 959  
QY 996 KDDGRCCEBGFVGNRCDCQCEENFYNRSWPGQCEPCACYRLVKDVADHRVKLQBLESL 1055  
Db 960 KDDGRCCEBGFVGNRCDCQCEENFYNRSWPGQCEPCACYRLVKDVADHRVKLQBLESL 1019  
QY 1056 IANLGTGDMVTDOAFEDRLKEAREVMDLLRAQDVQDQNLMDRLQVNNLTLSQIS 1115  
Db 1020 IANLGTGDMVTDOAFEDRLKEAREVMDLLRAQDVQDQNLMDRLQVNNLTLSQIS 1079  
QY 1116 RLQNRINTIETGNLQOARAHVENTERLLEIASRELEKAKAAVSVTQPESTGDPNN 1175  
Db 1080 RLQNRINTIETGNLQOARAHVENTERLLEIASRELEKAKAAVSVTQPESTGDPNN 1138  
QY 1176 MTLAEBARKLAERHKEADDIRVAKTANDTSTAYNLLRLTAGENOTAFIEBELNRK 1235  
Db 1139 MTLAEBARKLAERHKEADDIRVAKTANDTSTAYNLLRLTAGENOTAFIEBELNRK 1198  
QY 1236 YEOAKNISODLEKQAAARVHEEAKGADKAVEIYASVAQLSPDSELEANNIKWEAEN 1295  
Db 1199 YEOAKNISODLEKQAAARVHEEAKGADKAVEIYASVAQLSPDSELEANNIKWEAEN 1258  
QY 1296 LEQIDQKLDYEDLREDMRGKELEVKMLLEKGTQOQTADQLLADADAALAEBAKK 1355  
Db 1259 LDRIDQKLDYEDLREDMRGKELEVKMLLEKGTQOQTADQLLADADAALAEBAKK 1318  
QY 1356 GRDTLOEANDILNKLKDFDRVNDKNTAAEALRKIPAINQTTTEANEKTPREAOALGSA 1415  
Db 1319 GRDTLOEANDILNKLKDFDRVNDKNTAAEALRKIPAINQTTTEANEKTPREAOALGSA 1378  
QY 1416 AADATEAKNKAHEARITASAVQKNATSTKAEABERTFAEVTDLNENVMNLKQLEAEKEL 1475  
Db 1379 AADATEAKNKAHEARITASAVQKNATSTKAEABERTFAEVTDLNENVMNLKQLEAEKEL 1438  
QY 1476 KRQDDADQMMWAGNAGSQAQAEALNARKAKNSVSSLLSQNNLLDQQLGQDVTDLNKL 1535  
Db 1439 KRQDDADQMMWAGNAGSQAQAEALNARKAKNSVSSLLSQNNLLDQQLGQDVTDLNKL 1498  
QY 1536 NEIEGTINAKDEMKVSDLDKRVSDLENEAKQAEAAIMDYNDRIEEMKDIRNLEDIRKT 1595  
Db 1499 NEIEGSANAKDEMKASDLDRKVSLESEAKQAEAAIMDYNDRIEEMKDIRNLEDIRKT 1558  
QY 1596 LPSGCFNTPSIEKP 1609  
Db 1559 LPTGCFNTPSIEKP 1572

; Sequence 10, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Brunken, Robert  
; APPLICANT: Champilaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-10

Query Match 41.4%; Score 3611; DB 4; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 6.7e-202;  
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

QY 21 LAVLAAAAGCAQAMDECTDEGGPQRCMPEFVNAAPNVTVAATNTCGTPPEYCVQT 80  
DB 10 LALLAPRAAG----AGMGACYAGRPQCLPVFENAAFGRLAQASHTCGPPDFCPHV 65

QY 81 GVTGVTKSCHLDAGPHLQHGAAFLTDYNNQADTTWQSQMTLAGVQYPSINLHLG 140  
DB 66 GAAGAGAHQCRDAADPQRHNASYLTDFHSQDESTMWQSPMAFGVQYPTSVN:TLRLG 125

QY 141 KAPDITYVLKHTSRPESFAYKRTREDGPKTPYQYSGSCENTYSKANRGFIRTGDE 200  
DB 126 KAYEITYVLKHTSRPESFAYKYSRADGPEWYQFYASCKYTGPEGOYLPRGDE 185

QY 201 QOALCTDEPDISPLTGNVAFSTLEGPSAYFNDSNPSVLQEWVATDIRVTLNRLNTFG 260  
DB 186 RVAFCTSESDISPLSGNVAFSTLEGPSAYFNDSNPSVLQEWVATDIRVTLNRLNTFG 245

QY 261 DEVNDPKVLKSYIYALSPFAGCRCKNGHASECKWNEFDKLVCKNGHNTGVDCBCL 320  
DB 246 DQIFKDPKVLQSYIYAVDSFVGGRCCKNGHASECGPDVAGLACRCQHNITGTDCERCL 305

QY 321 PFENDPWRRAEASASECLPCDCNGRSQECYDFDELVASTGHGHCNTCQDNTDGAHCE 380  
DB 306 PFQDPRWARGTAAEAHECLPCNCSGRSECTFDRELFEFTGHGGRCHCRDHTAGPHE 365

QY 381 RCENPFRLGNNEACSSCHSPVGLSLSTQCDYGRCSCKPVGWMDKDCRCQPGFSLTEA 440  
DB 366 RCQENFYHWPMPQCPQDCQAGSLHLQCDTGTCAKCPVTVTGWKCDRCCLPFGFSLSEG 425

QY 441 GCEPCSDPSGSDENVTGRVCKDNGVEGFCNCRCKPFPNLSNPRGCTPCFCFGH 500  
DB 426 GCRPCTCNFAGSLDTCDPGRGRCPCKEVNEGMLCDRCRGTNLPQHPNAGSSCFYGH 485

QY 501 SSVCTNAVGYSVYSISTFTQIDEDGWABQRQDGESEASLEWSSERQDIAVISDSYFPRYFI 560  
DB 486 SKYCASTAQFQVHHILSDFHQAGEGWARSVGGSEHSPQWSPN----GVLLSPDEEBELT 541

QY 561 APAKFLGKQVLSGQNLSTSFVRDTRDRLSADLVLGAGLRVSVPLTAQNSYSESETT 620  
DB 542 APQKFLGQDRFSYQGLIITFRVPPGDSPLPVQ-URLEGTGLALS--LRHSSLSGFPQAR 598

QY 621 VKYVFLRH---EATDYPWRPALTPPEFKLLNLTSLIKIRGYISERSAG--YLDVDTLAS 675  
DB 599 ASQGGRAQVLPQETSEDVAPPLPPFPFQRLANLTSLRLVSPGSPAGPVFLTEVRLTS 658

QY 676 ARPGPGVATWESCTCPVGYGQPCMLSGVRRTPNLGYPSPCVLCACNGHSETCDP 735  
DB 659 ARFGLSPASWVBICSTGYTQGCESCAPGYKREMPQGGPYASCVPCTCNQHG-TCDP 717

QY 736 ETGVCNCRNTAGPCEKSDGVYGDSTAGTSSDQPCPCGGSSCAVVPKTKEVVCTNC 795  
DB 718 NTGICVCSHHTGSPCERCLPGFYGNPPFAGQADDQPCPCQOSACTTIPESGEVCTHC 777

QY 796 PTGTTGRCCELDDGYFGDPLGRNGFVRLCRICQCSNDIDPNAGVNCNRLTCECLKIYN 855  
DB 778 PPGQGRRCCEVDDGFFGDPGLGFHPQPCQCCSGNVDPNAVGNCDPLSGHCLRLCHN 837

QY 856 TAGFYCDRCXKDDGFFGNPLAPNADKCKACNCPYGTMTKQSSCNPNVTGCECLPHVTGD 915  
DB 838 TTGDHCEHCOEGFYGALAPRPAKCMPCSCHPQGSVSEQMPCDPVTGQSCPLPHVTARD 897

QY 916 CGACDPGFVNLQSGQCCERCDCHALGSTNGQCDIRTGQCECQPGITGQHCERCEVNHFF 975  
DB 898 CSRCTGFFDLPQGRGCRSKCHPLGSQEDQCHPKTGTCTCRPGVTGQACDRCOLGFFGS 957

QY 976 GPEGCPDCHPEGSLQCKDDRCCEGFGVNECDCEENYFYNRSPWQCECPACY 1035  
DB 958 SIRGCRACRCSPLGAASAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCPSCY 1017

QY 1036 RLKVDKVDADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAREVMDLLREADQKDV 1095  
DB 1018 ALVKEATAKLKARLTITEGWLQSDCGSPW---GPLDILLGEAPRG-DVYQGHLLPGA 1072

QY 1096 DONLMDRLQVNNLTSSQISRLQINRTIETONLAEQARAHVENTERLIEIASRELEKA 1155  
DB 1073 REAFLEQMGLEGAVKAAEQRLQNLKAGFCAQAGSKCTCTQLADLEAVLESSEELHA 1132

QY 1156 KVAANVSVTQPESTGDPNNMTLLABEARKLAEHRHKEADDIVRVAKTANDTSTEAYNLL 1215  
DB 1133 AAILASLEIFQ-BGPOPTKWSHLAIEARALASHRDTATKIAATWALLASNTSVALL 1191

QY 1216 LRTLAGENOTAFRIE-ELNRKYEQAKNI SODLEKQAAHVHEEAKRAGDKAVEIYASVQL 1274  
DB 1192 WNL--EGRVALETORDLEDYQEVQAAKALRTAVALPEAE-----SVLATVQQV 1242

QY 1275 SPLDSETL-----ENEANNKMEANLEQLIDQKLKDYEDLREDMRKGELEVK 1323  
DB 1243 GADTAPYALLASPGALPKQSRADGLKAKALEKT-----ASQHMATE-AARTLTQTA 1297

QY 1324 LLEKGTQEQT-----ADQLLARADAAKALAEAAKGRDLOEANDILNKLKDF 1373  
DB 1298 QATLRQTEPLTMARSRLTATFASQLHQGAALTAQSSVQAATVTVMGARTLLADLEG 1357

QY 1374 DRRVNDKNTAAEALRKIPAINOTITEANEKTEAQALGSAADATEAKYKAHEAERIA 1433  
DB 1358 KLOPPFPKQAAQLCKADSVSDRLADTRKTKTQAEFMGLGNAAPLSSAKKKGREAVLA 1417

QY 1434 SAVQKNTATSKABERTFAEVTDLNENNNMLKQL-QEAEKELRKQDDADQDMAGMA 1492  
DB 1418 KDSKALAKALLRERKQARRASRLTSQTQATLQASQOVLASEARQEEAEERVGAGLS 1477

QY 1493 SQAQAEINARKAKNSVTLSIINDLEQLGOLDT--VDLNKLAIEGTLNKAKDEM- 1549  
DB 1478 -----EMEQQIRRESRISLEKDIETLSSELLARGLSDTHQAPALNETQWALERLQLG 1532

QY 1550 KVSDDLDRKVSLENAKKQEAAMDNDRDTEEMKDIRNLEDIRKTLPSGC 1600  
DB 1533 SPGLQKRLSLQESQOQELQIQGFESDLAEIRADKQNLKLEALHSLPENC 1583

RESULT 12  
US-09-561-709B-3  
; Sequence 3, Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champilaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001

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; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-561-709B-3

Query Match      41.4%; Score 3611; DB 4; Length 1587;
Best Local Similarity 43.5%; Pred. No. 6.7e-202;
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

QY 21 LAVAIAAGAGCAQAAMDECTGGPQRCMPBPVNAANFVTVATNTCTGTPPEYCVQT 80
DB 10 LALLAPRAAG-----AGMGACYDAGRPQCLPVENAFAFRLAQASHCTGSPFPCPHV 65
QY 81 GVTGVTKSCHLDCAGPHLQHGAAFTLDVNNQADTTWQSQTMLAGVQVPPSSINILTLHLG 140
DB 66 GAAGAGAHQRCDAADPQRHNASYLTDPHSQDESTWQSPSWAFVQVPTSVNITLRLG 125
QY 141 KAFDITVRLKFTSPESPAIYKRTREDCGWPITPYOYSGSCENTYSKANRGIIRTGDE 200
DB 126 KAVEITVRLKFTSPESPAIYKRSRAGDQWEPYQFYASQCKTYGREGYLRPGDE 185
QY 201 QOALCTDFEFDISPLTGNVAFSTLGRPSAYNFDSVPLQEWVATDTRVTLNRLNTFG 260
DB 186 RVAFCTSEFSDISPLSGNVAFSTLGRPSAYNFDSVPLQEWVATDTRVTLNRLNTFG 245
QY 261 DEVFNDPKVLKSYIAISDFAVGRCCKNGHASECMKNEFDKLVNCKRNTYGVDCCKL 320
DB 246 DD1FKDPKVLQSYIYVSDFSVGRCKNGHASECGPDVAGVAGVACRCHNTTGTDCERCL 305
QY 321 PFENDRWRTAEASASECLPCDCNGRSORCYFDPBLYSTGTHGHCTNCOINTDGAHCE 380
DB 306 PFQDRPWARTAEAAHECLPCDCNGRSEECTFDRELFTSTGTHGHCHCHRTAGPHCE 365
QY 381 RCENFRLNGNEACSSCHSPVGSLSLTCQDSTYGRCSKRPVGMGRKDCRCQFPHSLTEA 440
DB 366 RCQENFYHWPQPCQDQCSAGSLHLQDDTGTCAKPTVTGMKDCRCLPGFHSLSG 425
QY 441 GCRPCSDPGSDIDECNVETGRCVKDNVEGFCERCKGCFNLESNPRGCTPCFCGH 500
DB 426 GCRPCTCNAGSLDTCPRSGRCPCKENVEGNLCDCRCPGTFLNLPNAGCCSCFCYGH 485
QY 501 SSVCTNAVGSVYSISSTFQIDEDGWRAEQDGSSEASLEWSSERQDIAVISDSYFPRYFI 560
DB 486 SKVCASTAQVQHILSDFHQAGWARSVGGSEHSPQWSPN---GVLLSPDEBELT 541
QY 561 APAFLKQVLQVQNLGSLFVRVDRTRLSAEDLVLEGAGLRVSVPLTAQNSYPSSETT 620
DB 542 APGKFLGDRFSYQPLILTRVPPGDSPLPQ--LRLEGTLALS--LRHSSLSGPDAR 598
QY 621 VKYVFLH---EATDYPWRALTPFEQKLNLTLSIKRTGYSERSAG--YLDVDTLAS 675
DB 599 ASQGRAPVLOETSESDVAPLPFFHFQRLANLTLRLVSPGSPAGPVFLTEVRLTS 658
QY 676 ARPQGPVATWVSECTCPVGVGGFCMCLSGVRRTPNLPYSPVCLACNHSHTCDP 735
DB 659 ARPGLSPPASVETCSCTGYTGQFCSCAPGVYKREMPQGGPYASCVPCTCNOHG--TCDF 717
QY 736 ETGVNCRDNTAGPHCKSDGYYGDSGTAGTSSDCPCPCPGSSCAVVPKTEVYCTNC 795
DB 718 NTGICVSHHTFEGSPSCRLPGFVGNFPAGQADDCPCPCPGSACTTIPSEGEVCTHC 777
QY 796 PTGTGKRCCLDDGFGDPLGRNGPVRLCRLCQCSNDIDPNVAGNRLTGELCKIYN 855
DB 778 PPGQGRRCCEVCDGDFGDLPLGLFHPQPCQCSGNVDPNAVGNCDPLSGHCLRLCHN 837

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856 TAGFYCDRCCKDGFNGLAPNADKACNCNPNYGMKQSSCNPNVTGQCECLPHVTQD 915
838 TTGDHCHCEGFGVGSALAPRPAKCMPCSCHPQSVSEQMPDPTVGTQCSCLPHVTARD 897
916 CGACDPFYNLQSGQGCRCCHALSTNGCQDIRTGQCECQPGITGCHCERCEVNHFGF 975
898 CSRCYPGFFDLQPGRCRSCKCHPLSGQEDQCHPKTGQCTCRPGVTGQACDRCOLGFFGS 957
976 GPEGCKPCDCHPEGSLQCKDGRCEGFGVGNRCNRCQCEENYFYNRSWPGQCEPCY 1035
958 SIKGRACRCSPLGAASAQCHYNGTCVCRPGFSGKCDRCHYNNFLTADGTHCQCFSCY 1017
1036 RLVDKQVADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAREVMDLLRQADYKDV 1095
1018 ALVXEETAKLKLRTLTTEGLWQSGDCGSPW---GPLDILLEGAPRG--DYVQGHLLPGA 1072
1096 DONLMDRLORVNTLSOISRLQINRNTIBETGNLAEOARAHVENTRLLIEIASRELEKA 1155
1073 REAFLEQWGLEGNVKAAREQLQLNKGARCAQAGSQKCTQLADLEAVLESSEELIHA 1132
1156 KVAANYSVTPQESTGDPNNMTLLAEARKLAERHKOADDIVRVAKTANDTSTEANLL 1215
1133 AAILASLEIPQ-EGPSQFTKWSHLAIEARALARSHRDTATKIAATAWRALLASNTSALL 1191
1216 LRTIAGENOTAFETE-ELNRKYEOKNI SODLEKQAAARVHEEAKRAGDKAVEIYASVAQL 1274
1192 WNLL--EGRVALETQRLDREYQVQAAKALRTAVAEVLPEAE-----SVLATVQOV 1242
1275 SPLDSETL-----ENEANNIKWEAENLEQLIDOKLYOVEDLREDMRGKLEVKN 1323
1243 GADTAPYLALLASPGALPQKSRAEDLGLKAKAEKTV---ASWQHMAE--AARTLQTA 1297
1324 LLEKGTQEQOT-----ADOLLARAADAALAEAAKKGRTDLEANDILNNLKDF 1373
1298 QATURQTEPLTMAISRITATFASQLHOGARAALTQASSVQAAATVYMGARTLLADLEG 1357
1374 DRRVNDKTRAEEALRKIPAINQITTEANBKTRTAAQALGSAADAATEAKNKAHEABRIA 1433
1358 KLQPPRPKQQAALQKADSVSDRLADTRKTKQAERMLGNAAAPLSSAKKGRAEVLA 1417
1434 SAVQKATSTKAEAEPTFAEVTDLIDNEVNNMLKL-QEAEKELKRDQDQDMMAGMA 1492
1418 KDSAKLAKALLERKQARRASRLTSQTATLQASQOVLASARRQELSEAEVAGLS 1477
1493 SQAQAEABINAKKNSVTSLLSIINDLLBQLGOLDT--VDLNKLNIEGTILNKADEM- 1549
1478 -----EMEQQIRESRISLEKDIETLSSELLARLGSLDTHQAPALNETOWALERLRLQ 1532
1550 KVSOLDKRVSLDENEAKQBAIMDYNDRIEIMKDIENLEDIRKTLPSGC 1600
1533 SPGSLQRKLSLLEQSQOQLQIQGFPSDLABIRADKQNLAILHSLPENC 1583

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RESULT 13
US-08-317-450B-13
; Sequence 13, Application US/08317450B
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kailunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

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581 -----EPVG-----CRSDGTVCCKPGFGPNCEH-----GAFS 608

1031 CPACYRLVKVADHRVRLKQLESLIANLGTGDEMVTQAFEDRLKEAREVMDLLEAQ 1090

609 CPACYNQKIQMDQFQQQORMEALISKAQGGDGVVPTLEGRMQQAQALQDLIRDAQ 668

1091 DVKDVQNLMDRLQVRNNTLSQISRLQWIRNTIETGNLAQARAHVENTERLEIASR 1150

669 ISEGARSGLGLQAKVRSQENSYQSRLLDKMTVSRVALGSQYQNRVDTLRLITQWL 728

1151 ELEKAKVAAANYSVTQPESTGDPNNMTLLAEARKLAERHKEADDIIVRAKTANDTTE 1210

729 SLAEEASLGNNTNIPASDHYVGNPGFKSLAQEAATRLAESHVESASMEQLTRETEDYSKQ 788

1211 AVNLLRLTL-----AGENQTAFFIEELNRKVEQAKNISOLEKOAARVHEEAKRAGDK 1263

789 ALSVKAHLHEGVGSGSPDGAV-VQGLVEKLEKTSLAQQLTREATQAEIADRSYQH 847

1264 AVEIYASVAQLSPDLSETLE-NEANNIKMEAEENLEQLIDQKLYEDLREDMRGKELEVY 1322

848 SLRLDSVSPLOGVSDQSFQVEEAKIKQKADSLSLVTRHMDFKTKQKLNKNKEBAQ 907

1323 NLEKGTQEQOTADQLLADADAALAEBAKKGRTQEQANDILLNLKDFERYNDNKT 1382

908 QLLQNGKSGREKSDQLLSRANLAKSRAQEALESNGNATFYVESILKNLUREFDLQVNRKA 967

1383 AAEELARKIPAINOTTITAEANEKTRAQOALGSAADATEAKNKAHEAERIASAVOKNATS 1442

968 EAEAMKRLSYISQKVSADSDTKQAERALGSAADADAQAKNGAGEALFISSEIEQIGS 1027

1443 TKAEARTFAEVTDLNVEVNNMLKQLEAEKELKQDDADQDMMAGMASQAQAEIN 1502

1028 LNLAEVNTADGALAMEKGLASLKSEMEVEGELEKELEFDTNMDAVQKVI TEAQKVOTR 1087

1503 ARKAKSVTSLLSIINDLLEQLQGLDVTDLNKLNEIEGTLNKAKDEMKSVDLDRKVSLE 1562

1088 AKVAGVTIOTLNTDGLLHMDQPLSVDBEGLVLEKLSRAKTQIN-SQLRPMWSELE 1146

1563 NEAKGEAAIMDYNRIEIMKDIRNLEDIRKTLPSGCNTPTSEIK 1608

1147 ERARQQRGHLHLETSIDGILADVKNLNIRDNLPPCYNTQALEQ 1192

RESULT 14

US-08-800-593-13

Sequence 13, Application US/08800593

Patent No. 6143505

GENERAL INFORMATION:

APPLICANT: Tryggvason, Karl

APPLICANT: Kallunki, Pekka

APPLICANT: Pyke, Charles

TITLE OF INVENTION: Laminin Chains: Diagnostic and

TITLE OF INVENTION: Therapeutic Use

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boenell Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,593

FILING DATE: 18-FEB-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/317,450

FILING DATE: 04-OCT-1994

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/317,450B

FILING DATE: 04-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Chao, Mark

REGISTRATION NUMBER: 37,293

REFERENCE/DOCKET NUMBER: 94,778

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 1193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-317-450B-13

Query Match 30.3%; Score 2637; DB 1; Length 1193;

Best Local Similarity 39.4%; Pred. No. 2.4e-145;

Matches 515; Conservative 235; Mismatches 419; Indels 138; Gaps 12;

319 CLPFFNDPWRATASASECLPCDNGRSQECYFDPPELYASTGHHCTNCQNTDCAH 378

9 CLCFSLLLPAARATSRRE-----VCDNGKSKRQCIPFRELHRTQNGFRCLNCNDNTDGIH 64

379 CERCEENFRLLGNNAACSSCHSPVGLSTOCDSYGRCSKPGVGMKDCRCQCPGFSLT 438

65 CEKCKNGFYRHERDRCLPCNCKNSKGLSARCDNSGRCSKPGVTGACDRCLGFFHMT 124

439 EAGC-----RPSCDPSSGIDECNVEGRVCVKONVEGFNCERCKPGFFNLESSNPR 490

125 DAGCTQDQRLDLSKDCDPAGIAGPC--DAGRCVCKPAVTGERCDRCRSGYINLDGNGPE 182

491 GCTPCFCGHSSVCTNAVGSYVS--SSTFQDEDEGWAEQDGSSEASLEWSESRQDIAVI 550

183 GTCQCFYGHSSASCSSAEYSVHKLTSTFHQVDQGWKAVQNGSPAKLQNSQRHQDVSS 242

551 SDSYFPRYFIAPAKFLGKQVLSYGQNLSSFSFVRDRDRRLSAEDLVLEGALRVSVPLIA 610

243 AQRLDPVYFVAPAKFLGQVSGYQSLSFDFYVDRGGRHPSAHDVILEGALRITAPLMP 302

611 QGNSYPSSETTKYVFLHEATDYPWRPALTPPEFQKLLNLTISIKRGTYSERSAGYLD 670

303 LGKTLPCGLTKTYTFLRNEHPSNNKSPQLSYFEXRLLRLNLTALIRATYGEYSTGYIDN 362

671 VTLGARPGPGVPATWVZSCTCPVGYGQFCMEMCLSGYRRETPNLGYPSPCVLCACNGHS 730

363 VTLISARPVSGAPAPWVEQCICPVGYKGQFCQDCASGYKRSARLGPFGTCIPCNCQG-G 421

731 ETCDBETGVNCRDNTAGPHCKSDGYGDSGTAGTSSDCQPCPCPGSSCAVVPKTEV 790

422 GACDPDGTGDCYSGDENPDTEACDPIGFYNDPHDPRS--CKPCCHNGFSCSVIPETSEV 479

791 VTCNCPGTGTKRCELCDGFGDPLGRNGPVRRLCRLCQCSNDIDPNVAGNCRNLTGEC 850

480 VCNKCPFGVTGARCELADGYGDFGEGHVPYRPPQPCQCSNVDPSASGNCRLTGEC 539

851 KCIYNTAGYCDRCXKDGFPNGPLANPADKACACNPNYGMKQSSCNVPTGQCECLPH 910

540 KCIHNTAGYCDQCKAGYFGDPLANPADKACACNPNMGS----- 580

911 VTGQDCGACDPGFYNLQSGQGCERCDHALGSTNGCQDIRTQGCBCQPGITGHCERCEV 970

581 ----- 580

971 NHFGFGECKPCDCHPEGSLSLQCKDGRCSREGFVGNRCDOCEENFYNRSWPGQCE 1030

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778-B  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-593-13

Query Match 30.3%; Score 2637; DB 3; Length 1193;  
Best Local Similarity 39.4%; Pred. No. 2,4e-145;  
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;

QY 319 CLPFFNDPWRRTATASASECLPCDNCGRSQEYFPDLYRSTGCHGCHTNCQDNTDGAH 378  
DB 9 CLCFSLPAAATSRRE-----VDCNCGSRQCFIDRELHRTGNGFRCLNCNDNTDGIH 64

QY 379 CERCRENFFELGNEACSSCHCSFVGLSTQCSYGRCSCKPGVMGDKCDRCQPGFHSIL 438  
DB 65 CEKCKGFFYHRDRCLPCNCKSKLSARCDNSRCCKPGVTGARCDCLPGFHLT 124

QY 439 EAGC-----RPSCDPSSIDEQNVETGRVCKDNVEGNCERCKPGFNLSSNPR 490  
DB 125 DAGCTDQRLDSKCDPAGIAGPC--DAGRCVCKPAVTVGRCDCRCSGYNLGNGPE 182

QY 491 GCTPCFCFHSVCTNAGVGVVYISSTFOIDGWRASORDGSEASLWSERQDIYI 550  
DB 183 GCTQCFCHGSHASCRSAEYVHKITSTFHQDDGKAVORNGSPAKQWSQHQDVFS 242

QY 551 SDSYFFRYTAPAKFLGKQVLSQNLFSFRVDRDRDLALSABDLVLEGAGLRVSVPLIA 610  
DB 243 AQRLDPVYFAPAKFLNGQVSYGSLSPDYRVDGRHPSAHDVILEGALRIITAPLM 302

QY 611 QGNSYSETTVKYVFRLEHATDPWRPALTPFFQKLIANNLTISIKIRGTYSERSAGYLD 670  
DB 303 LGKTLPCGLTKTYTFRLEHPSNNWSQLSYFBRLLRLNLTALRIATYGEYSTYIDN 362

QY 671 VTLASAPGPGVPATVYESCTCPVGVGGQFCMCLSGYRRETNLPGFSPCVLCAENGHS 730  
DB 363 VTLISAPVSGAPAPWVEQICPVYKGQFCQDCASGYKEDSARLPGFGTCPCNQG-G 421

QY 731 ETCDPETGVNCRDNTAGPHCEKSGDGYGDSGTAGTSSDCQPCPCPGGSSCAVPTKEV 790  
DB 422 GACDPDTGDCYSGDENPDIECADCPIGFYNDPHDPRS--CKPCCHNGFSCSVIPETEV 479

QY 791 VCTNCPGTGKRCLECDGDFGLGRNGFVRLCRLCQCSNDIDPNAVNCNRLTGECL 850  
DB 480 VVNCPPGVGTGARCELADGYGDFGDFGEPFVPCQPCQCNVNDPSASGNCDELGTGCL 539

QY 851 KCIYNTAGFYCDRCCKDGFNPLAPNADKCKACNCPYGTMTKQQSSCNVPTQCECLPH 910  
DB 540 KCIHNTAGYCDQCKAGYFGDPLAPNADKCRACNCPMGS----- 590

QY 911 VTGDCGACDPGFYNLQSGQGCERCDCALGSTNGQCDIRTGQCECPGIGTQHCEV 970  
DB 581 ----- 580

QY 971 NHFGFGECKPCDCHPEGSLSLQCKDDGRCECREGVGNRCDOCEYFNYSWFGQE 1030  
DB 581 -----EPVG-----CRSDGTVCVKPGFGGPNCEH-----GAFS 608

QY 1031 CPACRYLVKQVADHRVKLQLESILANLGTGDEMVTDOAFEDRLKEABEVMDLLEAQ 1090  
DB 609 CPACYNQYKIQDMFOQLOQMEALISKAQGGDGVVPTTELEGMQQAQEQALQDILDAQ 668

QY 1091 DVKDQDQNLMDRLQEVNNTLSSQISRLQNTIRNTIETGNTLAEQARAHVENTERLIEIASR 1150

RESULT 15

US-08-317-450B-15  
Sequence 15, Application US/08317450B  
Patent No. 5660982

GENERAL INFORMATION:  
APPLICANT: Tryggvason, Karl  
APPLICANT: Kallunki, Pekka  
APPLICANT: Pyke, Charles  
TITLE OF INVENTION: Laminin Chains: Diagnostic and  
TITLE OF INVENTION: Therapeutic Use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & ALLEGRETTI, LTD.

STREET: Ten South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/317,450B

FILING DATE: 04-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Chao, Mark

REGISTRATION NUMBER: 37,293

REFERENCE/DOCKET NUMBER: 94,778

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 1111 amino acids

DB 669 ISEGASRSLGLQAKVRSQENSYQSRLLDDDKMTVERVALGSGYQNVRRVTRHLITQMQL 728  
QY 1151 ELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKEQADDIVRVAKTANDTSTE 1210  
DB 729 SLAESEASLGNITNPASDHYVGNPKSLAQEAETRLAESHVESASNNWEQLTRETEDYSKQ 788  
QY 1211 AYNLLRLT-----AGENQTAPEIEELARKYQAKNIIISODLEKQARVHEBAKRGDK 1263  
DB 789 ALSIVRKALHEGVGSGSPDGAV-VQGLVEKLEKTSKLAQQLTREATQAEIADRSYQH 847  
QY 1264 AVEIYASVAOLSPUDSETLE-NEANNIKMEANLEQLIDQKLDYEDLREDMRGKELEVK 1322  
DB 848 SLRLDSVSPLOGVSDQSFQVEEAKRIKQKADSLSSLVTRHMDKFKTKQNLGNWKEEAQ 907  
QY 1323 NLLSEKGTQEQOTADOLLARADAKALAEBAKGRDITLQEQANDILNLLKDPDRVNDNKT 1382  
DB 908 QLLQNGSKSGREKSDQLSRANLAKSRAQEAALSNGENATFYVESILKNLRFDLQVDNRKA 967  
QY 1383 AAEALARKIPAINOTITTEANEKTRAQCALGSAADAATEAKNKAHEAERIASAVQKNATS 1442  
DB 968 EAEAMKRLSVISKVSDASDKTQQAERALGSAADAQAKNGAGALEISSEIEQEIGS 1027  
QY 1443 TKBAERTFAEVTOLDNEVNNMLQLOEAKELKRDQDADQDDMMAGMASQAQAEIN 1502  
DB 1028 LNLEANTVADGALAMEKGLASLSEMEVEGELEKELEFDTNMDAVQMVITEAQKYDTR 1087  
QY 1503 ARKAKNSVTSLSIINDLLEQLGOLDTVDLNKLNEIEGTLNKAKDEMKVSDLRKVSDE 1562  
DB 1088 AKNGVITQDTLNTDGLLHMDQPLSVDEGLVLEQLKSRKTQIN-SQLAPMKESE 1146  
QY 1563 NEAKQEAAMNDYNRDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1608  
DB 1147 ERAQQRGHLLHLETSIDGILLADVKLENIRDLNLPQCYNTQALEQ 1192

! TYPE: amino acid  
! TOPOLOGY: linear  
! MOLECULE TYPE: protein  
US-08-317-450B-15

Query Match 28.9%; Score 2516.5; DB 1; Length 1111;  
Best Local Similarity 39.7%; Pred. No. 2.2e-138;  
Matches 486; Conservative 215; Mismatches 385; Indels 137; Gaps 11;  
QY 319 CLPFFNDRPWRRAATAESASECLPCDNGRSQBCYFDPPELYRSTGHGHCNCQNDTGAH 378  
Db 9 CLCFSLLLPAARATSRRE----VCDNGKSRQCFIDRELLHRTGTNGFRCLNCNDNTDGIH 64  
QY 379 CBRCHENFRLLGNNAACSSCHGSPVGSLSQCDSTGRCSCKPGVWMDKDCRCQPGFSLT 438  
Db 65 CEKCKNGFYRHRDRCLPCNCSKGSLSARCDNSGRCSCKPGVTCARCDRLCPGFHMLT 124  
QY 439 BAGC-----RPGSCDPSGIDECNVETGRCVKDNVGFNCBRCCKPGFNFLESSNPR 490  
Db 125 DAGCTQDQRLDSKDCDPAAGTAGFC--DAGRCVCKPVTGRCDCRCRSGYNYLDGNGPE 182  
QY 491 GTPCPCFGHSSVCTNAVYSVYSISSTFQIDEDGNRAEQRDGSBASLEWSERODIAVI 550  
Db 183 GCTQCPCYCHSASCRSSAAYSVHKITSTPHQVDGKAVORNGSPAKLQWSQRHQDFSS 242  
QY 551 SDSYPRFYIAPAKELGKOVLSYGONLSPSFRVDRDRTLSAEDLVLEGAGLVSVPLIA 610  
Db 243 AQRLDPIYFVAPAKFLGNQVSGLSQSDPYRDRGRHPSAHDVILEGAGLRITAPLMP 302  
QY 611 QGNSYSETTVYFRLEHATDYPWRPALTPFEFOKLNNLTSIKIRGTYSERSAGYLD 670  
Db 303 LKLTLPGLTKTYTFRNLHPNSNWSPLSYFEYRLLRLNLTAIRATYGEYSTGYIDN 362  
QY 671 VTLASRPGFVPATVSECTCEVGVGQFCWELSGYRRETPNLGYPSPCVLCAACNGHS 730  
Db 363 VTLISARPVSGAPAPVVEQICIPVGYKQFCQDCASGYKRSARLPGFTCLPCNCQG-G 421  
QY 731 ETCDEPTGVCNCRDNTAGHCCKSCDGYGDTAGTSSDCQPCPGGSSCAVVPKTEV 790  
Db 422 GACDPTGDCYSGDENPDIEACDPIGFVNDPHDPRS--CKPCCHNGFSCSVIPETEEV 479  
QY 791 VCTNCPGTGTGRKCELCDDGYFGDPLGRNGPVRLCRLCQCSNDIDPNVAGNCNRLTGEC 850  
Db 480 VCNPCPGVGTGARCELCAQGYFGDPFGEHGPVRCPCQCCNSNDPFSASGNCNDRLTGRCL 539  
QY 851 KCIYNTAGFYCDRCCKDFFGNPLAPNADKCKACNCNPGYTMKQSSCNVPTGQCECLPH 910  
Db 540 KCIHNTAGIYCDCKAGYFGDPLAPNADKCRACNPNMGS----- 580  
QY 911 VTGQDCGACDPGYNLQSGGGERCDCHALGSTNGQCDIRTCQCECQPGITGQHCEV 970  
Db 581 ----- 580  
QY 971 NHFGFGECKPCDCHPEGSLSLQCKDDGRCEBGFVGNRCDOCEENFYNRSWPGQCE 1030  
Db 581 -----EPVG-----CRSDGTVCVKPGFGPNCEH-----GAFS 608  
QY 1031 CPACYRLVKDQVADHRVKLQELSLIANLGTGDEMVTQAFEDRLKEAREVMDLLRAQ 1090  
Db 609 CPACYNQVKIQMDQFMQQLQRMELISKAQGGGVVPTDELEGRMQAEALQDILRDAQ 668  
QY 1091 DVKDVONLMDRLQRYNNLSSQISFLQNTIETGNLAFQARAHVENTERLLEIASR 1150  
Db 669 ISGASRSLGLQAKVRSGENSQSRDLDDKMTVERVRLGSGYQNRVDRTHRLITQML 728  
QY 1151 ELEKAKVAAANVSQTPESTGDPNNMTLLAEAPKLAERHKQEADDIVRVAKTANDTSTE 1210  
Db 729 SLAASEASLGNTNIPASDHVGVFNGFKSLAQEATRLAESHVESASNMQLTRETEDYSKQ 788  
QY 1211 AYNLLRLTL-----AGENQTAFEIEELNRKYEQAKNISOLEKQAAARVHEEAKRAGD 1263  
Db 789 AUSLVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTKSLAQQLTREATQAEIADRSTQH 847

QY 1264 AVEIYASVAQLSPDSETLE-NEANNIKWEAENLEQIDQKLDKYEDLREDMRGKELEVK 1322  
Db 848 SLRLDSVSPLOGVSQSFQVEEAKIKQKADSLSLVTRHMDDEFKRTQKNLGNWKEEAQ 907  
QY 1323 NLEKKGKTEQQTADQLLARADAALAEBAAKKGRDTLOEANDILNNLKDFDRRVNDNKT 1382  
Db 908 QLLQNGKSGREKSDQLLSRANLAKSPAQEALESALSGNATFYEVEISILKNLREFDLQVDNRKA 967  
QY 1383 ABEALRKIPAINQTTTEANEKTRAQALGSAADAATAKAKKAHEAERIASAVQKNATS 1442  
Db 968 EABEAMKRLSYISQKVSADSKTQQAERALGSAADAQAKNGAGBALEISSIEQEIQS 1027  
QY 1443 TKAEABETFAEVTDLONEVNNMLKQLQEAEBELKRRKQDDADQDMMWAGVASQAAQAEIN 1502  
Db 1028 LNLEANTADGALAMEKGLASLASEMREVEGELERKELSPDTNMDAVQMVITEAQKVDIR 1087  
QY 1503 ARKAKSVTSLLSIINDLLEQLG 1525  
Db 1088 AKNAGVTIQDTLNTLDGILLHMG 1110

Search completed: May 18, 2004, 15:02:26  
Job time : 19.1718 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 40.9344 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-14

Perfect score: 8713  
Sequence: 1 MRGSHRAAPALPRGRMLWPV.....EDIRKTLPSGCFNTPSIEKP 1609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PTC\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PTCUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8713	100.0	1609	14	US-10-037-182-14
2	8713	100.0	1609	14	Sequence 14, Appl
3	8709	100.0	1609	9	US-10-299-058-12
4	8709	100.0	1609	15	US-09-938-275-11
5	8544	98.1	1576	14	US-10-372-683-36
6	8161	93.7	1607	9	US-10-037-182-16
7	8148	93.5	1605	14	US-09-938-275-10
8	8038	92.3	1572	14	US-10-037-182-18
9	3611	41.4	1587	9	US-09-845-583-10
10	3611	41.4	1587	12	US-10-262-839-210
11	3609	41.4	1575	12	US-10-262-839-212
12	3240	37.2	1575	12	US-10-369-493-6816
13	2637	30.3	1193	9	US-09-756-071B-13
14	2637	30.3	1193	12	US-10-392-113-14
15	2637	30.3	1193	14	US-10-171-311-115

Sequence 13, Appl	1193	30.3	1193	14	US-10-227-738-13
Sequence 31, Appl	1193	30.3	1193	14	US-10-053-662A-31
Sequence 390, App	1193	30.3	1193	15	US-10-295-027-390
Sequence 1269, Ap	1193	30.3	1193	15	US-10-295-027-1269
Sequence 26, Appl	1193	30.3	1193	15	US-10-603-725-26
Sequence 147, App	1193	30.3	1193	16	US-10-188-832-147
Sequence 28, Appl	1172	30.2	1172	15	US-10-603-725-28
Sequence 30, Appl	1193	30.2	1193	15	US-10-603-725-30
Sequence 32, Appl	1193	30.2	1193	15	US-10-603-725-32
Sequence 2, Appl	1172	30.1	1172	15	US-10-053-662A-2
Sequence 15, Appl	1190	30.0	1190	14	US-09-756-071B-15
Sequence 15, Appl	1111	28.9	1111	9	US-10-392-113-15
Sequence 36, Appl	1111	28.9	1111	14	US-10-227-738-15
Sequence 12, Appl	1171	28.2	1171	15	US-10-603-725-36
Sequence 32, Appl	1192	28.2	1192	12	US-10-392-113-12
Sequence 34, Appl	1192	28.2	1192	14	US-10-053-662A-32
Sequence 7, Appl	1192	28.2	1192	15	US-10-603-725-34
Sequence 4, Appl	3070	20.5	3070	10	US-09-961-403-7
Sequence 2, Appl	3084	20.5	3084	9	US-09-938-275-4
Sequence 2, Appl	3084	20.5	3084	14	US-10-262-670-2
Sequence 5, Appl	3075	20.0	3075	9	US-09-938-275-5
Sequence 8, Appl	1765	19.3	1765	14	US-10-037-182-8
Sequence 113, Appl	1786	19.3	1786	9	US-09-938-275-113
Sequence 6, Appl	1786	19.3	1786	9	US-09-938-275-6
Sequence 6, Appl	1786	19.3	1786	14	US-10-037-182-6
Sequence 7, Appl	1786	18.9	1786	9	US-09-938-275-7
Sequence 10, Appl	1786	18.9	1786	14	US-10-037-182-10
Sequence 5220, Ap	2823	18.7	2823	15	US-10-369-493-5220
Sequence 5221, Ap	2823	18.7	2823	15	US-10-369-493-5221
Sequence 12, Appl	1725	18.6	1725	14	US-10-037-182-12

ALIGNMENTS

RESULT 1  
US-10-037-182-14  
; Sequence 14, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggevason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 98-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-14

Query Match	100.0%	Score 8713;	DB 14;	Length 1609;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1609;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MRGSHRAAPALPRGRMLWPVLVLA	AAAAAGCAQAAMDECTDEGRPQRCMPFVNAAF	60
Db	1	MRGSHRAAPALPRGRMLWPVLVLA	AAAAAGCAQAAMDECTDEGRPQRCMPFVNAAF	60
Qy	61	VTVVAATTCGTPPEYCVQGTGVT	KSCHLDCAGQPHLQHGAAFLTDYNNADTTWQS	120
Db	61	VTVVAATTCGTPPEYCVQGTGVT	KSCHLDCAGQPHLQHGAAFLTDYNNADTTWQS	120
Qy	121	QTMLAGVQYSSINLTILHKGADIT	TVRLKFTSRPESAIYKRTDGDGPWPYQYSG	180



Db 121 QTMAGVQVPSINLTHLKGAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYSG 180  
QY 181 SCENTYSKANRGIRTGDEEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL 240  
Db 181 SCENTYSKANRGIRTGDEEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL 240  
QY 241 QEWVTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEF 300  
Db 241 QEWVTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEF 300  
QY 301 DKLVCKNHTYGVDECKLPFNDPRWRATASASECLPCDCNGRSOECYFDPDELVS 360  
Db 301 DKLVCKNHTYGVDECKLPFNDPRWRATASASECLPCDCNGRSOECYFDPDELVS 360  
QY 361 TGHGGCTNQQDNTDGAHCRCRENFRLGNNEACSSCHCSPVGSLSSTQCDYGRCSCKP 420  
Db 361 TGHGGCTNQQDNTDGAHCRCRENFRLGNNEACSSCHCSPVGSLSSTQCDYGRCSCKP 420  
QY 421 GVMGDKCDRCQPGFHSITAGCRPCSDPSGSDENCVETGRCVKDNVEGNCRCCKPG 480  
Db 421 GVMGDKCDRCQPGFHSITAGCRPCSDPSGSDENCVETGRCVKDNVEGNCRCCKPG 480  
QY 481 FPNLESNPRGCTPCFCFHSITAGCRPCSDPSGSDENCVETGRCVKDNVEGNCRCCKPG 540  
Db 481 FPNLESNPRGCTPCFCFHSITAGCRPCSDPSGSDENCVETGRCVKDNVEGNCRCCKPG 540  
QY 541 SSEEQDIAVISDSYFRPYFAPAKFLGKQVLSYQNLSPSFRVDRDRDRLSABDLVLEGA 600  
Db 541 SSEEQDIAVISDSYFRPYFAPAKFLGKQVLSYQNLSPSFRVDRDRDRLSABDLVLEGA 600  
QY 601 GLRVSVPLIAGNSYPSSETTKVFRLEHATDTPWRPALTPPFPQKLLNLSIKIRGY 660  
Db 601 GLRVSVPLIAGNSYPSSETTKVFRLEHATDTPWRPALTPPFPQKLLNLSIKIRGY 660  
QY 661 SERSAGYLDVTLASAPFGVPATWYESTCTPVGYGGQFCMCLSGYRRETNLGPYSP 720  
Db 661 SERSAGYLDVTLASAPFGVPATWYESTCTPVGYGGQFCMCLSGYRRETNLGPYSP 720  
QY 721 CVLCAHGSETCDPETHGVNCRDNTAGPHCEKSDGYGDSGTAGTSSDCQPCPCGGSS 780  
Db 721 CVLCAHGSETCDPETHGVNCRDNTAGPHCEKSDGYGDSGTAGTSSDCQPCPCGGSS 780  
QY 781 CAVVPKTEVVCNCPGTTGKRCCLDDGYFGDPLGRNGFVRLCRLCQSDNIDPNAV 840  
Db 781 CAVVPKTEVVCNCPGTTGKRCCLDDGYFGDPLGRNGFVRLCRLCQSDNIDPNAV 840  
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPLAPNADPKCKACNCPYGTMKQSSCMP 900  
Db 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNPLAPNADPKCKACNCPYGTMKQSSCMP 900  
QY 901 VTGOCECLPHVTGDCGACDPGFYNLQSGOCERCDCCHALGSTNGQCDIRTGCEQCPGI 960  
Db 901 VTGOCECLPHVTGDCGACDPGFYNLQSGOCERCDCCHALGSTNGQCDIRTGCEQCPGI 960  
QY 961 TGOHCERCEVNHFGFEGCKPCDCHPEGSLSLOKDDGRCCEGFGVGNRCQCEENYF 1020  
Db 961 TGOHCERCEVNHFGFEGCKPCDCHPEGSLSLOKDDGRCCEGFGVGNRCQCEENYF 1020  
QY 1021 YNRSWPGQCECPACVRLVKQVADHRVKLQLESILIANLGTGBMTWDOAFEDRLKEAR 1080  
Db 1021 YNRSWPGQCECPACVRLVKQVADHRVKLQLESILIANLGTGBMTWDOAFEDRLKEAR 1080  
QY 1081 EVMDDLREAQDVQDQVNDLRLQVNNLTSSQISRLQNRINTIETGNLAEOQARHVEN 1140  
Db 1081 EVMDDLREAQDVQDQVNDLRLQVNNLTSSQISRLQNRINTIETGNLAEOQARHVEN 1140  
QY 1141 TERLIEIASRELEKAKVAAANVSUPTGDPNNMTLLAEARKLAERHKEADDIRV 1200  
Db 1141 TERLIEIASRELEKAKVAAANVSUPTGDPNNMTLLAEARKLAERHKEADDIRV 1200  
QY 1201 AKTANDTTEANLLRLTAGENQTAPEIEELNRYEQAKNISODLEKQAAHYHEEAKRA 1260  
Db 1201 AKTANDTTEANLLRLTAGENQTAPEIEELNRYEQAKNISODLEKQAAHYHEEAKRA 1260

RESULT 2

US-10-299-058-12  
; Sequence 12, Application US/10299058  
; Publication No. US20030103975A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, JONATHAN C.R.  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION  
; FILE REFERENCE: 1720-1-002 CIP  
; CURRENT APPLICATION NUMBER: US/10/299,058  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/706,235  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/163,199  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-299-058-12

Query Match 100.0%; Score 8713; DB 14; Length 1609;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALRPRGRLPVLAFLAALAAAAAGCAQAAMDECTDEGGRPCRCMPEFVNAAFN 60  
Db 1 MRGSHRAAPALRPRGRLPVLAFLAALAAAAAGCAQAAMDECTDEGGRPCRCMPEFVNAAFN 60  
QY 61 VTVVATNTCGTPPEYCVQGTGVTGKTSCHLQDAGPHLOHGAFLTDYNNQADTTWQS 120  
Db 61 VTVVATNTCGTPPEYCVQGTGVTGKTSCHLQDAGPHLOHGAFLTDYNNQADTTWQS 120  
QY 121 QTMLAGVQVPSINLTHLKGAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYSG 180  
Db 121 QTMLAGVQVPSINLTHLKGAFDITYVRLKFTSRPESFAIYKRTREDGPWIPYQYSG 180  
QY 181 SCENTYSKANRGIRTGDEEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL 240  
Db 181 SCENTYSKANRGIRTGDEEQALCTDEFSDISPLTGNVAFSTLEGRPSAYNFNSPVL 240  
QY 241 QEWVTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEF 300  
Db 241 QEWVTATDIRVTNLNLTGDEVFNDPKVLKSYYYAISDFAVGGRCKNGHASECMKNEF 300



Db 421 GVMGDKCDRCQGFHSLTAGCRPCSCDPSGSDICNVETGRCVCKNVGFCNCRCKPG 480  
QY 481 FFNLESNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQDGEASLEW 540  
Db 481 FFNLESNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQDGEASLEW 540  
QY 541 SSRQDIIVISDYPFRPIAFAKELGKQVLSYGQNLVSFSFRVDRDTRLAEDLVLEGA 600  
Db 541 SSRQDIIVISDYPFRPIAFAKELGKQVLSYGQNLVSFSFRVDRDTRLAEDLVLEGA 600  
QY 601 GLRVSVELIAQGSYSESTTVKVFRLHEATDYPWRPALTPPEFQKLNILNLSIKIRGTY 660  
Db 601 GLRVSVELIAQGSYSESTTVKVFRLHEATDYPWRPALTPPEFQKLNILNLSIKIRGTY 660  
QY 661 SERAGYLDVTLASARPGGVPATWBSCTCPVGYGGQFCBMLCSGYRRTPLNGLYSP 720  
Db 661 SERAGYLDVTLASARPGGVPATWBSCTCPVGYGGQFCBMLCSGYRRTPLNGLYSP 720  
QY 721 CVLCAACGHSSETCDPPTGVCNCRDNTAGPHEKCSGDIYGGSTAGTSDCQPCPCPGSS 780  
Db 721 CVLCAACGHSSETCDPPTGVCNCRDNTAGPHEKCSGDIYGGSTAGTSDCQPCPCPGSS 780  
QY 781 CAVVPKTEWCTNCTGTTGRCBLCDGYPGDPGLRNGPVRCLRCQCSNDIDPNAV 840  
Db 781 CAVVPKTEWCTNCTGTTGRCBLCDGYPGDPGLRNGPVRCLRCQCSNDIDPNAV 840  
QY 841 NCNRLTGECLKIYNTAGFYCDRCCKDGGFNGPAPNADKCKACNCPYGTMKQSSCNP 900  
Db 841 NCNRLTGECLKIYNTAGFYCDRCCKDGGFNGPAPNADKCKACNCPYGTMKQSSCNP 900  
QY 901 VTGQCECLPHVTGQDCGACDPFYNLQSGQGCRCDCCHALSTWGQCDIRTGQCECQPGI 960  
Db 901 VTGQCECLPHVTGQDCGACDPFYNLQSGQGCRCDCCHALSTWGQCDIRTGQCECQPGI 960  
QY 961 TGQHCERCEVNHFGPGCEKPCDCHEGSLSLQCKDDGRCCEGFGVGNRCDOCEENYF 1020  
Db 961 TGQHCERCEVNHFGPGCEKPCDCHEGSLSLQCKDDGRCCEGFGVGNRCDOCEENYF 1020  
QY 1021 YNRSWPGCEACVYLVKQVADHRVKLOBESLIANLGTGDEMVDQAFEDRLKEAR 1080  
Db 1021 YNRSWPGCEACVYLVKQVADHRVKLOBESLIANLGTGDEMVDQAFEDRLKEAR 1080  
QY 1081 EVMDDLREAOQVQDQNDLMDRLQVNTLSQISRLQNIIRNTIETGNLAEQARAHVEN 1140  
Db 1081 EVMDDLREAOQVQDQNDLMDRLQVNTLSQISRLQNIIRNTIETGNLAEQARAHVEN 1140  
QY 1141 TERLIEIASRELEKAKVAANVSUPTQESTGDPNNMTLLAEARKLAERHKQADDIRV 1200  
Db 1141 TERLIEIASRELEKAKVAANVSUPTQESTGDPNNMTLLAEARKLAERHKQADDIRV 1200  
QY 1201 AKTANDTSTAYNLLRLTAGSNQTAPEIBELNRKYEQAQNIISQLEKQAARVHEAKRA 1260  
Db 1201 AKTANDTSTAYNLLRLTAGSNQTAPEIBELNRKYEQAQNIISQLEKQAARVHEAKRA 1260  
QY 1261 GKAVEIYASVQLSPLDSEITLNEANNIKWEAENLEOLIDOKLYEDLREDMRGKELE 1320  
Db 1261 GKAVEIYASVQLSPLDSEITLNEANNIKWEAENLEOLIDOKLYEDLREDMRGKELE 1320  
QY 1321 VKNLLEKGTQEQTDQDLARADAKALAEAAKKGRTDLOEANDIILNNLKDFDRRVND 1380  
Db 1321 VKNLLEKGTQEQTDQDLARADAKALAEAAKKGRTDLOEANDIILNNLKDFDRRVND 1380  
QY 1381 KTAABENLRKIPAINQTTIETANEKTRAQALGSAADATKAKAHEARISAVQKNA 1440  
Db 1381 KTAABENLRKIPAINQTTIETANEKTRAQALGSAADATKAKAHEARISAVQKNA 1440  
QY 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKQDDADQMMWAGMASQAAQAE 1500  
Db 1441 TSTKAEARTFAEVTDLNEVNNMLKQLEAEKELKQDDADQMMWAGMASQAAQAE 1500  
QY 1501 INARKAKNSVTLSLSIINDLLEIOLGOLDTVDLKNLEIEGLTNLAKDEMKSVDLDRKVS 1560  
Db 1501 INARKAKNSVTLSLSIINDLLEIOLGOLDTVDLKNLEIEGLTNLAKDEMKSVDLDRKVS 1560

QY 1561 LENEAKQOEAAIMDYNRDIEIMKDINLEDIRKTLPSGCNFTPSIEKP 1609  
Db 1561 LENEAKQOEAAIMDYNRDIEIMKDINLEDIRKTLPSGCNFTPSIEKP 1609

## RESULT 4

US-10-372-683-36  
; Sequence 36, Application US/10372683  
; Publication NO. US20040009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRITSEN, MARY E.  
; APPLICANT: PEALE JR, FRANKLIN V.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
; FILE REFERENCE: P1928R1P1  
; CURRENT APPLICATION NUMBER: US/10/372,683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271,690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344,534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 36  
; LENGTH: 1609  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; US-10-372-683-36

Query Match 100.0%; Score 8709; DB 15; Length 1609;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGSHRAAPALPRGRLLPWLAVLAAAAAGCAQAAMDECTDEGGPQRCMPFVNAAFN 60  
Db 1 MRGSHRAAPALPRGRLLPWLAVLAAAAAGCAQAAMDECTDEGGPQRCMPFVNAAFN 60  
QY 61 VTVATNTCGTPPEYCVQGTGVTATKASCHLCAQOPHLOHGAFLTDYNNQADTTWQS 120  
Db 61 VTVATNTCGTPPEYCVQGTGVTATKASCHLCAQOPHLOHGAFLTDYNNQADTTWQS 120  
QY 121 QTMLAGVQYSSINLTLHLGKAFDITYVRLKFTSPESFAIYKRTREDGPMIPYQYSG 180  
Db 121 QTMLAGVQYSSINLTLHLGKAFDITYVRLKFTSPESFAIYKRTREDGPMIPYQYSG 180  
QY 181 SCENTYSKANEFTRTGDEQQAALCTDEPSDI SPLTGGNVAFSTLGRPSAYNFDNSPVL 240  
Db 181 SCENTYSKANEFTRTGDEQQAALCTDEPSDI SPLTGGNVAFSTLGRPSAYNFDNSPVL 240  
QY 241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF 300  
Db 241 QEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGRCCKNGHASECMKNEF 300  
QY 301 DKLVCNCKHNTYGVDCBKCLPFNDPRWRATASASECLPCDCNCRSOSCYFDPLEYRS 360  
Db 301 DKLVCNCKHNTYGVDCBKCLPFNDPRWRATASASECLPCDCNCRSOSCYFDPLEYRS 360  
QY 361 TGHGCHTNCODNTDGAHCRCRENFRLLGNNEACSSCHSPVGSLSSTQCDSYGRCSCKP 420  
Db 361 TGHGCHTNCODNTDGAHCRCRENFRLLGNNEACSSCHSPVGSLSSTQCDSYGRCSCKP 420  
QY 421 GVMGDKCDRCQGFHSLTAGCRPCSCDPSGSDICNVETGRCVCKNVGFCNCRCKPG 480  
Db 421 GVMGDKCDRCQGFHSLTAGCRPCSCDPSGSDICNVETGRCVCKNVGFCNCRCKPG 480  
QY 481 FFNLESNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQDGEASLEW 540  
Db 481 FFNLESNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFQIDEDGWRAEQDGEASLEW 540  
QY 541 SSRQDIIVISDYPFRPIAFAKELGKQVLSYGQNLVSFSFRVDRDTRLAEDLVLEGA 600  
Db 541 SSRQDIIVISDYPFRPIAFAKELGKQVLSYGQNLVSFSFRVDRDTRLAEDLVLEGA 600

QY 601 GLRVSVPLIAAGNSVSPSETTVKVFRLHEATDY PWRPALTPFPEFQKLLNNLTSIKIRGT 660  
DB 601 GLRVSVPLIAAGNSVSPSETTVKVFRLHEATDY PWRPALTPFPEFQKLLNNLTSIKIRGT 660  
QY 661 SRSAGYLDVTLASARPGVGPATWVSCCTPVGYGQPCFEMCLSGYRRRTPLNLPYSP 720  
DB 661 SRSAGYLDVTLASARPGVGPATWVSCCTPVGYGQPCFEMCLSGYRRRTPLNLPYSP 720  
QY 721 CVLCAAGHSETCDPBTGVCNCRDNTAGPHCKSDGYVGDSTAGTSSDCPCPCPGSS 780  
DB 721 CVLCAAGHSETCDPBTGVCNCRDNTAGPHCKSDGYVGDSTAGTSSDCPCPCPGSS 780  
QY 781 CAVVPKTEVCTNPTGTTGKRCBLCDGYPGDFLGRNGPVRCLRCQCSNDIDPNAVG 840  
DB 781 CAVVPKTEVCTNPTGTTGKRCBLCDGYPGDFLGRNGPVRCLRCQCSNDIDPNAVG 840  
QY 841 NCNRLTGECLKCIYNTAGYCDRCXGDFGNGFLAPNADKCKACNCNPGYGMKQSSCNP 900  
DB 841 NCNRLTGECLKCIYNTAGYCDRCXGDFGNGFLAPNADKCKACNCNPGYGMKQSSCNP 900  
QY 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCERCDCHALGNTGQCDIRTGQCECPGI 960  
DB 901 VTGQCECLPHVTGQDCGACDPGFYNLQSGQCERCDCHALGNTGQCDIRTGQCECPGI 960  
QY 961 TQHCERCENHFGPGPECKCDCHPEGSLSLOCKDGRCEGFGVGNRCDCQCEENYF 1020  
DB 961 TQHCERCENHFGPGPECKCDCHPEGSLSLOCKDGRCEGFGVGNRCDCQCEENYF 1020  
QY 1021 YNRSWPGCQCPACVRLVKDVADHRVKLQELLESILIANLGTDEMVTQDAFEDRLKEAER 1080  
DB 1021 YNRSWPGCQCPACVRLVKDVADHRVKLQELLESILIANLGTDEMVTQDAFEDRLKEAER 1080  
QY 1081 EYMDLLREADQVQDVQDNLQVNNLTLSSQISRLQNRINTIETGNLABQARAHVEN 1140  
DB 1081 EYMDLLREADQVQDVQDNLQVNNLTLSSQISRLQNRINTIETGNLABQARAHVEN 1140  
QY 1141 TERLIISARELEKAKVAANVSVPQSTGPNNTLLAEARKLAERHKEADDDIVRV 1200  
DB 1141 TERLIISARELEKAKVAANVSVPQSTGPNNTLLAEARKLAERHKEADDDIVRV 1200  
QY 1201 AKTANDTSEAYNLLRTLAGEQTAFIEELNRKYEQAKNISQDLEKQAAVHBEAKRA 1260  
DB 1201 AKTANDTSEAYNLLRTLAGEQTAFIEELNRKYEQAKNISQDLEKQAAVHBEAKRA 1260  
QY 1261 GDKAVEIYASVACLSPIDSETLENEANNIKMAENLQLIQKLDYEDLREDMKGKLE 1320  
DB 1261 GDKAVEIYASVACLSPIDSETLENEANNIKMAENLQLIQKLDYEDLREDMKGKLE 1320  
QY 1321 VKNLLKKGTEQQTADOLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFDRRVNDN 1380  
DB 1321 VKNLLKKGTEQQTADOLLARADAAKALAEAAKKGRTDLOEANDILNNLKDFDRRVNDN 1380  
QY 1381 KTAABEALRKIPAINQTIITEANEKTRAQALGSAADAATEAKNKAHEARTASAVQKNA 1440  
DB 1381 KTAABEALRKIPAINQTIITEANEKTRAQALGSAADAATEAKNKAHEARTASAVQKNA 1440  
QY 1441 TSTKABAEARTFAVTDLDNEVNNMLKQLEAEKELKRKODDADQDMWAGMASQAAQAE 1500  
DB 1441 TSTKABAEARTFAVTDLDNEVNNMLKQLEAEKELKRKODDADQDMWAGMASQAAQAE 1500  
QY 1501 INARKAKNSVTSLLSIINDLLEQLGOLDTVDLNKLNEIEGTLNKAKDEMKVSDLDKQVSD 1560  
DB 1501 INARKAKNSVTSLLSIINDLLEQLGOLDTVDLNKLNEIEGTLNKAKDEMKVSDLDKQVSD 1560  
QY 1561 LENEAKQQAIAINDYNRDIEEMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
DB 1561 LENEAKQQAIAINDYNRDIEEMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609

RESULT 5  
US-10-037-182-16  
; Sequence 16, Application US/10037182  
; Publication No. US20030044899A1

; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-16

Query Match 98.1%; Score 8544; DB 14; Length 1576;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 QAAWDECTDEGGPQRCMPPEFVNAAFNVTVANTTCGTPEEYCVQTVGTGVTKSHCLCD 93  
DB 1 QAAWDECTDEGGPQRCMPPEFVNAAFNVTVANTTCGTPEEYCVQTVGTGVTKSHCLCD 60  
QY 94 AGPHLOHGAFLITVNNQADTTWQSQTMLAGVQVPSINLTLHLGKAPDITVRLKPH 153  
DB 61 AGPHLOHGAFLITVNNQADTTWQSQTMLAGVQVPSINLTLHLGKAPDITVRLKPH 150  
QY 154 TSPESEFAIKYRTREDDGFWPIQYVYSGSCENTYSKANRGFIRTGGBEQQALCTDEFSDIS 213  
DB 121 TSPESEFAIKYRTREDDGFWPIQYVYSGSCENTYSKANRGFIRTGGBEQQALCTDEFSDIS 180  
QY 214 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTAIDIRVTLNRLNTFGDEVNDPKVLKSY 273  
DB 181 PLTGGNVAFSTLEGRPSAYNFDNSPVLQEWVTAIDIRVTLNRLNTFGDEVNDPKVLKSY 240  
QY 274 YYAISDFAVGCRCKCNHASECMKNFEKLVCKNCKNTYGVDCCKLPPNDRPWRATA 333  
DB 241 YYAISDFAVGCRCKCNHASECMKNFEKLVCKNCKNTYGVDCCKLPPNDRPWRATA 300  
QY 334 ESASECLPCDCNCRSQBCYDPPELYRSTGHGCHTNCQDNTDGAHCRCRNFRLGNNE 393  
DB 301 ESASECLPCDCNCRSQBCYDPPELYRSTGHGCHTNCQDNTDGAHCRCRNFRLGNNE 360  
QY 394 ACSCHSCPVGSLSTQCDISYGRCSCKPGVMDKCDRCQPGFHSILTBAQCPCSDPSGSI 453  
DB 361 ACSCHSCPVGSLSTQCDISYGRCSCKPGVMDKCDRCQPGFHSILTBAQCPCSDPSGSI 420  
QY 454 DECNVETGRVCVKDNVEGFNCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNNAVGSVY 513  
DB 421 DECNVETGRVCVKDNVEGFNCERCKPGFNLSSNPRGCTPCFCFGHSSVCTNNAVGSVY 480  
QY 514 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 573  
DB 481 SISSTFQIDEDGWRAEQRDGSEASLEWSSERQDIAVISDSYFPFYFIAPAKFLGKQVLSY 540  
QY 574 GONLSRFRVDRDTRLASDELVLGAGLAVSVPLIAQNSYSPSETTVKVPFLHEATDY 633  
DB 541 GONLSRFRVDRDTRLASDELVLGAGLAVSVPLIAQNSYSPSETTVKVPFLHEATDY 600  
QY 634 PWRPALTPFPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVGPATWVSCCTCP 693  
DB 601 PWRPALTPFPEFQKLLNNLTSIKIRGTYSERSAGYLDVTLASARPGVGPATWVSCCTCP 660  
QY 694 VGYGQCECLSGYRRETPNLGPSPCVLCACNHSETCDPBTGVCNCRDNTAGPHCKE 753  
DB 661 VGYGQCECLSGYRRETPNLGPSPCVLCACNHSETCDPBTGVCNCRDNTAGPHCKE 720  
QY 754 CSDGYGDSTAGTSSDCQPCPCPGSSCAVVPKTKVWCTNCTGTTGKRCCELCDGCFG 813

Db 721 CSBGYYGDSSTAGTSSDCQPCPCFGSSCAVVPKTVCTNGTCTTKRCELDGDFG 780
QY 814 DPLGRNGPVLRLCLCOCSNDIDNAGVNCNRLTGBCLKCIYNTAGFYCDRCXGDFGNPL 873
Db 781 DPLGRNGPVLRLCLCOCSNDIDNAGVNCNRLTGBCLKCIYNTAGFYCDRCXGDFGNPL 840
QY 874 APNPADKCAKACNCPYGTWKQSSCNPTVGTGQCECLPHVTGQCGACDPGFYNLQSGQCE 933
Db 841 APNPADKCAKACNCPYGTWKQSSCNPTVGTGQCECLPHVTGQCGACDPGFYNLQSGQCE 900
QY 934 RCDCHALGSTNGGCDIRTCQCECPGIGITQHCERCEVNHFGPGGCKPCDCHPEGSL 993
Db 901 RCDCHALGSTNGGCDIRTCQCECPGIGITQHCERCEVNHFGPGGCKPCDCHPEGSL 960
QY 994 QCKDDGRCEGFGVGNRCQCEENFYNRSWFGQCEPCACVRLVKDQVADHRVKLOELE 1053
Db 961 QCKDDGRCEGFGVGNRCQCEENFYNRSWFGQCEPCACVRLVKDQVADHRVKLOELE 1020
QY 1054 SLITANLTGDEWMTDOAFEDRLKEABREVMDLRLRAQDVQDQNLMDRLQVNTLSQ 1113
Db 1021 SLITANLTGDEWMTDOAFEDRLKEABREVMDLRLRAQDVQDQNLMDRLQVNTLSQ 1080
QY 1114 ISRLQNRITBETGNLAQCAHVAHNTERLIEIASRELEKAKVAAANVSVPQESTGDP 1173
Db 1081 ISRLQNRITBETGNLAQCAHVAHNTERLIEIASRELEKAKVAAANVSVPQESTGDP 1140
QY 1174 NMWTLAABARKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTAGENOTAFIEBELN 1233
Db 1141 NMWTLAABARKLAERHKEADDIIVRAKTANDTSTEAYNLLRLTAGENOTAFIEBELN 1200
QY 1234 RYEQAKNTSQLEKQAAVHEEAKRAGDKAVEIYASVAQLSPIDSETLEANEANNIWEA 1293
Db 1201 RYEQAKNTSQLEKQAAVHEEAKRAGDKAVEIYASVAQLSPIDSETLEANEANNIWEA 1260
QY 1294 ENLEQIDQKDYEDLREDMRGKEVKNLEKGTQEQOTADQOLARADAALABEAA 1353
Db 1261 ENLEQIDQKDYEDLREDMRGKEVKNLEKGTQEQOTADQOLARADAALABEAA 1320
QY 1354 KXGRDTLQANDILNNLKDFDRVNDNKTAAEALRKIPAINQITTEANEKTRAEQAALG 1413
Db 1321 KXGRDTLQANDILNNLKDFDRVNDNKTAAEALRKIPAINQITTEANEKTRAEQAALG 1380
QY 1414 SAAADATEAKNAKHAERIASVQKATSTKAEABRTFAEVTDLQNEVNNMLKQLEAEK 1473
Db 1381 SAAADATEAKNAKHAERIASVQKATSTKAEABRTFAEVTDLQNEVNNMLKQLEAEK 1440
QY 1474 ELKRRQDDADQDMMAGMASQAQAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1533
Db 1441 ELKRRQDDADQDMMAGMASQAQAEINARKAKNSVTSLLSIINDLLEQLGQDITVDLN 1500
QY 1534 KLEIEGTLLKAKDEMYSDLDKVSQDLENAKQAEAAINDYNDIEEIMKDINLEDIR 1593
Db 1501 KLEIEGTLLKAKDEMYSDLDKVSQDLENAKQAEAAINDYNDIEEIMKDINLEDIR 1560
QY 1594 KTLPSGCFNTPSIEKP 1609
Db 1561 KTLPSGCFNTPSIEKP 1576
RESULT 6
US-09-938-275-10
; Sequence 10, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938.275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1607
; TYPE: PRT
; ORGANISM: Mus Musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P02468
; DATABASE ENTRY DATE: 1989-07-01
US-09-938-275-10

Query Match 93.7%; Score 8161; DB 9; Length 1607;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 1492; Conservative 61; Mismatches 54; Indels 2; Gaps 1;

QY 1 MRGSHRAAPALRPRGRLPVLAALAAACACAAAMDECTDDEGRPQRCWPFVNAAFN 60
Db 1 MTGGGGAALANQPRGLNPLLAFL--HAGACVRAAMDECADEGRPQRCWPFVNAAFN 58
QY 61 VTVVATNTCGTPPEYCVQGTGVTGKSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQS 120
Db 59 VTVVATNTCGTPPEYCVQGTGVTGKSCHLCDAGQPHLQHGAAFLTDYNNQADTTWQS 118
QY 121 QTMLAGVOYPPSINLTLLHGAFOITVYRLKFHTSRPESPAIKYKTRDGDPMIPYQYSG 180
Db 119 QTMLAGVOYPPSINLTLLHGAFOITVYRLKFHTSRPESPAIKYKTRDGDPMIPYQYSG 178
QY 181 SCENTYSKANRGFIRTGDEBOQALCTDEFSDISPLTGNVAFSTLEGPSAYNFDNSPVL 240
Db 179 SCENTYSKANRGFIRTGDEBOQALCTDEFSDISPLTGNVAFSTLEGPSAYNFDNSPVL 238
QY 241 QEWVTATDIRVTLNRLNTFGDEVENDPKLKYVYAIISDPAVGRCCKNGHASECKNEF 300
Db 239 QEWVTATDIRVTLNRLNTFGDEVENDPKLKYVYAIISDPAVGRCCKNGHASECKNEF 298
QY 301 DKLVNCHNTYGVDCSKLPPFNDRPWRATASASECLPCDCNGRSQECYDPELYRS 360
Db 299 DKLVNCHNTYGVDCSKLPPFNDRPWRATASASECLPCDCNGRSQECYDPELYRS 358
QY 361 TGHGHCHTNCODNDGAHCRCRNFRLGNNAEACSSCHSPVGSLSSTOCDSDYGRCSCKP 420
Db 359 TGHGHCHTNCODNDGAHCRCRNFRLGNNAEACSSCHSPVGSLSSTOCDSDYGRCSCKP 418
QY 421 GVMGDKDCRCOPGPHSITTEAGCRPCSCDPSGSDIDECNVETGRCVCKNDVEGFNCERCKPG 480
Db 419 GVMGDKDCRCOPGPHSITTEAGCRPCSCDPSGSDIDECNVETGRCVCKNDVEGFNCERCKPG 478
QY 481 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFOIDEDGWRAEORDGEASLEW 540
Db 479 FFNLESSNPRGCTPCFCFGHSSVCTNAVGYSVYSISSTFOIDEDGWRAEORDGEASLEW 538
QY 541 SSERQDIATVSDSYPPRYPTAPAKPLGKQVLSYQMLSPSFVDRDRDTRLASDLDVLEGA 600
Db 539 SSDRQDIATVSDSYPPRYPTAPAKPLGKQVLSYQMLSPSFVDRDRDTRLASDLDVLEGA 598
QY 601 GLRYSVPLIAQNSYPSSETTVKIVFRLHEATDYPWRPALTPPFFQKLLNNLTISKIRGTY 660
Db 599 GLRYSVPLIAQNSYPSSETTVKIVFRLHEATDYPWRPALTPPFFQKLLNNLTISKIRGTY 658
QY 661 SERSAGYLDVTLASARPGGVPATWVESCTCPVGGGQFCMCLSGYRRETNLGPYSP 720
Db 659 SERTAGYLDVTLASARPGGVPATWVESCTCPVGGGQFCMCLSGYRRETNLGPYSP 718
QY 721 CVLCAKNGHSETCDPETGVNCNCRDNTAGPHCEKCSQDGYTGDSTAGTSSDCQPCPCGSS 780
Db 719 CVLCAKNGHSETCDPETGVNCNCRDNTAGPHCEKCSQDGYTGDSTAGTSSDCQPCPCGSS 778
QY 781 CAVVPKTKVNVCTNCPGTGKCELCDDGYFDDPLGRNGPVLRLCLCOCSNDIDNAGV 840
Db 779 CAVVPKTKVNVCTNCPGTGKCELCDDGYFDDPLGRNGPVLRLCLCOCSNDIDNAGV 838
QY 841 NCNLTGECCLKIYNTAGFYCDRCXGDFGNPLAPNPADKCAKACNCPYGTWKQSSCN 900
Db 839 NCNLTGECCLKIYNTAGFYCDRCXGDFGNPLAPNPADKCAKACNCPYGTWKQSSCN 898

QY 901 VTGQCECLPHVTGQCGACDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGI 960  
DB 899 VTGQCCQLPHVSGRDCGTDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGI 958  
QY 961 TGOHCERCEVNHFGPGPECKEPCDCHPEGSLSLQCKDDGRCEBREGFGVGNRCDCQCEENYF 1020  
DB 959 TGOHCERCEVNHFGPGPECKEPCDCHPEGSLSLQCKDDGRCEBREGFGVGNRCDCQCEENYF 1018  
QY 1021 YNRSWFGQCECPACRYLVKDVADHRVKLQELLESILIANLGTGDMVTDOAFEDRLKEAER 1080  
DB 1019 YNRSWFGQCECPACRYLVKDVADHRVKLQELLESILIANLGTGDMVTDOAFEDRLKEAER 1078  
QY 1081 EWDLLREAOYKVDONLMDRLQVNNLTLSQISRLQNRNRTIETGNLAEOABAHVEN 1140  
DB 1079 EYTDLLREAOYKVDONLMDRLQVNNLTLSQISRLQNRNRTIETGNLAEOABAHVEN 1138  
QY 1141 TERLLEIASRELEKAKVAAANVSVPQSTGPNPNMTLLAEBARKLABRHKQEAADDIVRV 1200  
DB 1139 TERLLEIASRELEKAKVAAANVSVPQSTGPNPNMTLLAEBARKLABRHKQEAADDIVRV 1198  
QY 1201 AKTANDTSTEANVLLRLTLAGENQTAPEIEBLNRKYEQAKNISQLEKQAAARVHEAKRA 1260  
DB 1199 AKTANETSAAEYNLLRLTLAGENQTAPEIEBLNRKYEQAKNISQLEKQAAARVHEAKRA 1258  
QY 1261 GDAVEIIVASVAQLSPDSETLNENANNIKMAENLEOLIDOKLXDYEDLREDMRGKELE 1320  
DB 1259 GDAVEIIVASVAQLSPDSETLNENANNIKMAENLEOLIDOKLXDYEDLREDMRGKELE 1318  
QY 1321 VKNLLEKGTBEOQTADQLLARAADAKALAEBAEAAKYGRDTLOEANDILNNLKDFFRRVNDN 1380  
DB 1319 VKNLLEKGTBEOQTADQLLARAADAKALAEBAEAAKYGRDTLOEANDILNNLKDFFRRVNDN 1378  
QY 1381 KTAABEALRKIPAINCTTAEANEKTRAEQAQALGSAADAATAEAKNAKHAERIASAVQKNA 1440  
DB 1379 KTAABEALRKIPAINCTTAEANEKTRAEQAQALGSAADAATAEAKNAKHAERIASAVQKNA 1438  
QY 1441 TSKABAEARTFAEVTDLNENVMNLKQLOAEKELKRRKODDADQMMAGMASQAQAE 1500  
DB 1439 TSKABAEARTFAEVTDLNENVMNLKQLOAEKELKRRKODDADQMMAGMASQAQAE 1498  
QY 1501 INARAKNSVTSLSITNDLLEQLGOLDTVDLNKLNEIEGTLNKAKDMKYSDLDKRVSD 1560  
DB 1499 INARAKNSVTSLSITNDLLEQLGOLDTVDLNKLNEIEGTLNKAKDMKYSDLDKRVSD 1558  
QY 1561 LENEAKQEAAMNDYNDRIEEMKDIRNLEDIRKTLPSGCFNTPSIEKP 1609  
DB 1559 LENEAKQEAAMNDYNDRIEEMKDIRNLEDIRKTLPSGCFNTPSIEKP 1607

RESULT 7  
US-10-037-182-18  
; Sequence 18, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tyggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1605  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-18

Query Match 93.5%; Score 8148; DB 14; Length 1605;  
Best Local Similarity 92.8%; Pred. No. 0;  
Matches 1493; Conservative 59; Mismatches 53; Indels 4; Gaps 3;  
QY 1 MRGSHRAAPALRRGRGLPVLAVLAAAAAGCAQAAMDECTDEGGPQRCMEPFVNAAFN 60  
DB 1 MTGGRAALALQPRGLPFLAVL--AAVAGCVRAAMDECADEGGPQRCMEPFVNAAFN 58  
QY 61 VTVVATNTCTPPEEYCVGTGVTGKSHLCHDAGQPHLQHGAAFLTDYNNQADTTWOS 120  
DB 59 VTVVATNTCTPPEEYCVGTGVTGKSHLCHDAGQPHLQHGAAFLTDYNNQADTTWOS 118  
QY 121 QTMLAGVQYESSNLTLHLGKAFDIYVRLKFTSRPESFAIYKRTREGDPMIPYQYSG 180  
DB 119 QTMLAGVQYESSNLTLHLGKAFDIYVRLKFTSRPESFAIYKRTREGDPMIPYQYSG 178  
QY 181 SCENTYSKANRGFIRTGDEBQALCTDEFSDISPLTGGNVAFSTLREGRSAYNFDNSPVL 240  
DB 179 SCENTYSKANRGFIRTGDEBQALCTDEFSDISPLTGGNVAFSTLREGRSAYNFDNSPVL 238  
QY 241 QEWVATDITRVTLNRLNTGDEVNDPKVLKSYVYAIISDFAVGGRCKNGHASECMKNEF 300  
DB 239 QEWVATDITRVTLNRLNTGDEVNDPKVLKSYVYAIISDFAVGGRCKNGHASECMKNEF 298  
QY 301 DKLVCNCKHNTYGVDCCKLFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYS 360  
DB 299 DKLVCNCKHNTYGVDCCKLFFNDRPWRRAATAESASECLPCDCNGRSQECYFDPPELYS 358  
QY 361 TGHGCHCTNODNTDGAHCERENFRIGNREACSSCHCSPVGSLSSTOCDSVGRCSCKP 420  
DB 359 TGHGCHCTNODNTDGAHCERENFRIGNREACSSCHCSPVGSLSSTOCDSVGRCSCKP 418  
QY 421 GVMGDKCDRCQPFHSLTEAGRCPCSDPSGSDIENCVETGRCVCKDNVEGFNCERCKPG 480  
DB 419 GVMGDKCDRCQPFHSLTEAGRCPCSDPSGSDIENCVETGRCVCKDNVEGFNCERCKPG 478  
QY 481 FFMLESNPGCTPCFPGHSSVCTNAVGSYVSISSSTFQIDEDGWRARQDSEASLEW 540  
DB 479 FFMLESNPGCTPCFPGHSSVCTNAVGSYVSISSSTFQIDEDGWRARQDSEASLEW 538  
QY 541 SSERQDIATVSDSYFPFYPIAPAKFLGKQVLSYQNLSPSFVRDRDRTLSEAEDLVLEGA 600  
DB 539 SSERQDIATVSDSYFPFYPIAPAKFLGKQVLSYQNLSPSFVRDRDRTLSEAEDLVLEGA 598  
QY 601 GLRVSVPLIAQGNYSYPSSETTVKYVFLRHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 660  
DB 599 GLRVSVPLIAQGNYSYPSSETTVKYVFLRHEATDYPWRPALTPFEFQKLLNNLTSIKIRGTY 658  
QY 661 SERSAGYLDVTLASARPGVDPATVWESCTCPVGYGGQFCMCLSGYRRETPNLGPSP 720  
DB 659 SERSAGYLDVTLASARPGVDPATVWESCTCPVGYGGQFCMCLSGYRRETPNLGPSP 718  
QY 721 CVLTCNCGHSETCDPETGVCDRCRDNTAGPHCEKSDGYIGDSSTAGTSSDCQPCPCGGSS 780  
DB 719 CVLTCNCGHSETCDPETGVCDRCRDNTAGPHCEKSDGYIGDSSTAGTSSDCQPCPCGGSS 778  
QY 781 CAVVPKTKVVCNCTGTGTGKRCCLDDGYFGDPLGRNGPVRLCHLCOCSNIDNNAV 840  
DB 779 CAVVPKTKVVCNCTGTGTGKRCCLDDGYFGDPLGRNGPVRLCHLCOCSNIDNNAV 838  
QY 841 NCNRLTGECLKCIYNTAGFYCDRCCKDGFENPLAPNADKCKACNCPYGTMKQSSCNP 900  
DB 839 NCNRLTGECLKCIYNTAGFYCDRCCKDGFENPLAPNADKCKACNCPYGTMKQSSCNP 897  
QY 901 VTGQCECLPHVTGQCGACDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGI 960  
DB 899 VTGQCCQLPHVSGRDCGTDPGFYNLQSGQGCERCDCHALGSTNGQCDIRTGQCECQPGI 957  
QY 961 TGOHCERCEVNHFGPGPECKEPCDCHPEGSLSLQCKDDGRCEBREGFGVGNRCDCQCEENYF 1020  
DB 958 TGOHCERCEVNHFGPGPECKEPCDCHPEGSLSLQCKDDGRCEBREGFGVGNRCDCQCEENYF 1017





Db 1139 MTLAEEARLAEHRKQEAADDIVRAKANTETSAYANLLRLTAGENQTALEIELNRK 1198  
Qy 1236 YEOAKNISQDLKQOARVHEEAKRAGDKAVEIYASVAQLSPDSETLEANEANNIMEAEN 1295  
Db 1199 YEOAKNISQDLKQOARVHEEAKRAGDKAVEIYASVAQLTPVDSEALENEANKIKKEAAD 1258  
Qy 1296 LEQOLDQKLYEDLREDNRGHELVKNLLEKQTEQOQTADOLLIARADAALAEAAK 1355  
Db 1259 LBRLLDQKLYEDLREDNRGHELVKNLLEKQTEQOQTADOLLIARADAALAEAAK 1318  
Qy 1356 GRDTLQEAANDIINLLKDFRRVNDNKTAAEEALRKIPAINQITTEANEKTRQAQALGSA 1415  
Db 1319 GRSTLQEAANDIINLLKDFRRVNDNKTAAEEALRKIPAINRTIAEANEKTRQAQALGNA 1378  
Qy 1416 ADATAEKNAKAEERIASAVOKNATSTKAEARTFAEVTDLNENVMKLOLEAEKEL 1475  
Db 1379 AADATEAKNAKAEERIASAAQKNATSTKADAERTFGEVTDLDNENVMKLOLEAEKEL 1438  
Qy 1476 KRQDDADQDMWAGMASQAQAEAINARKAKNSVTSLSIINDLLEQLGQDLDVLDNKL 1535  
Db 1439 KRQDDADQDMWAGMASQAQAEALNARKAKNSVSSLSQLNNLLDQLGQDLDVLDNKL 1498  
Qy 1536 NIEGTLNKADEMKVSDLDLQKVSLEENAKQEAAMNDYNDIEBIIMKDINLEDIRKT 1595  
Db 1499 NIEGSLNKADEMKASDLQKVSLESEARKQEAAMNDYNDIAEIIKDIHNLEDIRKT 1558  
Qy 1596 LPSGCENTPSIEKP 1609  
Db 1559 LFTGCENTPSIEKP 1572

RESULT 9  
US-09-845-583-10  
; Sequence 10, Application US/09845583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champliand, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-10

Query Match 41.4%; Score 3611; DB 9; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 3.8e-197;  
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;

Qy 21 LAVLAAAAAGCAQAAMDECTEGGRPQRCMEFVNAAFTVTVATNCTGTPPEYCVQT 80  
Db 10 LALLAPRAAG----AGMGACYDAGRPQRCLEPVFENAAFGRLAQASHTCGSPEDFCPHV 65  
Qy 81 GVTGVTKSCHLDCAGQPHLQHGAAFLTDVNNQADTTWQSQOTMLAGVOYPPSSINTLHLG 140  
Db 66 GAAGAGACQRCDAADPQRHNASYLTDFHSODESTWQSPMAFGVQVPTSVNITLRLG 125  
Qy 141 KAFDITVRLKHTSPESFAYIKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTGDE 200  
Db 126 KAYEITVRLKHTSPESFAYIKGRADGPWEPIQYFASQKTYGRPEGYLRPGEDE 185  
Qy 201 QCALCTDEESDLSPLTGGNVAESTLEGRESAYNFDSNPSVLQEWVTATDIRVTLNLTNFG 260

Db 186 RVAFTCTSEFSDISPLSGGNVAFSTLEGRPSAYNFEBSPGLQEWVTSTELLISLDRLNTFG 245  
Qy 261 DEVFNDPKVLKSYIYAIISDFAVGCRCKCNCHGASECMKNFEDKLVCKNKHNTYGVDCCKCL 320  
Db 246 DDIFKDPKVLQSYIYAVSDFVSGRCKCNCHGASECGPQVAGLACRQHNTTGTDCERCL 305  
Qy 321 PFNDPRWRATAESASECLPCDCNCRSQBCYEDPELRYSTGHGHCTNCQDNTDGAHCE 380  
Db 306 PFTQDRPWARGTAAEAHECLPCNCSGRSEBCTFDELFRSTGHGRCHCRDHTAGPHCE 365  
Qy 381 RCENPFRLGNNAEACSSCHSPVSGISLSTQDSCVGRCSCKPVGWMDKCDRCQPFHSLTEA 440  
Db 366 RCQENFYHNDPRMPCQPCDCQSAGSLHLQCDDTGTCAKPTVTGKWCDCRCLPFGHSLSEG 425  
Qy 441 GCSPCSDPGSGIDECNVETGRCVCKDNVEGFNCERCKPFGFNLESNNPGRCTPCFCFGH 500  
Db 426 GCPCCTCNAGSLDTCDCPRSGRCPCKENVEGNLDCRCPTGNLQPHNPAGCSCSCFCYGH 485  
Qy 501 SSVCTNAVGVSVYSISTFOIDEGWRAEQOROSEASLEWSSERQDIATVSDSYFFRYFI 560  
Db 486 SKVCASTAQVQHILLSDFHQGAEGWARSVSGSEHSPQWSPN----GVLLSPDEBELT 541  
Qy 561 APAKFLGKQVLSYXGNLSFSGFRVDRDRDRLSADLVLEGAGLRVSVPLIAQGSNYPSETT 620  
Db 542 APGKFLGQDQSFSGQPLILITFRVPPGDSPLPVG--LLEGTGLALS--LRHSSLSGGQDAR 598  
Qy 621 VKYVFRLLH---EATDVPWRPALTPFEFQKLLNNLTSIKIRGTYSERSAG--YLDDVTLAS 675  
Db 599 ASQGGRAQVPLQETSEDVAPLPFPFHQRLANLTSLRLEAVSPGSPAGPVFLTEVLTS 658  
Qy 676 ARGPGVPATWBSCTCPVGVGQPCCEMLSGYRRETNPLNGYSPCVLCAACNHSSETCDP 735  
Db 659 ARPLSPASWVEICSCFTGTGTQFCESCAPGYKREMPQGGPYASCVPCTCNQHG--TCDP 717  
Qy 736 ETGVNCRNDNTAGPHCEKSDGYGSDTAGTSDCQPCPCGGSSCAVVPKTKKEVCTNC 795  
Db 718 NTGICVCSHTEGSEPCERCLPGFYGNPFAQADDCQPCPCGQSACTTIPESGEVVCTHC 777  
Qy 796 PTGTTGRCELDGDTGDPDLGRNGPVRLCRLCCSDNDIDPNAVGNLRTGELCIAYN 855  
Db 778 PPGQRRRCREVCDDGDFGDFLGFHPQPCQCQCSGNVDPNVAGNCDPLUGSHCLKCLHN 837  
Qy 856 TAGFYCDRCXGDPFNGNLAENPADKCAKNCNPGYTWKQSSCNPNVTGQCECLPHVTGQD 915  
Db 838 TTGDHCEHCEGFGYGSALAPRADKCMPCSCHPQSVSEQMPCDPVTGQCSCLPHVTARD 897  
Qy 916 CGACDPGFYNLQSGQGCERCDCALGSTNGQCDIRTGQCECQPGITGQHCHERCEVNHFGF 975  
Db 898 CSRCYPGFDFLQFGRGCRCKCHPLGSDQEDQCHPKTQCTCRFGVTGQACDRCLQGFSG 957  
Qy 976 GPEGKPCDCHPBGSLSLQCKDDGRCBREGFVGNRCDOCEENYFYNRSWPGQCECPACY 1035  
Db 958 SIKGCRACRSPPLGAASAQCHYNGTCVCRPGFEGYKCDRCHYNNFLTADGTHCQCPSCY 1017  
Qy 1036 RLVKQKVADHRVKLOELIESLIANLGTGDEMVTQAFEDRLKEAREVMDLLRBAQDVKV 1095  
Db 1018 ALVKEETAFLKARLTLTEGMLQSGSDGSPW---GPLDILLGEAPRG--DVGQGHLLPGA 1072  
Qy 1096 DONLMDRLQVNNLTSSQISRLQNIENRTIETGNLAEQARAHVENTERLEIASRELEKA 1155  
Db 1073 REAPLEQMGLEGAAAREQLQRLNKARCAQAGSQKTCQLADLEAVLESEEEELHA 1132  
Qy 1156 KVAANYSVTQPESTGDPNNMTLLAEARKLAERHKEADDIVRVAKTANDTSTEAYNLL 1215  
Db 1133 AAILASLEIPQ--EGPSQPTKWSHLATEARALASRHRDTATKIAATAWRALLASNTSVALL 1191  
Qy 1216 LRTLAGENQTAFLIE--ELNRYEAKNI SODLEKQARVHEEAKRAGDAVEIYASVAQL 1274  
Db 1192 WNLL--EGRVALETORDLEDREYQEVQAAQKALSTAVAEVLPEAE-----SVLATVQQV 1242  
Qy 1275 SPLDSETL-----ENEANNIKMEANLEQLIDQKLDYEDLREDMRKELEVN 1323  
Db 1243 GADTAPYALLASPGALPKSRAEDLGLKAKALEKTV---ASWQHMAE--AARTLQATA 1297

QY 1324 LLEKGTQOOT-----ADQLARADAALAEAAKGRDLOEANDILNNKDF 1373  
Db 1298 QATLRQTEPLTARSRLTATFASQLHOGAARALTQASSVQAATVTVMGARTLLADLEGW 1357  
QY 1374 DRVNDNKTAAEALRKIPAINQITIFANEKTRQAQALGSARADATEAKNKAHERIA 1433  
Db 1358 KLOFFPRKQAAQORQADSVDRLADTRKTKQABRMUGNAAPLSSAKKUGREAEVLA 1417  
QY 1434 SAVQKATSTKAAERTFAEVTDLNENNNMLKQL-QEAEKELKRRKQDDADQDMMAGMA 1492  
Db 1418 KDSAKLALLRRKQAHRRASRLTSQTQATLQQAQQVLAASARQEELEAEAVGAGLS 1477  
QY 1493 SQAAQAEIINARKXNVSITLSIINDLLEQLQOLDT--VDLNKLEIGETLNKAKDEM- 1549  
Db 1478 -----ENEQIRESRISEKDIETLSSELLARLSLTHQAPALNETOMALERLQLG 1532  
QY 1550 KVSLDLRKVSLENAEKQAAMNDYNRDIEEMKDIRNLEDIRKTLPSGC 1600  
Db 1533 SPGSLQRKLSLLEQESQQELQIQGFESDLAEIRADQNLEAILHSIPENC 1583  
RESULT 10  
US-10-262-839-210  
; Sequence 210, Application US/10262839  
; Publication No. US20040038877A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, John,  
; APPLICANT: Anderson, David W.,  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Burgess, Catherine,  
; APPLICANT: Catterton, Elina,  
; APPLICANT: Edinger, Shlomit,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Guo, Xiaojia,  
; APPLICANT: Ji, Weizhen,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Leach, Martin,  
; APPLICANT: Li, Li,  
; APPLICANT: Miller, Charles,  
; APPLICANT: Patturajan, Meera,  
; APPLICANT: Reiger, Daniel,  
; APPLICANT: Rothenberg, Mark,  
; APPLICANT: Shimkets, Richard,  
; APPLICANT: Smithson, Glenda,  
; APPLICANT: Spytek, Kimberly,  
; APPLICANT: Taupier, Raymond, Jr.,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Voss, Edward,  
; APPLICANT: Zerhusen, Brian,  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-462A  
; CURRENT APPLICATION NUMBER: US/10/262,839  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,029  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/328,056  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/381,101  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/371,972  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/327,342  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/328,044  
; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/374,738  
; PRIOR FILING DATE: 2002-04-23  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 210  
; LENGTH: 1587  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-839-210  
Query Match 41.4%; Score 3611; DB 12; Length 1587;  
Best Local Similarity 43.5%; Pred. No. 3.8e-197;  
Matches 701; Conservative 264; Mismatches 578; Indels 68; Gaps 21;  
QY 21 LAVLAAAAAGCAQAAMDECTDEGGRPORCMPEFNAAFNVTVVATVTCGTPPEYCVQT 80  
Db 10 LALLAPRAAG---AGMGACYDGAQRPCRLPFVFNAAFGELAQASHTCGSPDPDFCPHV 65  
QY 81 GVTGVTCKSLCDAGQPHLQHGAAFLTDYNNQADTTWQSOTMLAGVQYPSINLTLHLG 140  
Db 66 GAAGAGAHQCRDAADPORHNASYLTDFHSQDSTWQSPMAFGVQYPTSVNITLRLG 125  
QY 141 KAFDITYVRLKFHTSRPESFAIYKRTREDGPWIPYQYVSGSCENTYKANKGFIRTGDE 200  
Db 126 KAYEITYVRLKFHTSRPESFAIYKRSRADGPWEPYQFYASQKTYGRPEGYLRGDE 185  
QY 201 QOALCTDFSDISPLTGGNVAFTLEGPSAYNFDNSPVLOEWVTATDIRVTLARLNTFG 260  
Db 186 RVAFCTSEFSDISPLSGGNVAFSTLEGPSAYNEEESFGLQEWVTSTELLISLRLNTFG 245  
QY 261 DEVFNDPKVLKSYVYVAISDFAVGGRCKNGHSHASCKMNEFDKLVNCKXNTYGVDCSKCL 320  
Db 246 DDIFKDPKVLQSYVYVAVSDFSVGGRCCKNGHSHASCGPDVAGQACRQOHTTGTDCBRCL 305  
QY 321 PFNDRPWRRTATASASCLPCDCNQRSQCYFPDELYRSTGHGCHTNCODNTDGAHCE 380  
Db 306 PFFQDRPWARGTAAEAHECLPCNCSRSEECTFRELFRSTGHRGRCHCHDHTAGPCE 365  
QY 381 RCRENFRLGNNEACSSCHCPVGSLSLTCQDSYGRCKCPGVMDGKCDRCQPGFHSITEA 440  
Db 366 RCQENFYWDPMPCQPCDCQASGLHLCDDTGTCAKPTVTGWKDCRCLPGFHSISEG 425  
QY 441 GCRPCSDPSGIDECNVETGRCVCKDNVEGFNCERCKPGFNFLESNPRCTCFCEGH 500  
Db 426 GCRPCTCNPAGSLDTCPRSGRCPCKENVEGNLDCRCPGTFTNLOPHNPAGCSSCFYGH 485  
QY 501 SSVCTNAVGSVYSISSTFQIDEGWRAEQRDGSEASLEWSERQDIAVSDSYPPRYFI 560  
Db 486 SKVCASTAQFQVHHLSDFHQAGWARSYVGSSEHSPQWSPN---GVLLSPEDESELT 541  
QY 561 APAKELGKVLQVSYGNLQSLFSPRVDRDRTRLSAEDLVLEGAGLRVSVPLIAQNSYPSSET 620  
Db 542 APCKELGDRFSGYQPLITLTFRVPPGSPPLVQ-LRLEGTGLALS--LRHSLSGFPQDAR 598  
QY 621 VKYVFLH---EATDYPWRPALTPFEOKLNNLTSIKIRGTYSRASAG--YLDQVTLAS 675  
Db 599 ASQGGRAQVLOETSEDVAPPLPPHFORLLANLTSRLRVSPGSPAGVPFLTEVRLTS 658  
QY 676 ARPGGVPATWYESTCPVYGQFCENCLSGYRRETNLPGLPSPCVLCANGHSETCDP 735  
Db 659 ARPLSPASPASVWEICSPGTGYTQFCESCAPGYKREMPQGGPYASCPVCTCNQHG-TCDP 717  
QY 736 ETGVNCRDNTAGPCEKSDGYIGDSTAGTSSDCQPCPCGSSCAVVPKTEVVCTNC 795  
Db 718 NTGICVCSHTEGSPCERCLPGFYGNPPFAGQADDQPCPCPGQSQACTTIPESGEVVCTHC 777  
QY 796 PTGTTGKRCLELDDGYFGDPLGRNGFVRLCRLCQCSNDINPNAVGNLRLTCELUKCIYN 855  
Db 778 PFGQGRRCVCDGDDGFFGDFGLGFGHPQCHQCQCSGNVDPNAVGNCDPLSGHCLRLCLHN 837

QY 856 TAGFYCDRCXGDFGNPLAPNADKCKACNCFYGTMEQSSCNFVTGQCECLPHVTGQD 915  
Db 838 TTGDHCEHCQEGFYGSALAFRPAADKCMPCSCHPQSVSEQMPQCDVTCQCSCLPHVTARD 897  
QY 916 CGACDPGFYNLQSGQCCERCDCHALGSTNGQCDIRTCQCEQPGITGQHCFERCEVNHFGF 975  
Db 898 CSRCYPGFDPQPGRCRCKCHPLGSDQDCHPXTGQCTCRPGVTGQACDRCQLGFFGS 957  
QY 976 GPEGKPCDCHPEGLSLOKDDGRCEBCEGFGVGNRCDOCEBENFYNRSWPGCCPCPAC 1035  
Db 958 SIKGRACRCSPLGASAOCHYNGTCVCRPGFEGYKDRCHYNFFLTADGTHCQCPSCY 1017  
QY 1036 RLVKQKVADHRVKLOELESILANLGTGDEMVTDOAFEDRLKEAREVMDLLREAOQDVX 1095  
Db 1018 ALVKSETAKLAKRLTILTEGWLQSDGSPW---GFLDILLGEAPRG--DVYQGHLLPGA 1072  
QY 1096 QNLMRQVRNNTLSSQISRLQNTNITETGNLAQBARHVENTERLIELIASBELEKA 1155  
Db 1073 REAFLEQMGLEGAVKAAREQLRKNKGARCAQAGSQKTCTQADLEAVLESSEBIIHA 1132  
QY 1156 KYAANVSVTPESTGDPNNMTLLAEHAKLAERHKEADDIVRVAKTANDTSTAYNLL 1215  
Db 1133 AAILASLEIPQ--EGSPQTKWHLAIEAALARSHTATKTAATAWRALLASNTSYALL 1191  
QY 1216 LRTLAGENQTAPEIE--ELNKRYEQAKNISQDLEKQAAHVHEAKRAGKAVEIYASVQL 1274  
Db 1192 WNL--EGRVALETQDLEDYQVQAQKALRTAVAEVLPEAE-----SVLATVQOV 1242  
QY 1275 SPLDSETL-----ENANNIKMEANLEQLIDQKDYEDLREDMGEKLEVK 1323  
Db 1243 GADTAPYLALLASPGALPKSRAREDGLKAKALEKTIV-----ASWQHMAE--AARTLQTA 1297  
QY 1324 LLEKGTQEQT-----ADQLARADAALAEAAKKGRTDLOEANDILNNLKDF 1373  
Db 1298 QATLRQTEPTWARSRLTATFASQLHOGARALTQASSSVQAATVTVMGARTLLADLEG 1357  
QY 1374 DRVNDKTAAREALKRIPAINQITTEANEKTRQAQALGSAADATEAKNKAHEARIA 1433  
Db 1358 KLOFRPKQQAALQORADSVDRLLADTRKTKQAEIMIGNAAPLSSAKKKGREAEVIA 1417  
QY 1434 SAVQKNATSTKAEARTFAEVTDLNENVMNMLKQL--QEAKEKLRKQDDADQMMAGMA 1492  
Db 1418 KOSAKLAKALLERKQAHRRASRLTSTQATLQASQVQLASEARRQEEBAEVRGAGLS 1477  
QY 1493 SQAAQAEINARKAKNSVTLISINDILLEQLGOLDT--VDLNKLINEIEGTINKAKDEM- 1549  
Db 1478 -----EMEQQIRESISLEKDIETUSSELLARIGSLDTHQAPQALNETQWALERLQLG 1532  
QY 1550 KYSDLRKVSLENEAKQBAAIMDYNRDIEIMKDIRNLEDIRKTLPGSC 1600  
Db 1533 SPSLQRLKSLLEQESQOQELQIQGFESDLAEIRADKQNLAILHSLPENC 1583

RESULT 11  
US-10-262-839-212

; Sequence 212, Application US/10262839  
; Publication No. US20040038877A1

; GENERAL INFORMATION:

; APPLICANT: Alsbrook, John,  
; APPLICANT: Anderson, David W.,  
; APPLICANT: Boldog, Ferenc,  
; APPLICANT: Burgess, Catherine,  
; APPLICANT: Catterton, Elina,  
; APPLICANT: Edinger, Shlomit,  
; APPLICANT: Ellerman, Karen,  
; APPLICANT: Gerlach, Valerie,  
; APPLICANT: Gorman, Linda,  
; APPLICANT: Guo, Xiaojia,  
; APPLICANT: Ji, Weizhen,  
; APPLICANT: Kekuda, Ramesh,  
; APPLICANT: Leach, Martin,  
; APPLICANT: Li, Li,  
; APPLICANT: Miller, Charles,

; APPLICANT: Patturajan, Meera,  
; APPLICANT: Reiger, Daniel,  
; APPLICANT: Rothenberg, Mark,  
; APPLICANT: Shimkets, Richard,  
; APPLICANT: Smithson, Glenda,  
; APPLICANT: Spytek, Kimberly,  
; APPLICANT: Taupier, Raymond, jr.,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Voss, Edward,  
; APPLICANT: Zerhusen, Brian,  
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD;  
; FILE REFERENCE: 21402-462A

; CURRENT APPLICATION NUMBER: US/10/262,839

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: 60/326,483

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/327,917

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,029

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,056

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/381,101

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/371,972

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/327,342

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/328,044

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/374,738

; PRIOR FILING DATE: 2002-04-23

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 367

; SOFTWARE: Curaseq1ist version 0.1

; SEQ ID NO 212

; LENGTH: 1575

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-262-839-212

Query Match 41.4%; Score 3609; DB 12; Length 1575;

Best Local Similarity 43.7%; Pred. No. 4.9e-197;

Matches 699; Conservative 265; Mismatches 577; Indels 60; Gaps 21;

QY 21 LAVLAAGAGCAQAAMDECTDEGRRPQRCMPFVNAFNVTVVVAINTGCTPPPEEYCVQT 80  
Db 10 LALLAPRAAG---AGMGACYDGAQRPCQLPVFENAAFGRLAQASHTCGSPPEFCPHV 65  
QY 81 GVTGVTXSKLCDAGOPHLOHGAFLTDYNNQADTTWQSQOTMLAGVQVPSINLTLHLG 140  
Db 66 GAAGAGAHQRCDAADPQRHNNASYLTFHQSDESTWQSPSMAFGVQVPTSVNITRLG 125  
QY 141 KAFDITVRLKFTSRPESFAIYKRTREDGFWIPYQYSGSCENTYTSKANRGFIRTGDE 200  
Db 126 KAVEITVRLKFTSRPESFAIYKRSRADGFWPEYQFYSASQCKTYGRPEGVYLRPEGE 185  
QY 201 QOALCTDEFSDISPLTGNVAFSTLEGRPSAYNFDSPLQEWVTATDITVNLNLTG 260  
Db 186 RVAFCTSEFSDISPLSGNVAFSTLEGRPSAYNFDSPLQEWVTATDITVNLNLTG 245  
QY 261 DEVENDPKLVKSYIYALSDFAVGRCRCKNGHASECMKNEPDKLVNCKNHTYGVDCCKL 320  
Db 246 DDIFDKVQLQSYIYAVSDFSVGRCKNGHASECGPDVAGQLACRQHNITGTDCECL 305  
QY 321 PFFNDRPWRATASASECLPCDCNGRSQBCYFDPPELYRSTGTGHHGHTNCQDNDGAC 380  
Db 306 PFFQDRPWARGTAEAHAHECLPCNCSGRSEBCTFDRELFRSTGTGHHGHTNDRHTAG 365  
QY 381 RCNRFELGNNEACSSCHSCSPVGSLSLTQCDYSYGRCSCKPGVMGDKCDRCQPGFHS 440

Db 366 RQENFYHDPMPQCFDCQAGSLHLQCDTGTACKFTVTGKCDRCLPFGFSLSEG 425  
Qy 441 GCRPCSDPGSGTDCGNVETGRCKVNDVEGNCERCKPFFNLSSNPRGCTPCFCFQH 500  
Db 426 GCRPTCNAGSLDTCDPGRGCPCKENVEGNLCRCRGTNLOPHNPAGSCSCFCYGH 485  
Qy 501 SSVCTNAVGVSVYSSTTQIDBDGWRARQORGSSEASLEWSSERQDIAVISDSYPRFVI 560  
Db 486 SKVCASTAQFQVHHILSDHQAEGHWAARSVGGSEHSPQWSPN----GVLLSPEDEBELT 541  
Qy 561 APAKFLGKOVLSYGNLSFRVDRDRTLSEADLVLLEGAGLRVSVPLIAQNSVPSETT 620  
Db 542 APKFLGDORFSYQGLPIITFRVPPGDSPLPVQ-LELEGTGLALS--LRHSLSPQDAR 598  
Qy 621 VKTVFRLH---EATDYPWRPALTPFFFKLNNLTSIKIRGYBSRSAG--YLDVDTLAS 675  
Db 599 ASQCGRAQVPLQSTSDVAPLPPFFHFORILLATSLRLVSPGSPAGPVLTEVRLTS 658  
Qy 676 ARPQGVPAWVWSCCTCPVYGQCFCEMCLSGVRRETNLPVSPCLVCAACNGHSETCDP 735  
Db 659 ARFGLSPASWVSCPTGYTQFCESCAPGYKREMPQGGPVASVCPCTCNQHG-TCDP 717  
Qy 736 ETGVCNCRDNTAGPHCEKSDGYGDSGTAGTSSDCQPCPCGSSCAVVPKTKYVCTNC 795  
Db 718 NTGICVCSHTEGSCERCCLPGFYGNPFAGADDCCQPCPGQSACTTIPESGEVVCTHC 777  
Qy 796 PTGTTGKRCLODGGFDPGLRANGPVLRLCQCSNDIDPNAVCNRLTGCCLKCIYN 855  
Db 778 PPGQGRRCVCDGDFGDFGLFGRHPQCHQCGSGNVDPNAVGNCDPLSGHCLRLCLN 837  
Qy 856 TAGFYCDRCXGDFPGLAPNADKACACNCPYGMKQSSCNPVTCQCECLPHVTGQD 915  
Db 838 TTGDHCBEGYVGSALAPRPAKMPSCHPQGSVSEQMPCDPVTGQCSCLPHVTARD 897  
Qy 916 CGACDPGFYNLQGGQGERCDCHALGSTNQCDIRTGQCEQCPGITGQHCERCEVNHFF 975  
Db 898 CSRCYPGDFDLPQGRGCRSKCHPLGASQEDQCHPKTGCTCRPGVTGQACDRCOLGFFOS 957  
Qy 976 GPECKCDCHPEGLSLQCKDGRCEGRGFGVNRCDQCEENFYFNRSWPGQCEPCAPY 1035  
Db 958 SIKGRACRCSPLGAABAQCHYNGTCVCRPGFEGYKCDRCHYNFFLTADGTHCQCPSCY 1017  
Qy 1036 RLVRKDVADHRVKLELESILANLGTGDEMVTQAFEDRLKEAERVMOLLREAOQKDV 1095  
Db 1018 ALVKEETAKLKAULTLLEGWLOGSDCGSPW--GPLDILLGEAPRG--DVIQGHLLPGA 1072  
Qy 1096 DONLMDRLQVNNLSSQISLQNIQNTIBETGNLAEQABAHVENTERLIEIASRELEKA 1155  
Db 1073 REAFLEQWGLGAVKAARBOQLNKGARCAQGSQKTCTQADLEAVLESSEBILHA 1132  
Qy 1156 KVAANQSVTPQESTGDPNNMTLAEARKLAERHKEQADDIVRVAKTANDTSTAYNLL 1215  
Db 1133 AAILASLEIPQ-EGPSQPTKWSHLAIEARALARSHRDTATKIAATAWRALLASNTSYALL 1191  
Qy 1216 LRTLAGEHOTAFETE-ELNRKYEQAKNIQDLEKQARVHEEAKRAGDAVEIYASVQOL 1274  
Db 1192 WNL--EGRVALETQDRLDREYQVQAQKALRTAVAEVLPEAB-----SVLATVQQV 1242  
Qy 1275 SPLDSETL-----ENEANNIKWEAENLEQLDQKLKDYEDLREDMRGKELEVKN 1323  
Db 1243 GADTAPYLLALLASPCALFOKSRADDLGLKAKALEKTIV---ASQWEMATE-AAARTIQTA 1297  
Qy 1324 LLEGKTEQQTADQLLAPADIAKALAEAAKGRDITLOEANDILNLIKDFDRVNDKTA 1383  
Db 1298 QATLRQTEPLT--KLHOZARAALTQASSSVQAATVTVNGARTLLADLEGWKLQFPKPKQ 1355  
Qy 1384 ABEALRKIPALNOTITEANEKTRACQALGSAADATEAKNKAHEABERIASAVQKATST 1443  
Db 1356 AALQKADSVDRLLADTRKTKTQARWLGNAAPLSSAKKKGAEAEVLAKDSAKLAKAL 1415  
Qy 1444 KAEARTFAEVTDLNEVNNMLKQI-QEAEKELKQKODDADQDMMGAMASQAQAEAIN 1502

Db 1416 LRERKQHRASRLTSQTQATLQOASQVULASERRQEELEAERVGAGLS-----EWEQQ 1470  
Qy 1503 ARKAKSVTSLLSIINDLLEQLQCLDT--VDLNKLANEIBGTLNKAKDEM-KVSDLRKVS 1559  
Db 1471 IRESRISELDXIETLSSELLARGLSLDTHQAPALNATQWALERLRLQLGSPGLQRLKS 1530  
Qy 1560 DLENAKQOEAAMNDYNDIRDEEMKDIRNLEDIRKTLPSGC 1600  
Db 1531 LLEGESQOQLQIQGFESDLAEIRAKQNLLEALHSLPENC 1571  
RESULT 12  
US-10-369-493-6816  
; Sequence 6816, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6816  
; LENGTH: 1557  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6816

Query Match 37,24; Score 3240; DB 15; Length 1557;  
Best Local Similarity 39.08; Pred. No. 5,4e-176;  
Matches 636; Conservative 289; Mismatches 541; Indels 166; Gaps 32;  
Qy 40 CTDEGR-PQRCMPFVNAAPNVTVATNTCGTP-PEEYCVQTGVTGVTKSHLCDAGQP 97  
Db 25 CYDRATQPCQPCVDFVNAAFNLEVQVNTCGTKRPTKFCVQSGHTQQRSVCTCDDRHE 84  
Qy 98 HLQCAAPLTDYNNQADTTWQSOTMLAGVQYSSINLTLHLKAPDITVYRLKPHTSRP 157  
Db 85 GFSHPAKYLTDFVGNNTWQSDTMQEGQQYPTTNLTLVLGKSFDTYVRLKFSRPP 144  
Qy 158 ESFAIKRTREDGPWIPYQYVSGSCENTYSKANRGFIRTTGGDEQOALCTDEFSDISPLT 217  
Db 145 ESFTYKXTHDSEWEPQWQFYSGSCRATYGLSDRAPI-LPGNEATAQCTKEFSDISPTG 203  
Qy 218 GNVAFTLEGPSAYNPDSNPLQEWYATDIRVTANLNTFGDEVNDPKVLSYYVAI 277  
Db 204 GNIAFTLEGPSAHAFEESEVLQKRWTAIRISLRNMTFGDEVKDFQVLSYYVAI 263  
Qy 278 SDFAVGGRCKNGHASECMKNEF---DKLYCNCKHNTYGVDCBKCLPFFNDRPWRATA 333  
Db 264 SDFAVGGRCKNGHASECMKNEF---DKLYCNCKHNTYGVDCBKCLPFFNDRPWRSGTS 323  
Qy 334 ESASECLPCDNGRSQBCYFPPELYRSTGHGHCNTCODNTDGAHCRCRNFELGNE 393  
Db 324 VEANEICACNSQLSNRCYFDQQLFEETGHGHCIDCOGNTQGVHCEOCIANHWRPGEN 383  
Qy 394 ACSCHCSPVSGSLSTQCDYSGRCCKPGVMGDKDRQOPGFHSTEAAGRCPCSDPGSSI 453  
Db 384 YCVACGCGNEISLSTQCDNECKGCKQCKPGVTGRFCQDCLDGFYDFSTNGCKNCGCETSGL 443  
Qy 454 D---ECNVETGRVCCKNVGFCNBERCKPGFNFENLESSNPRCTPCFCFSGHSSVCTNAVGY 510  
Db 444 NNQPRCDSSSGSCSKLNVGRCQDKCKPGYFDLSTENQFCTPCFCFSGHSSICNTADGY 503  
Qy 511 SVYSLSSTFQDDEGWRAEQDGSSEASLEWSSERQDIAVISDSYPRFYIAPKFLGQV 570

504	FAMNVSVFDDQOKQWAGQNRIGLQ--DTQWAEILDKAVASDSTDNSPVFVFAPEQFLGDQR	566
571	LSYGNLSFSFPRDRDRTR.SAEDVLLEGAGLR-VSVPLIAQNSYVPSETTVMKYVRLHE	629
563	SSYNQDLVFTLKVAKVHTNQDVXDIIVGADROELSTSTAQGNPFPTTEAQTVAFRVAHA	622
630	ATDPWRPALPFPFQKLANLTSIKIRGYNSRSAGYLDVTLASARPGGV----PAT	685
623	DYFGWYPRINELDFIGILSNITAKIRGYISYKD:GYLSNNVLGTAGVAPSAANPKQAT	682
686	WVEGCTCPVGYGGQFCWCVLSGYVRETPNIPGYSPCVLCACNHGHEBTDPTFTGVNCNRDN	745
683	WIEHCFLPGVGQFCSCSGFRETFCGPFNFHICIKDCHNHNSCBAESGSGCIEHN	742
746	TAGPHCEKCSGYGYGDSITAGTSSDCQCPFCGGSSCAVVPKTEVVCTNCPITGTTGKRC	805
743	TAGDTCERCASGYGDALQGTEDCQCPNDGPC-ILHADGDVICTECPNGYTGRECD	801
806	LCDDGYFGDPLGRNGPVRLCRLCOCSNIDPNVAGNCNRLTGBCLKCIYNTAGFCVDRCK	865
802	ECSDDYFGNP--XDGTE--CYECACSGNTDPSIGNCDKITGECKKCIPTHTGFENCECK	857
866	DOFFGNPLAPNADPKKACNCPYGTMKQOS-----SCNPVTGQCBCLPHVVTGQDCGACD	920
858	PGYWGDAII-EPKGNCSGCGFAAGTRPNNDYTLECNQDQDCDCLFNVIIGIQDOCA	916
921	PGFYNLQSGQGERCDHALGSTNGQCDITGQCEQCPGITGQHCBCRBVWFHFGPBGCG	980
917	HGFYNTITSLGQCQCCNDPLGSEBNTCDVNTGCOCKPGVTGQCDRCADYHFGFSANGC	976
981	KPCDCHPBGSLSLQCK--DDGRCRECFVGNRCDQCEBNFYFNRSWPGQCECPACVRLVK	1039
977	QPCDCEYIENQCCDYNSSGCLCKENVEGRRCQCAENRY--GITQGCLPCDDCVYTLIQ	1034
1040	DKVADHRVULOELSLIANLGTGDMYTDOAFEDRLKEABR---EVMULLRBAQDVKQVD	1096
1035	SRVNVFBEKVXSLDNTLOEIIENPAPVNDYTFKEVKETSRASEVWEAVK--QKTKSGG	1092
1097	QNLMDRLQRVNTLSSQISRLQNTRIETETGNLAEQARAHVENTERLLTETIASREL---	1152
1093	GTIKTKSKAIKDEIVAALKLTSIDESAQKYGADAAENDMKRWEIIEENARREIENVL	1152
1153	-----EKAKVAANVSUTOPSTGDPNNMTLLAEARKLAEHKQPADDIVRAKTA	1204
1153	HYLETEGERAQI-AYNASQKYBQS---KRMSELASGTREBEAKHLKQASEIQLSSQA	1208
1205	NDTSTEAYNLLRLTAGENQTAPEIEELNKRYEQA-KNISQDLEKQAARVHEEAKRAGDK	1263
1209	IANATOANKEASDAIYGEOI:SKQIAELKEKQNLNESIHTLD-----LASEQKKSAD	1263
1264	AVEIYA-----SVAQJSLPDSSETLENNIKWEABNLEQLIDQKLD---YEDLRDM	1314
1264	ANMLAAVSLTNVEAKVPSPDKPLRNDVAGVLESEN---LVDSVKENSANDSELPDEV	1320
1315	RGKELEVNLLKKGTEQOQTADQLARADAAKALABEAAKGGRTTLQEAANDILNKLKDFD	1374
1321	NRSVADARNELQSQQOQVSDQLMLELXSRERIVDSVSTADKTLKDAEALQVLEBFG	1380
1375	RVYNONKTAEBEALRKIPATNQ---TITEANETREA---QOALGSAADAATEAKNAH	1427
1381	AKIEKSRNDVAEAPFAGVBEINQRLLDDIIAQDKRNSLPIDKGFVIDYKRSADVLLNETH	1440
1428	E-AERIASAVQKNA-TSTKAPAEFTFAEVTDLONEVNMMLKQLEABEKELKKQDADAOD	1485
1441	ALADRYKDI:IHSDVDTRDSTEA-----VQVDIEQLMEELTDSNENLQYKQQAQSD	1491
1486	MMWAGMASQ-----AAQEAEBINAKKNSVTSILSTIINDLLBQLQGLDQDVLNKLN	1536
1492	KQMAATEAVRKQLLPRILPESKQMLPFSIRKMKRSKSLIVL-----	1532
1537	ETEGTLNKAQEMKVSDDLDRKXVSDLENEAKKQEAAMINDYNRDIETEMKDIRKTL	1596
1533	-----NLESIRNLL-----NLESIRNLL-----	1541

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QY      1597 PGSCFNTPSIEK 1608  
       |: ||| :::  
DB      1542 PTKCFNVINLEQ 1553  
  
RESULT 13  
US-09-756-071B-13  
 / Sequence 13, Application US/09756071B  
 / Patent No. US20020052307A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Tryggvason, Karl  
 /           Kallunki, Pekka  
 / Pyke, Charles  
 / TITLE OF INVENTION: Laminin Chains: Diagnostic Uses  
 / NUMBER OF SEQUENCES: 20  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Ray Sharpe Fagan Winnich & McKee  
 / STREET: 1100 Superior Ave, Suite 700  
 / CITY: Cleveland  
 / STATE: Ohio  
 / COUNTRY: USA  
 / ZIP: 44114  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 /   APPLICATION NUMBER: US/09/756,071B  
 /   FILING DATE: 08-Jan-2001  
 / CLASSIFICATION: <unknown>  
 / PRIOR APPLICATION DATA:  
 /   APPLICATION NUMBER: US 09/663,147  
 /   FILING DATE: 150-September 2000  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Minnich, Richard J.  
 / REGISTRATION NUMBER: 24,175  
 / REFERENCE/DCKET NUMBER: TRV 20014  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 216-861-5582  
 / TELEFAX: 216-241-1666  
 / INFORMATION FOR SEQ ID NO: 13:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 1193 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-756-071B-13  
  
Query Match          30.3%; Score 2637; DB 9; Length 1193;  
Best Local Similarity 39.4%; Pred.No. 9.4e-142;  
Matches 515; Conservative 235; Mismatches 418; Indels 138; Gaps 12;  
  
QY      319 CLFFPFNDPRWRATASAECLPDCDNGRSQBECYPDFELRYSTGHGHCNCDTGDGAH 378  
         |||||  
DB      9    CLCFSLLPAARATSRR-----VCDCNGKSQCIFDRHLHRQTGNGFRCNLNCNDTDGIH 64  
  
QY      379 CEBCRFNFRLGNNEACSSCHSPVGSLSITOCDSYGCRCKPKVMGDKDCRCPGGHSLT 438  
         ||:::||:  
DB      65  CEKKCNKFYHRERDRCLPCNCKSGSLGARCDNSGRCSCKPGVTGARDRCILPGFHMLT 124  
         |||||  
  
QY      439 EAGC-----RPCCSDPSGSTDECVETGTGCVKDNVEFGFCRKPKGFFNLESNNPR 490  
         |  
DB      125 DAGCTODQRLLDSKCDDCPAGIAGPC--DAGRVCVPKPAVTGERCDCRSGYYNLDGKNPE 182  
         |||||  
  
QY      491 GCTPCFCFGSHSVCTWAVGYSVYSISSTEQIDEDGWRAEORDGEASELWSSEQQDIAMI 550  
         |||||  
DB      183 GCTQCFCYGHSACSRSAASYVHKHTSTTHQDVDTGMKA VORNESPAKLQWSRHQDVFS 242  
         |||||  
  
QY      551 SDSYFPFYTIAPAKFLGKVQLSYQGONLSFSFRVDNRDLTLASDLVLLEGAGLRVSVELIA 610  
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Db 243 AQLDVPVYFVAPAKFLGNQVSVGQSLSFYRVDGRHPSAHDVILEGAGLRIITAPLMP 302  
Qy 611 QGNSYPSSETTKVYVRLHEATDYPWRPALTPFEFQKLLNNLTISIKIRGTYSERSAGYLD 670  
Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSQSLSYFVRELLNLALIRATYGVSTGYIDN 362  
Qy 671 VTLASARPFGVPATWVESCTCPVYGQFCMCLSGYRETPNLPYSPCVLCACNHGS 730  
Db 363 VTLISARPVSGAPAPWVEQICPVYKGFQCDQASGYKRD SARLPGFTGICPCNQG-G 421  
Qy 731 ETCDPBTGVNCRDNTAGHCEKSDGYGDSSTAGTSSDCQPCPGGSCCAVVPKTEV 790  
Db 422 GACDPTGDCYSGDENPDIEADCPIGFYNDPHDRS--CKPCFCHNGFSCVPIPETEV 479  
Qy 791 VCTNCPGTGKRCBELCDDYFGDPLGRNGPVLRLCLCOCSNDIDPNAVGNCRNLGTGCL 850  
Db 480 VCNCPGPGVTGARCELADYFGDPLGRNGPVLRLCLCOCSNDIDPNAVGNCRNLGTGCL 539  
Qy 851 KCIYNTAGYCDRCCKDGFNGPLAPNADKCAKCNCPYGTWKQSSCNVPTGQCECLPH 910  
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCAKCNCPYGTWKQSSCNVPTGQCECLPH 580  
Qy 911 VTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECOPGITQHCERCEV 970  
Db 581 -----  
Qy 971 NHFGPPEGCKPCDCHPEGSLSLQCKDGRCEGFGVGNRCDOCEENFYNRSWPGQCE 1030  
Db 581 -----EVG-----CRSDGTVCVKPFGFGPNCHE-----GAPS 608  
Qy 1031 CPACYRLVKDKVADHRVYKLOELESLLANLGTGDEMVTQAFEDRLKEAREVMDLLREAO 1090  
Db 609 CPACYNKVQIMQDFMQLQMEALISKAQGGGVDPDELEGRMQQAQALQDILRLDAQ 668  
Qy 1091 DVKDVQNLMDRLQVNTLSSQISRLQNTIETGNLAEOARAHVENTERLIEASR 1150  
Db 669 ISEGAASRLQLAKVRSQNSQSLDLDKMTVERVRLGSGYQNRVDRTHRLITQMQL 728  
Qy 1151 ELEKAKVAANVSVTQESTGDPNNMTLLAEARKLAERKOEADDIRVAKTANDTST 1210  
Db 729 SLAEASLGNWNTIPASDHYVGNPKSLAQEATRLAESHVESASNEQLTRETEDYSQ 788  
Qy 1211 AYNLLRLTL-----AGENQTAPEIHELNRKYEQAKNISQDLEKQAAVHEEAKGDK 1263  
Db 789 ALSIVRKALHEGVSGSGSPDGAV-VQGLVEKLEKTSLAQQLTREATQATEADRSYOH 847  
Qy 1264 AVEIYASVAOLSPILDSSTLE-NEANNIKMAENLEQLIDOKLXDYEDLREDMEGKELEVK 1322  
Db 848 SLRLDSVPLQVSDGQSFQVEAKRIKQKADSLSLVTHMDEFKXTQKLGKNWKEEAQ 907  
Qy 1323 NLEKGTQEQTDQLARADAALAEFAAKKGRDITLQANDILANLKDFFRVDNKT 1382  
Db 908 QLLQNGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVSILKNLREFDLQVDRKA 967  
Qy 1383 AAEALRKIPAINQTIETAEKTEAQAALGSAADAATEAKNAHEAERIASAQKNATS 1442  
Db 968 EAEAMKRLSVISQVSDASDKTQABRALGSAADAQRAKNGAGEALEISSIEQEIGS 1027  
Qy 1443 TKABAERTFAEVTDLDEVNMLKQLOEAKELKRCQDDADQDMWAGMASQAQAEN 1502  
Db 1028 LNLEANTADGALAMEKGLASLXSEMREVEGELERKELEFDTNMDAVQWVITEAQKYDTR 1087  
Qy 1503 ARKAKNVSLSLILNLEQLGOLDVTLNKLNEIGTLNKADEKMSDLDKYSVLE 1562  
Db 1088 AKNAVGTQTLNTLDGLLHMDQPLSVDEGLVLEQLSRKTQIN-SQLRPMNSELE 1146  
Qy 1563 NEAKKQEAAMIDYNRDIEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1608  
Db 1147 ERARQORGHLLLETSIDGILADVKNLENIRDLNLPFCYNTQALEQ 1192

RESULT 14

US-10-392-113-14

; Sequence 14, Application US/10392113  
; Publication No. US2003024993A1  
; GENERAL INFORMATION:  
; APPLICANT: Land, Hartmut  
; APPLICANT: Deleu, Laurent  
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION  
; TITLE OF INVENTION: OF CANCER CELLS  
; FILE REFERENCE: 21108.0005U3  
; CURRENT APPLICATION NUMBER: US/10392.113  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: 60/365,078  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: PCT/US01/32127  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/239,705  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence./Note =  
; OTHER INFORMATION: Synthetic Construct  
; US-10-392-113-14

Query Match 30.3%; Score 2637; DB 12; Length 1193;  
Best Local Similarity 39.4%; Pred. No. 9.4e-142;  
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;  
Qy 319 CLPFDNRPMRRAEASASECLPDCNGRSGQECYFDELYRSTCHGCHCTNCDDTDGAH 378  
Db 9 CLCFSLLLPARATSRRE---VDCNKGSRQCFIDREHRTQGTNGFRCLNCNDTIDGII 64  
Qy 379 CERENRPFRLGNNEACSSCHSCSPVGSLSLSTQCSYGRCSCKPGVMGDKCDRCQFPHSLT 438  
Db 65 CEKANGFYRHREDRLCLPCNCKSGLSARCDNSGRCSCKPGVTGARCDRLPGPHMLT 124  
Qy 439 BAGC-----RPSCDPSGIDE CNVETGRCVCKNVGFCNRCERCKPFFNLESSNPR 490  
Db 125 DAGCTQDRLDSDKCDCPAGIAGFC--DAGRCVCKPAVTGERCDRCRSGYINLDGNGPE 182  
Qy 491 GCTPCFCFHSVCTNAVGYSVYSISSTFQIDEDGWAEQDGEASLEWSSERQDIAMI 550  
Db 183 GCTQCFYGHASACRSAAEYSVHKITSTFHQVDGKAVQENGSPAKLQWSQRHQDVFS 242  
Qy 551 SDSYFPRYFIAPAKFLGKQVLSYQNTLSFSFRVDRDRTRLSAEDLVLEGALRVSVPLIA 610  
Db 243 AQLDVPVYFVAPAKFLGNQVSVGQSLSFYRVDGRHPSAHDVILEGAGLRIITAPLMP 302  
Qy 611 QGNSYPSSETTKVYVRLHEATDYPWRPALTPFEFQKLLNNLTISIKIRGTYSERSAGYLD 670  
Db 303 LGKTLPCGLTKTYTFRLNEHPSNNWSQSLSYFVRELLNLALIRATYGVSTGYIDN 362  
Qy 671 VTLASARPFGVPATWVESCTCPVYGQFCMCLSGYRETPNLPYSPCVLCACNHGS 730  
Db 363 VTLISARPVSGAPAPWVEQICPVYKGFQCDQASGYKRD SARLPGFTGICPCNQG-G 421  
Qy 731 ETCDPBTGVNCRDNTAGHCEKSDGYGDSSTAGTSSDCQPCPGGSCCAVVPKTEV 790  
Db 422 GACDPTGDCYSGDENPDIEADCPIGFYNDPHDRS--CKPCFCHNGFSCVPIPETEV 479  
Qy 791 VCTNCPGTGKRCBELCDDYFGDPLGRNGPVLRLCLCOCSNDIDPNAVGNCRNLGTGCL 850  
Db 480 VCNCPGPGVTGARCELADYFGDPLGRNGPVLRLCLCOCSNDIDPNAVGNCRNLGTGCL 539  
Qy 851 KCIYNTAGYCDRCCKDGFNGPLAPNADKCAKCNCPYGTWKQSSCNVPTGQCECLPH 910  
Db 540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCAKCNCPYGTWKQSSCNVPTGQCECLPH 580  
Qy 911 VTGQDCGACDPGFYNLQSGQGCRCDCCHALGSTNGQCDIRTGQCECOPGITQHCERCEV 970

581 ----- 580  
581 ----- 580  
971 NHFGPEGCKPCDCHPGSLQCKDDGRCEBGFVGNRCDOCEENFYNRWPGQCE 1030  
581 -----EPVG-----CRSDGTCVCKPFGGPNCEH-----GAFS 608  
1031 CPACYRLVKDKVADHRVKLOELSLANLGTGDEMVTDOAFEDRLKEAREVMDLLREAO 1090  
609 CPACYNQVKIQMDQFMQQLQRMALISAKQGGDVVPDTELEGRMQQAEQALQDILRDAQ 668  
1091 DVKDQDQMLDRQVRNNTLSSQISRLQNRNTIETGNLAQARAHVENTERLIEIASR 1150  
669 ISEGASRSLGLQAKVRQSENSYQRLDLDKMTVERVRLGSGYQNRVRDTHRLITOMQL 728  
1151 ELEKAKYAAANVSUTQPESTGDPNNMTLLAEARKLAERHKEADDDIVRVAKTANDTSTE 1210  
729 SLAESEASLGNITNPASDHYVGNFGFKSLAQAEATLAESHVESASNMQLTRETEDYSKQ 788  
1211 AYNLLRLTL-----AGENQTAFAEIEELNRKYEQAKNISODLEKQAAARVHEEAKRAGDK 1263  
789 ALSLVKALHEGVGSGSPDCAV-VQGLVEKLEKTKSLAQQLTREATQABIEADRSYQH 847  
1264 AVEIVASVAQLSPDSEITL-NEANNIKMEANLEQLIDOKLDYEDLREDMRGKELEVX 1322  
848 SURLDSVSRLOQSDQSFQVEEAKIKQKADSLSTLVRHMDPEFRQKMLGNWKEEAQ 907  
1323 NLEKXKTBQQTADQALLARADAALABEAAKGRDITLQEAANDILNNLKDFDRVNDNKT 1382  
908 QILQNGKREKSDQLLSHANLAKSRAQEAQSMGNATFVEVESILKNLREFDQVDRKA 967  
1383 ABEALRKIPALNQTITENETRAOQALGSAADATEAKNKAHEABERIASAVQKNATS 1442  
968 EABEAMKRLSYISQKVSADSDTQOABRALGSAADAAQAKNGAGEALEISEIEQETGS 1027  
1443 TRAEABRTFAEVTDLIDNEVNNMLKQLEAEKELKQDADQDMMAGNASQAQAEABIN 1502  
1028 LNLEANTVADGALAMEKGLASLSEMRVEGELEKELEFDINMDAVQVITEAQKVDTR 1087  
1503 ARKAKNSVTSLSIINDLEQIQLDQTDVNLKLNIEIGTLNKAQEMKVSDDLDRKVSLE 1562  
1088 AKNAGVTIQDTLLGLHLHLDQPLSVDEGLVLEQLKLSRAKTQIN-SQLRPMWSELE 1146  
1563 NEAKQEAAMVDNRDIEIMKDIRNLEDIRKTLPSGCFNTPSIEK 1608  
1147 ERARQORGHLLHLETSIDGILADVKNLEIRNLRNLPFGCYNTOALEQ 1192

RESULT 15

US-10-171-311-115  
; Sequence 115, Application US/10171311  
; Publication No. US20030087270A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Chen, Yan  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Monahan, John  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Glatt, Karen  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Hoerish, Sebastian  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
; FILE OF INVENTION: OF CERVICAL CANCER  
; FILE REFERENCE: MRI-035  
; CURRENT APPLICATION NUMBER: US/10/171,311  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US 60/298,159  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,155  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/335,936  
; PRIOR FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 1193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-171-311-115  
Query Match 30.3%; Score 2637; DB 14; Length 1193;  
Best Local Similarity 39.4%; Pred. No. 9.4e-142;  
Matches 515; Conservative 237; Mismatches 416; Indels 138; Gaps 12;  
319 CLPFFNDRPWRRTAASASECLPCDNGRSQBCYFPPELYRSTGHGHCNTCNDNTDGAH 378  
9 CLCFSLLFAARATSRRE----VDCNKGSRQCFDREHLHRTGTNGFRCLNCNDNTDGLH 64  
379 CERENRFRRLGNEACSSCHGSPVGLSTQCDSDSYGRCSCKPFGVMGDKCDRCQPGFHSIT 438  
65 CEKCKNGFYHRREDKCLPNCNCKSLGSLARCDNSGRCSCKPFGVTGARCDCLPGFHMILT 124  
439 EAQC-----RPCSDPSGSIENVTGRCVCNVEGFCNCRCKPFPNLESNPR 490  
125 DAGCTDQRLDLSKDCDPAGIAGPC--DAGRCVCKPAVTGRCDCRSGSYNLDGDNPE 182  
491 GCTPCFCFHHSSVCTNAGVSVYSISSTFTQIDBDGWAPQRDQSGSEASLEWSERQDIAVI 550  
183 GCTQCFYGHSSACRSAEYSVHKITSTFHQVDGHWKAVQRNGSPAKLQWSQHQDFVSS 242  
551 SDSYFPFYPIAPAKFLGKQVLSYQNLSPFRVDRDTRLASBDLVLEGAGURSVVPLIA 610  
243 AQRLDPVYFVAPAKFLGNQOVSYQSLSFDRYDRGRHPSAHDVILEGAGLRITAPLMP 302  
611 QGNSYSEITTKVVRHLHEATDYPWRPALTPPBFQKLLNLTISI KIRGTYSRSACYLDD 670  
303 LGKTLPCGLTKTTFRLNHPNNSWSPQLSYFYRRLRLNLTAIRIRATYGEVSTGYIDN 362  
671 VTLASAPFGVGPATWVESCTCPVYGQGFCEMCLSGYRRETNLPYSPCVLCACNHGS 730  
363 VTLISARPVSGAPAPWVEQICFPVYKGFQCDQASGYKRD SARLPGFTGTCPCNQCG-G 421  
731 ETCDPETGVNCDNTAGPHCEKCSQGYGDSGTAGTSSDCQPCPCPGSGSACVVPKTEV 790  
422 GACDPDGTGDCYSGDENPDIEACDPIGFYNDPHDPRS--CKPCPCNNGFSCSWPTEEV 479  
791 VCTNCPGTGTTGKECELCDGDFGDPGLGRNGPVRCLQCQSDNIDPNAVGNCRNLRTGEC 850  
480 VCNCPPGVTGARGELCAGYFGDPFGEHGFVAPQPCQCNVNVDPFSASGNCRLTGRL 539  
851 KCIYNTAGFYCDRCXGDFGNPLAPADKCKACNCPYGTMKQOQSSCNPTVQCCECLPH 910  
540 KCIHNTAGIYCDQCKAGYFGDPLAPNADKCRACNCPMGS----- 580  
911 VTGQDCGACDPGFYNLQSGQGCERCDCALGSTNGQDIRTGQCECQPGITGQRCERCEV 970  
581 ----- 580  
971 NHFGPEGCKPCDCHPGSLQCKDDGRCEBGFVGNRCDOCEENFYNRWPGQCE 1030  
581 -----EPVG-----CRSDGTCVCKPFGGPNCEH-----GAFS 608  
1031 CPACYRLVKDKVADHRVKLOELSLANLGTGDEMVTDOAFEDRLKEAREVMDLLREAO 1090  
609 CPACYNQVKIQMDQFMQQLQRMALISAKQGGDVVPDTELEGRMQQAEQALQDILRDAQ 668  
1091 DVKDQDQMLDRQVRNNTLSSQISRLQNRNTIETGNLAQARAHVENTERLIEIASR 1150  
669 ISEGASRSLGLQAKVRQSENSYQRLDLDKMTVERVRLGSGYQNRVRDTHRLITOMQL 728  
1151 ELEKAKYAAANVSUTQPESTGDPNNMTLLAEARKLAERHKEADDDIVRVAKTANDTSTE 1210  
729 SLAESEASLGNITNPASDHYVGNFGFKSLAQAEATLAESHVESASNMQLTRETEDYSKQ 788  
1211 AYNLLRLTL-----AGENQTAFAEIEELNRKYEQAKNISODLEKQAAARVHEEAKRAGDK 1263



Db 789 ALSIVRKALHEGVSGSGSPDGA-VQGLVEKLEKTSLAQQLTREATQAEIEADRSYQH 847  
Qy 1264 AVEIYASVAQLSPDSETLE-NEANNIKVEAENLEQLIDQKLKDYEDLREDMRGKELEVYK 1322  
Db 848 SLRLDSVSRLOQVSDQSFQVEEAKRIKQKADSLSTLVTRHMDFFKRTQKNLGNWKEEAQ 907  
Qy 1323 NLEKGYTEQQTADOLLARADAARAAKAKGRDTLOEANDILANLKDFDRRVNDNKT 1382  
Db 908 QLLONGKSGREKSDQLLSRANLAKSRAQEAALSMGNATFYEVESILKNLREFDLQVDRKA 967  
Qy 1383 AABEALRKIPAINQTIITEANEKTRAQALGSAADATEAKNKAHAEIRIASAVQKNATS 1442  
Db 968 EAEEMKRLSVISQKVSADSKTQQAERALGSAADAQRAKNGAGEALEISSIEQIEIGS 1027  
Qy 1443 TKAEARTFAEVTDLNNEVNNMLKQLOEAEKELKRQDDADQDMWAGMASQAAQAEIN 1502  
Db 1028 INLEAVNTADGALAMEKGLASLKSEMEFEVEGELEKELEFDTNMDAVQMVITEAQKVDT 1087  
Qy 1503 ARKAKNSVTSLLSTINDLLEQLGQDVTVDLKNLNEIEGTILNKAKDEMKVSDLDKRVSDLE 1562  
Db 1088 AKNAGVTIQTINTLDGLHMDPLSVDBEGLVLEQLSRAKTQIN-SOLRPMWSELE 1146  
Qy 1563 NEAKQBAAMNDYNRDIEEIMKDIRNLEDIRKTLPSCCFNTPSIEK 1608  
Db 1147 ERARQQRGHLHLETSIDGILADYKNLENIRDNLPFGCYNTQALEQ 1192

Search completed: May 18, 2004, 15:42:52  
Job time : 47.9344 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 14.8077 Seconds

(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-14

Perfect score: 8713

Sequence: 1 WRGSHRAPALPRGRLWPV.....EDIRKTLPGCFNTPSIEKP 1609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	8709	100.0	1609	1	MMHUB2	laminin gamma-1 ch
2	8161	93.7	1607	1	MMHUB2	laminin gamma-1 ch
3	3433	39.4	1639	1	MMHUB2	laminin gamma-1 ch
4	3240	37.2	1557	2	T28811	hypothetical prote
5	2637	30.3	1193	2	A44018	laminin B2t chain
6	2454.5	28.2	1192	2	S69000	laminin gamma 2 ch
7	1782.5	20.5	3084	1	MMHUBA	laminin alpha-1 ch
8	1774.5	20.4	3106	1	S53868	laminin alpha-2 ch
9	1739.5	20.0	3075	2	S14458	laminin alpha-1 ch
10	1680.5	19.3	1786	1	MMHUB1	laminin beta-1 cha
11	1669.5	19.2	1790	1	MMHUB1	laminin beta-1 cha
12	1651	18.9	1786	1	MMHUB1	laminin beta-1 cha
13	1626.5	18.7	2823	2	T23064	hypothetical prote
14	1626.5	18.7	2823	2	P87908	protein T22A3.8 li
15	1626.5	18.7	3102	2	T43291	laminin alpha chai
16	1613.5	18.5	1801	1	MMHUB1	laminin beta-2 cha
17	1608	18.5	1808	2	S15099	hypothetical prote
18	1598.5	18.3	1798	2	S53869	laminin beta-2 cha
19	1496	17.2	1797	2	A55677	laminin beta-2 cha
20	1486.5	17.1	3712	2	S18253	laminin alpha-1 ch
21	1394	16.0	3672	2	T23433	hypothetical prote
22	1394	16.0	3704	2	T10053	probable laminin a
23	1327.5	15.2	3635	2	T10053	laminin alpha 5 ch
24	1173	13.5	606	2	A54665	netrin-1 precursor
25	1070	12.3	581	2	A54665	netrin-2 precursor
26	989	11.4	612	2	JH0799	laminin-related pr
27	923	10.6	1170	2	A53612	laminin B1k chain
28	887.5	10.2	1168	2	I56985	kalinin B1 - mouse
29	880	10.1	4391	2	A38096	perlecan precursor

## ALIGNMENTS

### RESULT 1

MMHUB2

laminin gamma-1 chain precursor

human

laminin chain B2

N/Alternate names: laminin chain B2

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C/Accession: S13548; A28158; S13549; B34961; S14664; S23567

R/Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.

J. Biol. Chem. 265, 221-228, 1991

A/Title: Structure of the human laminin B2 chain gene reveals extensive divergence from t

A/Reference number: S13548; MUID: S1093128; PMID: 1955895

A/Accession: S13548

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1609 <KAL>

A/Cross-references: GB:M55217; NID:G186937

A/Note: the nucleotide sequence was submitted to GenBank, February 1991

R/Pikkarainen, T.; Kallunki, T.; Tryggvason, K.

J. Biol. Chem. 263, 6751-6758, 1988

A/Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the

A/Reference number: A28158; MUID: 88198245; PMID: 3360804

A/Accession: A28158

A/Molecule type: mRNA

A/Residues: 1-211, 'I', 213-1609 <PIK>

A/Cross-references: EMBL:J03202; NID:G186916; PIDN:AAA59488.1; PID:G307107

R/Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; Her

Cytogenet. Cell Genet. 48, 137-141, 1988

A/Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene to

A/Reference number: S13549; MUID: 89169663; PMID: 3234037

A/Accession: S13549

A/Molecule type: mRNA

A/Residues: 1393-1609 <PIK>

A/Cross-references: EMBL:M27654; NID:G186923; PIDN:AAA59489.1; PID:G186924

R/Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.

Lab. Invest. 60, 772-782, 1989

A/Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha

A/Reference number: A34961; MUID: 89280632; PMID: 2733383

A/Accession: B34961

A/Molecule type: mRNA

A/Residues: 868-1551, 'N', 1553-1609 <OLS>

A/Cross-references: EMBL:J13939; NID:G34237; PIDN:CAA32122.1; PID:G34238

R/Santos, C.L.S.; Sabbaga, J.; Brentani, R.

DNA Seq. 1, 275-277, 1991

A/Title: Differences in human laminin B2 sequences.

A/Reference number: S14664; MUID: 92216129; PMID: 1806043

A/Accession: S14664

A/Molecule type: mRNA

A/Residues: 1282-1609 <SANT>

A/Cross-references: EMBL:XI3939; NID:G34237; PIDN:CAA32122.1; PID:G34238

R/Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.

In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P

A/Title: Genes for the human laminin B1 and B2 chains.

A/Reference number: S23566

A;Accession: S23567		421	GVMGDKCDRCQPGFHSUTEAGCRPCSDPSGSDIBCNVETGRVCVKDNVGFNCERCKPG	480
A;Molecule type: DNA		481	FFNLESSNPRGCTPCFCFHSSVCTNAVGYSVYSISSTFOIDEDGMRABORDSEASLEW	540
A;Residues: 801-1481, 'R', 1483-1609 <VUO>		481	FFNLESSNPRGCTPCFCFHSSVCTNAVGYSVYSISSTFOIDEDGMRABORDSEASLEW	540
A;Note: mRNA was also sequenced		541	SSERQDIATVSDSYFPRYFTAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA	600
C;Genetics:		541	SSERQDIATVSDSYFPRYFTAPAKFLGKQVLSYGQNLSPFSFRVDRDRTRLSAEDLVLEGA	600
A;Gene: GDB:LAMC1; LAMB2		601	GLRVSVELIAAQNSYPSETTKVYFRLEHATDYPWRPALTPPFQKLLNNLTISKIRGT	660
A;Cross-references: GDB:120136; OMIM:150290		601	GLRVSVELIAAQNSYPSETTKVYFRLEHATDYPWRPALTPPFQKLLNNLTISKIRGT	660
A;Map position: 1q31-1q31		661	SERAGYLDVMTLASARPGQVATWVESCCTCPVGVGGQFCMCLSYRRETNLGYSYP	720
A;Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1; 731; 1525/1		661	SERAGYLDVMTLASARPGQVATWVESCCTCPVGVGGQFCMCLSYRRETNLGYSYP	720
C;Function:		721	CVLCAKNGHSETCDPETGVCNCRDNTAGPHEKCSGYYGDSSTAGTSSDQCPGCGSS	780
C;Description: Interact with cells and with other basement membrane proteins to promote		721	CVLCAKNGHSETCDPETGVCNCRDNTAGPHEKCSGYYGDSSTAGTSSDQCPGCGSS	780
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology		781	CAVVPKTKVVCNCPGTTGKCELCDDGDFGDLGRNGPVRCLRCQCSQDNDPNAVG	840
C;Keywords: Basement membrane; calcium binding; cell binding; coiled coil; extracellular		781	CAVVPKTKVVCNCPGTTGKCELCDDGDFGDLGRNGPVRCLRCQCSQDNDPNAVG	840
F;1-33/Domain: signal sequence #status predicted <SIG>		841	NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNLPADKCKACNCNPNYGTMTKQSSCNP	900
F;34-1609/Product: laminin gamma-1 chain #status predicted <MAT>		841	NCNRLTGECLKCIYNTAGFYCDRCCKDGFNGNLPADKCKACNCNPNYGTMTKQSSCNP	900
F;34-285/Domain: VI <DOM6>		901	VTGQCECLPHVTGQDCACDPGFNLOSOGGCRCDCHALGSTNGQCDITGQCECPGI	960
F;286-504/Domain: V <DOM5>		901	VTGQCECLPHVTGQDCACDPGFNLOSOGGCRCDCHALGSTNGQCDITGQCECPGI	960
F;286-339/Domain: laminin-type EGF-like homology <LE01>		961	TGQHCERCEVNHFGPGECKPCDCHPEGSLSLQCKDDGRCCEGFGVGNRCQCEBNYF	1020
F;342-395/Domain: laminin-type EGF-like homology <LE02>		961	TGQHCERCEVNHFGPGECKPCDCHPEGSLSLQCKDDGRCCEGFGVGNRCQCEBNYF	1020
F;398-442/Domain: laminin-type EGF-like homology <LE03>		1021	YNRWPGQCEPCACRYLVKQVADHRVKLOESLILANLGTGBMVTQDAFEDRLKEAR	1080
F;445-492/Domain: laminin-type EGF-like homology <LE04>		1021	YNRWPGQCEPCACRYLVKQVADHRVKLOESLILANLGTGBMVTQDAFEDRLKEAR	1080
F;495-504/Domain: laminin-type EGF-like homology <LE05>		1081	EVMDLLREAOQVQDVQDNLMDRLORVNTLSQISRLQNTIETETGNLAEQARAHVEN	1140
F;505-689/Domain: IV <DOM4>		1081	EVMDLLREAOQVQDVQDNLMDRLORVNTLSQISRLQNTIETETGNLAEQARAHVEN	1140
F;690-1034/Domain: III <DOM3>		1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQAEADDIVRV	1200
F;690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>		1141	TERLIEIASRELEKAKVAAANVSVTQPESTGDPNNMTLLAEARKLAERHKQAEADDIVRV	1200
F;724-770/Domain: laminin-type EGF-like homology <LE07>		1201	AKTANDTSTEAYNLLRLTLAGENQTAFEIELNRYEQAKNISQLEKQAAARVHEEAKRA	1260
F;773-825/Domain: laminin-type EGF-like homology <LE08>		1201	AKTANDTSTEAYNLLRLTLAGENQTAFEIELNRYEQAKNISQLEKQAAARVHEEAKRA	1260
F;828-881/Domain: laminin-type EGF-like homology <LE09>		1261	GDKAVEIYASVAQLSPDSETELEANNIKMEAEENLSQLIDQKLYOYEDUREDRGRKELE	1320
F;884-932/Domain: laminin-type EGF-like homology <LE10>		1261	GDKAVEIYASVAQLSPDSETELEANNIKMEAEENLSQLIDQKLYOYEDUREDRGRKELE	1320
F;935-980/Domain: laminin-type EGF-like homology <LE11>		1321	VNKLKQKTEBOQTADQLARADAAKALAEAAKKGRTDLOEANDILNNLKDFRRVNDN	1380
F;983-1028/Domain: laminin-type EGF-like homology <LE12>		1321	VNKLKQKTEBOQTADQLARADAAKALAEAAKKGRTDLOEANDILNNLKDFRRVNDN	1380
F;1035-1609/Region: heptad repeats		1381	KTAAEALRKIPAINQITTEANEXTREAAQQAALGSAADAATAEAKNKAHEAERIASAVQKNA	1440
F;140-50/Disulfide bonds: #status predicted		1381	KTAAEALRKIPAINQITTEANEXTREAAQQAALGSAADAATAEAKNKAHEAERIASAVQKNA	1440
F;60,134,576,502,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbonyl		1441	TSTKAAERTFAEVTDLNNEVNNMLKQLOAEAKELKQDQDQDMMAGWASQAQAE	1500
F;1031,1034,1600/Disulfide bonds: interchain #status predicted		1441	TSTKAAERTFAEVTDLNNEVNNMLKQLOAEAKELKQDQDQDMMAGWASQAQAE	1500
Query Match 100.0%; Score 8709; DB 1; Length 1609;		1501	INARKAKNSVTSLSIINDLLEQLGQDVTDLNKLNEIETGLNKAKDEMKYSDLDKRVSD	1560
Best Local Similarity 99.9%; Pred No. 4e-314;		1501	INARKAKNSVTSLSIINDLLEQLGQDVTDLNKLNEIETGLNKAKDEMKYSDLDKRVSD	1560
Matches 1609; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	MRGSHRAAPALPRGRUWPLVLAIAAAGCAQAAWDECTDEGGRPQRCMPFVNAAFN	60	
Db	1	MRGSHRAAPALPRGRUWPLVLAIAAAGCAQAAWDECTDEGGRPQRCMPFVNAAFN	60	
Qy	61	VTVATNTCGTPPEYCVQGVTVTKSCHLDCAGOPHLOHGAFLTDYNNQADTTWQS	120	
Db	61	VTVATNTCGTPPEYCVQGVTVTKSCHLDCAGOPHLOHGAFLTDYNNQADTTWQS	120	
Qy	121	QTMLAGVQYPPSSINLTLHLKAFDITYVRLKFTSRPESPAIYKRTREDGPMIPYQYSG	180	
Db	121	QTMLAGVQYPPSSINLTLHLKAFDITYVRLKFTSRPESPAIYKRTREDGPMIPYQYSG	180	
Qy	181	SCENTYSKANRGFTRTGGDQQAALCTDFESDI SPLTGNVAFSTLGRPSAYNFNSPVL	240	
Db	181	SCENTYSKANRGFTRTGGDQQAALCTDFESDI SPLTGNVAFSTLGRPSAYNFNSPVL	240	
Qy	241	QEWVTATDIRVTNLRLNTFGDEFNDPKVLKSYIYAIISDFAVGRCCKNGHASECMKNEF	300	
Db	241	QEWVTATDIRVTNLRLNTFGDEFNDPKVLKSYIYAIISDFAVGRCCKNGHASECMKNEF	300	
Qy	301	DKLVNCKHNTYGVDCSKCLPFNDPRWRATASASECLPCDNGRSQECYEDPELYRS	360	
Db	301	DKLVNCKHNTYGVDCSKCLPFNDPRWRATASASECLPCDNGRSQECYEDPELYRS	360	
Qy	361	TGHGGHCTNCOQDNDGHAFCRCRNFRLGNNEACSSCHSPVGSLSLSTQCDSYGRCSCKP	420	
Db	361	TGHGGHCTNCOQDNDGHAFCRCRNFRLGNNEACSSCHSPVGSLSLSTQCDSYGRCSCKP	420	
Qy	421	GVMGDKCDRCQPGFHSUTEAGCRPCSDPSGSDIBCNVETGRVCVKDNVGFNCERCKPG	480	

QY 1561 LENEAKQEAALMDYNRDIEIMKIDIRNLEDIRKTLPSGCNTPSIEKP 1609  
DB 1561 LENEAKQEAALMDYNRDIEIMKIDIRNLEDIRKTLPSGCNTPSIEKP 1609

RESULT 2  
MMMS2  
laminin gamma-1 chain precursor - mouse  
N:Alternate names: laminin chain B2  
C:Species: Mus musculus (house mouse)  
C>Date: 28-Feb-1985 #sequence revision 30-Jun-1991 #text change 10-Dec-1999  
C:Accession: A28469; A27729; A28082; S02680; S05327; S02037; A02870; S13544; S14552  
R:Sasaki, M.; Yamada, Y.  
J. Biol. Chem. 262, 17111-17117, 1987  
A>Title: The laminin B2 chain has a multidomain structure homologous to the B1 chain.  
A:Reference number: A28469; MUID:88059118; PMID:3680290  
A:Accession: A28469  
A:Molecule type: mRNA  
A:Residues: 1-1607 <SAS>  
A:Cross-references: EMBL:J03484; NID:G198594; PIDN:AAA39405.1; PID:G293688  
R:Durkin, M.E.; Batic, B.B.; Liu, S.H.; Phillips, S.L.; Chung, A.E.  
Biochemistry 27, 5198-5204, 1988  
A>Title: Primary structure of the mouse laminin B2 chain and comparison with laminin B1.  
A:Reference number: A27729; MUID:89000737; PMID:3167041  
A:Accession: A27729  
A:Molecule type: mRNA  
A:Residues: 1-263, 'D', 265-336, 'C', 338-446, 'PS', 449-661, 'S', 663-885, 887-1155, 1157-1433, 'A'  
A:Cross-references: EMBL:J03749; NID:G198704; PIDN:AAA39409.1; PID:G554184  
R:Fukuiwaka, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A>Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02680  
A:Molecule type: protein  
A:Residues: 227-238 <FUJ>  
R:Hartl, L.; Oberbauer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A>Title: The N terminus of laminin A chain is homologous to the B chains.  
A:Reference number: S00624; MUID:88225080; PMID:3267223  
A:Accession: S05327  
A:Molecule type: protein  
A:Residues: 227-238; 387-393, 'F', 395-405; 881-912; 1022-1034 <HAR>  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A>Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te  
A:Reference number: S01790; MUID:89030593; PMID:3181157  
A:Accession: S02037  
A:Molecule type: protein  
A:Residues: 1362-1377, 'X', 1379-1392, 'X', 1394-1406 <DEU>  
R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.  
EMBO J. 3, 2355-2362, 1984  
A>Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a  
A:Reference number: A02870; MUID:85051302; PMID:6209134  
A:Accession: A02870  
A:Molecule type: mRNA  
A:Residues: 1391-1474, 'K', 1476-1575, 'N', 1577-1607 <BAR>  
A:Cross-references: EMBL:X05211; NID:G52862; PIDN:CAA28838.1; PID:G817975  
R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
EMBO J. 4, 309-316, 1985  
A>Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
A:Reference number: S13543; MUID:85257455; PMID:3848400  
A:Accession: S13544  
A:Molecule type: protein

A:Residues: 1506-1523, 'X', 1525 <PAU>  
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, M.  
Lab. Invest. 60, 772-782, 1989  
A>Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A:Reference number: A34961; MUID:89280632; PMID:2733383  
A:Accession: S14552  
A:Molecule type: protein  
A:Residues: 881-912; 1022-1034; 1364-1377; 1379-1392; 1394-1409; 1506-1525; 1593-1606 <OLS>  
C:Genetics:  
A:Gene: Lamb-2  
A:Map position: 1  
A:Introns: 138/1; 239/3  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:34-1607/Product: laminin gamma-1 chain #status predicted <MAT>  
F:34-283/Domain: VI <DOM6>  
F:284-502/Domain: V <DOM5>  
F:284-337/Domain: laminin-type EGF-like homology #status atypical <LE01>  
F:340-393/Domain: laminin-type EGF-like homology <LE02>  
F:396-440/Domain: laminin-type EGF-like homology <LE03>  
F:443-490/Domain: laminin-type EGF-like homology <LE04>  
F:493-502/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:503-687/Domain: IV <DOM4>  
F:688-1032/Domain: III <DOM3>  
F:688-719/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F:722-768/Domain: laminin-type EGF-like homology <LE07>  
F:771-823/Domain: laminin-type EGF-like homology <LE08>  
F:826-879/Domain: laminin-type EGF-like homology <LE09>  
F:882-930/Domain: laminin-type EGF-like homology <LE10>  
F:933-978/Domain: laminin-type EGF-like homology <LE11>  
F:981-1026/Domain: laminin-type EGF-like homology <LE12>  
F:1033-1607/Domain: II/I <DOM2>  
F:1033-1607/Region: heptad repeats  
F:38-48/Disulfide bonds: #status predicted  
F:58,132,574,648,1020,1105,1159,1173,1203,1221,1239,1437/Binding site: carbohydrate (Asn)  
F:1029,1032/Disulfide bonds: interchain (Asn) #status predicted  
F:1378,1393/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:1598/Disulfide bonds: interchain (to chain B1) #status experimental

Query Match 93.7%; Score 8161; DB 1; Length 1607;  
Best Local Similarity 92.7%; Pred. No. 6.7e-294;  
Matches 1492; Conservative 61; Mismatches 54; Indels 2; Gaps 1;

QY 1 MRGSHRAAPALRRGRILWPLVLAIAAAAGCAQAAMDECTDEGGRPQRCMPEFVNAAFN 60  
DB 1 MTGGRAALALQPRGLMPLAVL--AAVAGCVRAAMDECADEGGRPQRCMPEFVNAAFN 58  
QY 61 VTVAINTCCTPPEEYCVQVTGVTGKSKCHLDAGQPHLQHGAAFLTDYNNQADTTWQS 120  
DB 59 VTVAINTCCTPPEEYCVQVTGVTGKSKCHLDAGQPHLQHGAAFLTDYNNQADTTWQS 118  
QY 121 QTMAGVQVPSINLTLHLGKAFDITVRLKFTSPESFAIYKRTREDGPMIPYQYSG 180  
DB 119 QTMAGVQVPSINLTLHLGKAFDITVRLKFTSPESFAIYKRTREDGPMIPYQYSG 178  
QY 181 SCENTYSKANRGFIRTGDEQQALCTDEFSIDISPLTGGNVAFSTLGRFSAYNFNSPVL 240  
DB 179 SCENTYSKANRGFIRTGDEQQALCTDEFSIDISPLTGGNVAFSTLGRFSAYNFNSPVL 238  
QY 241 QEWATATDIRVTNRLNTGTDEVFNPKVLKSYVYAI SDFAVGGRCKNGHASECMKNEF 300  
DB 239 QEWATATDIRVTNRLNTGTDEVFNPKVLKSYVYAI SDFAVGGRCKNGHASECMKNEF 298  
QY 301 DKLVCMCKNTYGVDCCKLPFFNDPRWRATAESCLPCDCNGRSQECYFDPPELYRS 360  
DB 299 DKLVCMCKNTYGVDCCKLPFFNDPRWRATAESCLPCDCNGRSQECYFDPPELYRS 358  
QY 361 TGGGCTNCDNTDGAHCRERENFRILGNNEACSSCHSPVGSISTOCDSYGRCSCKP 420

359 TGHGGCTNCRDNTDGAKECRERENFRNLGNTAEACSPCHCSPVGSLSTQCDYGRCSCKP 418  
421 GVMGDKCDRCQPGFHSILTEAGRCPCSDPGSGIDECEVETGRVCVKNVGEFCNCRKPG 480  
419 GVMGDKCDRCQPGFHSILTEAGRCPCSDPGSGIDECEVETGRVCVKNVGEFCNCRKPG 478  
481 FFLNLSNPRGCTPCFCFSGHSSVCTNAGVSVVYSISSTFOIDEDGWRAROGSGSASLEW 540  
479 FFLNLSNPRGCTPCFCFSGHSSVCTNAGVSVVYSISSTFOIDEDGWRAROGSGSASLEW 538  
541 SSSRQDIANTSDSYFFRYFIAPAKFLGKQVLSYQNLSPFSFRVDRDRTLSAEDLVLEGA 600  
539 SSSRQDIANTSDSYFFRYFIAPAKFLGKQVLSYQNLSPFSFRVDRDRTLSAEDLVLEGA 598  
601 GLRVSVPLIAQGNYSYSETTKVFRHLHEATYDWPALTPPEFQKLNLSIKIRGTY 660  
599 GLRVSVPLIAQGNYSYSETTKVFRHLHEATYDWPALTPPEFQKLNLSIKIRGTY 658  
661 SERSAGVLDVTLASAPGPGVPATVWVESCCTPVGSGGFCFNCISGYSYRRETNLPYSP 720  
659 SERSAGVLDVTLASAPGPGVPATVWVESCCTPVGSGGFCFNCISGYSYRRETNLPYSP 718  
721 CVLCAANGHSETCDPFTGVNCRDNTAGPHCEKCSGYYGDSSTAGTSYSDCQPCPPGGSS 780  
719 CVLCTGNHSETCDPFTGVNCRDNTAGPHCEKCSGYYGDSSTAGTSYSDCQPCPPGGSS 778  
781 CAUVPTKEVVTNCPGTGKCELCDDGYFGDPLGRNGPVLCRLCOCSDNIDNNAV 840  
779 CAUVPTKEVVTNCPGTGKCELCDDGYFGDPLGRNGPVLCRLCOCSDNIDNNAV 838  
841 NCNRLTCEGLKCIYNTAGFYCDRCXGDFGNPLAPNADPKACACNPNYGTWKQSSCNP 900  
839 NCNRLTCEGLKCIYNTAGFYCDRCXGDFGNPLAPNADPKACACNPNYGTWKQSSCNP 898  
901 VTGOCCLPHVTGDCACDPGPNVLOSOGCERCDCHALGSTNGODIRTGOCCEQPGI 960  
899 VTGOCCLPHVTGDCACDPGPNVLOSOGCERCDCHALGSTNGODIRTGOCCEQPGI 958  
961 TGQHCERCEVNHFGFEGEGKPCDCHPEGSLSLQCKDGRCEKRGFVGNRCQCENYF 1020  
959 TGQHCERCEVNHFGFEGEGKPCDCHPEGSLSLQCKDGRCEKRGFVGNRCQCENYF 1018  
1021 YNRSWPCQCPACRYLVKQVADHRVKLOELESILANTGTGDEMVTDOAFEDRLKEAR 1080  
1019 YNRSWPCQCPACRYLVKQVADHRVKLOELESILANTGTGDEMVTDOAFEDRLKEAR 1078  
1081 EVMOLLREADQVNDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEOARHVN 1140  
1079 EVTLLEAEQVNDQNLMDRLQRVNNTLSSQISRLQNRNTIETGNLAEOARHVN 1138  
1141 TERLIEIASRELEKAKVAANVSITQPESTGDPNNMTLLAEBAKLAERHKEADIVRV 1200  
1139 TERLIEIASRELEKAKVAANVSITQPESTGDPNNMTLLAEBAKLAERHKEADIVRV 1198  
1201 AKTANDTSTAYNLLRLTAGENOTAFIEBELNRKYEQAKNISQDLKQARVHEBAKRA 1260  
1199 AKTANETSAYNLLRLTAGENOTAFIEBELNRKYEQAKNISQDLKQARVHEBAKRA 1258  
1261 GDKAVEIYASVAQSPILDSEPLENANNKWEANLEPOLIDOKLYEDLREDMRGKELE 1320  
1259 GDKAVEIYASVAQSPILDSEPLENANNKWEANLEPOLIDOKLYEDLREDMRGKELE 1318  
1321 VKNLLEKTKTQOQTADQLARADAKALAEBAKKGRTDILQEANDILNNLKDFDRVNDN 1380  
1319 VKNLLEKTKTQOQTADQLARADAKALAEBAKKGRTDILQEANDILNNLKDFDRVNDN 1378  
1381 KTAEEALRKIPAINOTITEANEXTREAAQALGSAADATEAKNKAHEERIASAVQKNA 1440  
1379 KTAEEALRKIPAINOTITEANEXTREAAQALGSAADATEAKNKAHEERIASAVQKNA 1438  
1441 TSTKAEABERTFAEVTDLNNEVNNMLKQLOEAKESIKKQDADODMMAGWASQAQAEAE 1500  
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QY 1501 INARKXNVSITLLSIINDILLEGQLDQTDVINKLNEIEGTAKAKEMKVSDLDKRVSD 1560  
DB 1499 INARKXNVSITLLSIINDILLEGQLDQTDVINKLNEIEGTAKAKEMKVSDLDKRVSD 1558  
QY 1561 LENEAKQEAALIMYDNRDIEBEIMKDRINLEDIRKTLPSGCFNTPSIEKP 1609  
DB 1559 LENEAKQEAALIMYDNRDIEBEIMKDRINLEDIRKTLPSGCFNTPSIEKP 1607  
RESULT 3  
NMFFB2  
laminin gamma-1 chain precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: laminin chain B2  
C:Species: Drosophila melanogaster  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000  
C:Accession: A31483; A33737; S01733; A40502  
R:Chi, H.C.; Hui, C.F.  
J. Biol. Chem. 264, 1543-1550, 1989  
A:Title: Primary structure of the Drosophila laminin B2 chain and comparison with human.  
A:Reference number: A31483; MUID:89109164; PMID:2912972  
A:Accession: A31483  
A:Molecule type: mRNA  
A:Residues: 1-1639 <CHI>  
A:Cross-references: EMBL:IM25063; NID:G157803; PIDN:AAA28664.1; PID:G157804  
R:Montell, D.J.; Goodman, C.S.  
J. Cell Biol. 109, 2441-2453, 1989  
A:Title: Drosophila laminin: sequence of B2 subunit and expression of all three subunits  
A:Reference number: A33737; MUID:90037237; PMID:2808533  
A:Accession: A33737  
A:Molecule type: mRNA  
A:Residues: 1-39, 'T', '41-991, 'L', 893-1106, 'T', 1108-1459, 'HV', 1462-1591, 'G', 1583-1639 <MON  
A:Note: 831-Tyr was also found  
R:Chi, H.C.; Hui, C.F.  
Nucleic Acids Res. 16, 7205-7206, 1988  
A:Title: cDNA and amino acid sequences of Drosophila laminin B2 chain.  
A:Reference number: S01733; MUID:88303364; PMID:3405777  
A:Accession: S01733  
A:Molecule type: mRNA  
A:Residues: 344-1639 <CH2>  
A:Cross-references: EMBL:X07806; NID:G8179; PIDN:CAA30665.1; PID:G1335618  
A:Note: The authors translated the codon GGC for residue 409 as Phe  
R:Chi, H.C.; Juminaga, D.; Wang, S.Y.; Hui, C.F.  
DNA Cell Biol. 10, 451-466, 1991  
A:Title: Structure of the Drosophila gene for the laminin B2 chain.  
A:Reference number: A40502; MUID:91299161; PMID:1840513  
A:Accession: A40502  
A:Molecule type: DNA  
A:Residues: 1-891, 'L', 893-1639 <CH3>  
A:Cross-references: GB:M58417; NID:G157805; PIDN:AAA28665.1; PID:G157806  
C:Genetics:  
A:Gene: lamB2  
A:Cross-references: FlyBase:FBgn0002528  
A:Map position: 3L 67C  
A:Introns: 65/3; 110/2; 153/1; 358/1; 495/2; 1357/2; 1469/3; 1570/1  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:34-1639/Product: laminin gamma-1 chain #status predicted <MAT>  
F:34-297/Domain: VI <DOM6>  
F:298-528/Domain: V <DOM5>  
F:299-356/Domain: laminin-type EGF-like homology <LE01>  
F:359-411/Domain: laminin-type EGF-like homology <LE02>  
F:414-458/Domain: laminin-type EGF-like homology <LE03>  
F:461-511/Domain: laminin-type EGF-like homology <LE04>  
F:514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:529-705/Domain: IV <DOM4>  
F:706-1057/Domain: III <DOM3>  
F:710-741/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F:744-790/Domain: laminin-type EGF-like homology <LE07>

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 9.14821 Seconds  
(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-14

Perfect score: 8713

Sequence: 1 MRGSHRAPALPRGRLWPV.....EDIRKTLPSGCFNTSIEKP 1609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8709	100.0	1609	1	LMG1 HUMAN
2	8161	93.7	1607	1	LMG1 MOUSE
3	3611	41.4	1587	1	LMG3 HUMAN
4	3492.5	40.1	1581	1	LMG3 MOUSE
5	3440	39.5	1639	1	LMG1 DROME
6	3222	37.0	1535	1	LMG1 CAEL
7	2637	30.3	1193	1	LMG2 HUMAN
8	2529	29.0	1191	1	LMG2 MOUSE
9	1782.5	20.5	3084	1	LMG1 MOUSE
10	1782.5	20.5	3110	1	LMG2 HUMAN
11	1774.5	20.4	3106	1	LMG2 MOUSE
12	1739.5	20.0	3075	1	LMG1 HUMAN
13	1680.5	19.3	1786	1	LMG1 HUMAN
14	1669.5	19.2	1790	1	LMG1 DROME
15	1651	18.9	1786	1	LMG1 MOUSE
16	1613.5	18.5	1801	1	LMG2 RAT
17	1592.5	18.3	1798	1	LMG2 HUMAN
18	1572	18.0	1799	1	LMG2 MOUSE
19	1486.5	17.1	3712	1	LMG1 DROME
20	1394	16.0	3672	1	LMG2 CAEL
21	1373.5	15.8	3718	1	LMG5 MOUSE
22	1318	15.1	3695	1	LMG5 HUMAN
23	1174	13.5	604	1	NET1 MOUSE
24	1173	13.5	604	1	NET1 HUMAN
25	1173	13.5	606	1	NET1 CHICK
26	1141.5	13.1	3333	1	LMG3 MOUSE
27	1070	12.3	581	1	NET2 CHICK
28	989	11.4	612	1	UNC6 CAEL
29	930	10.7	1172	1	LMG3 HUMAN
30	887	10.2	727	1	NETA DROME
31	886.5	10.2	1168	1	LMG3 MOUSE
32	880	10.1	4351	1	PGM1 HUMAN
33	867.5	10.0	793	1	NET5 DROME

34 867.5 10.0 3707 1 PGBM MOUSE  
35 640.5 7.4 539 1 NTG1 MOUSE  
36 609 7.0 3375 1 UNS2 CAEL  
37 581 6.7 530 1 NTG2 HUMAN  
38 571.5 6.6 1816 1 LMA4 HUMAN  
39 554.5 6.4 1816 1 LMA4 MOUSE  
40 545 6.3 589 1 NTG2 MOUSE  
41 510 5.9 1713 1 LMA3 HUMAN  
42 485 5.6 303 1 LMB1 CHICK  
43 474.5 5.4 2524 1 NOTC XENIA  
44 454.5 5.2 2437 1 NTC1 BRARE  
45 453.5 5.2 2703 1 NOTC DROME

#### ALIGNMENTS

RESULT 1  
LMG1 HUMAN  
ID LMG3 HUMAN STANDARD; PRT; 1609 AA.  
AC P11047;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin gamma-1 chain precursor (laminin B2 chain).  
GN LAMC1 OR LAMB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91093128; PubMed=1985895;  
RA Kallunki T., Ikonen J., Chow L.T., Kallunki P., Tryggvason K.;  
RT "Structure of the human laminin B2 chain gene reveals extensive  
RT divergence from the laminin B1 chain gene.";  
EL J. Biol. Chem. 266:221-228(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89198245; PubMed=3360804;  
RA Pikkariainen T., Kallunki T., Tryggvason K.;  
RT "Human laminin B2 chain. Comparison of the complete amino acid  
RT sequence with the B1 chain reveals variability in sequence homology  
RL between different structural domains.";  
RN [3]  
RP SEQUENCE OF 1393-1609 FROM N.A.  
RX MEDLINE=89169663; PubMed=3234037;  
RA Fukushima Y., Pikkariainen T., Kallunki T., Eddy R.L., Byers M.G.,  
RA Haley L.L., Henry W.M., Tryggvason K., Shows T.B.;  
RT "Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of  
RT the gene to chromosome region 1q25-->q31.";  
RN [4]  
RP SEQUENCE OF 1282-1609 FROM N.A.  
RX TISSUE-Endothelial cells;  
RX MEDLINE=92216129; PubMed=1806043;  
RA Santos C.L.S., Sabbaga J., Brentani R.;  
RT "Differences in human laminin B2 sequences.";  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITE ASN-650.  
RX MEDLINE=22660472; PubMed=12754519;  
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;  
RT "Identification and quantification of N-linked glycoproteins using  
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";  
RN [6]  
RP Nat. Biotechnol. 21:660-666(2003).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound





Query Match				100.0%; Score 8709; DB 1; Length 1609;
Best Local Similarity				99.9%; P-Id: 1.5e-315; Indels 0; Gaps 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1	MRGSHRAAPALPRGRWLPVLA	1	MRGSHRAAPALPRGRWLPVLA
DB	1	MRGSHRAAPALPRGRWLPVLA	1	MRGSHRAAPALPRGRWLPVLA
QY	61	VTVAINTCGTPPEEYCVGTGVT	61	VTVAINTCGTPPEEYCVGTGVT
DB	61	VTVAINTCGTPPEEYCVGTGVT	61	VTVAINTCGTPPEEYCVGTGVT
QY	121	QTMLAGVQVPSINLTGKAFDIT	121	QTMLAGVQVPSINLTGKAFDIT
DB	121	QTMLAGVQVPSINLTGKAFDIT	121	QTMLAGVQVPSINLTGKAFDIT
QY	181	SCENTYSKANRGFIRFGDQOAL	181	SCENTYSKANRGFIRFGDQOAL
DB	181	SCENTYSKANRGFIRFGDQOAL	181	SCENTYSKANRGFIRFGDQOAL
QY	241	QEWATATDRTVTLNRLNTGDE	241	QEWATATDRTVTLNRLNTGDE
DB	241	QEWATATDRTVTLNRLNTGDE	241	QEWATATDRTVTLNRLNTGDE
QY	301	DKLVCKNTGYGDCCKLPFNDP	301	DKLVCKNTGYGDCCKLPFNDP
DB	301	DKLVCKNTGYGDCCKLPFNDP	301	DKLVCKNTGYGDCCKLPFNDP
QY	361	TGHHGCTCQDNTDGAHCRCP	361	TGHHGCTCQDNTDGAHCRCP
DB	361	TGHHGCTCQDNTDGAHCRCP	361	TGHHGCTCQDNTDGAHCRCP
QY	421	GVNGDKCDRCQPGFHSILT	421	GVNGDKCDRCQPGFHSILT
DB	421	GVNGDKCDRCQPGFHSILT	421	GVNGDKCDRCQPGFHSILT
QY	481	FFNLESNPRGCTPCFCFHS	481	FFNLESNPRGCTPCFCFHS
DB	481	FFNLESNPRGCTPCFCFHS	481	FFNLESNPRGCTPCFCFHS
QY	541	SSERQDIIVSDSYFPRYI	541	SSERQDIIVSDSYFPRYI
DB	541	SSERQDIIVSDSYFPRYI	541	SSERQDIIVSDSYFPRYI
QY	601	GLRVSVPLIAQNSYSEST	601	GLRVSVPLIAQNSYSEST
DB	601	GLRVSVPLIAQNSYSEST	601	GLRVSVPLIAQNSYSEST
QY	661	SERSAGVLDVTLASARPG	661	SERSAGVLDVTLASARPG
DB	661	SERSAGVLDVTLASARPG	661	SERSAGVLDVTLASARPG
QY	721	CVLCAACNGHSETCDP	721	CVLCAACNGHSETCDP
DB	721	CVLCAACNGHSETCDP	721	CVLCAACNGHSETCDP
QY	781	CAVVPKTEVVCNCTGT	781	CAVVPKTEVVCNCTGT
DB	781	CAVVPKTEVVCNCTGT	781	CAVVPKTEVVCNCTGT
QY	841	NCNRLTGECLKCIYNT	841	NCNRLTGECLKCIYNT
DB	841	NCNRLTGECLKCIYNT	841	NCNRLTGECLKCIYNT
QY	901	VTGQCECLPHVTGDCG	901	VTGQCECLPHVTGDCG
DB	901	VTGQCECLPHVTGDCG	901	VTGQCECLPHVTGDCG
QY	961	TGQHCECEVNHFGF	961	TGQHCECEVNHFGF
DB	961	TGQHCECEVNHFGF	961	TGQHCECEVNHFGF

QY	1021	YNSWPCQCPACRYLVKQVAD	1021	YNSWPCQCPACRYLVKQVAD
DB	1021	YNSWPCQCPACRYLVKQVAD	1021	YNSWPCQCPACRYLVKQVAD
QY	1081	EYMDLLREAOQVQKVDQND	1081	EYMDLLREAOQVQKVDQND
DB	1081	EYMDLLREAOQVQKVDQND	1081	EYMDLLREAOQVQKVDQND
QY	1141	TERLIETASRELEKAKVAA	1141	TERLIETASRELEKAKVAA
DB	1141	TERLIETASRELEKAKVAA	1141	TERLIETASRELEKAKVAA
QY	1201	AKTANDTSTAYNLLRTLAG	1201	AKTANDTSTAYNLLRTLAG
DB	1201	AKTANDTSTAYNLLRTLAG	1201	AKTANDTSTAYNLLRTLAG
QY	1261	GDKAVEIYASVAQLSPUD	1261	GDKAVEIYASVAQLSPUD
DB	1261	GDKAVEIYASVAQLSPUD	1261	GDKAVEIYASVAQLSPUD
QY	1321	VKNLEKGTKEQQTADQOL	1321	VKNLEKGTKEQQTADQOL
DB	1321	VKNLEKGTKEQQTADQOL	1321	VKNLEKGTKEQQTADQOL
QY	1381	KTAEEBALRKIPAINQIT	1381	KTAEEBALRKIPAINQIT
DB	1381	KTAEEBALRKIPAINQIT	1381	KTAEEBALRKIPAINQIT
QY	1441	TSTKAEAEERITFAEYTD	1441	TSTKAEAEERITFAEYTD
DB	1441	TSTKAEAEERITFAEYTD	1441	TSTKAEAEERITFAEYTD
QY	1501	INARKAKSVTSLSIINDL	1501	INARKAKSVTSLSIINDL
DB	1501	INARKAKSVTSLSIINDL	1501	INARKAKSVTSLSIINDL
QY	1561	LENKAKQEAIAIMDYNR	1561	LENKAKQEAIAIMDYNR
DB	1561	LENKAKQEAIAIMDYNR	1561	LENKAKQEAIAIMDYNR
RESULT 2				
LMG1 MOUSE				
ID	LMG1_MOUSE	STANDARD;	PRT;	1607 AA.
AC	P02458;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Laminin gamma-1 chain precursor (Laminin B2 chain).			
GN	LAMC1 OR LAMC-1 OR LAMB-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=88059118; PubMed=3680290;			
RA	Sasaki M., Yamada Y.;			
RT	"The laminin B2 chain has a multidomain structure homologous to the			
RT	B1 chain.";			
RL	J. Biol. Chem. 262:17111-17117(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89000737; PubMed=3167041;			
RA	Durkin M.E., Bartos B.B., Liu S.-H., Phillips S.L., Chung A.E.;			
RT	"Primary structure of the mouse laminin B2 chain and comparison with			
RT	laminin B1.";			
RT	Biochemistry 27:5198-5204 (1988).			
RN	[3]			
RP	SEQUENCE OF 1-239 FROM N.A.			
RP	MEDLINE=8828071; PubMed=2836421;			
RA	Ogawa K., Burbeio P.D., Sasaki M., Yamada Y.;			
RT	"The laminin B2 chain promoter contains unique repeat sequences and			

RT is active in transient transfection.";  
RL J. Biol. Chem. 263:8384-8389(1988).  
RN [4].  
RP SEQUENCE OF 1391-1607 FROM N.A.  
RX MEDLINE=85051302; PubMed=6209134;  
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
coiled-coil alpha-helix.";  
RL EMBO J. 3:2355-2362(1984).  
RN [5].  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 771-932.  
RX MEDLINE=96196434; PubMed=8648630;  
RA Stetefeld J., Mayer U., Timpl R., Huber R.;  
RT "Crystal structure of three consecutive laminin-type epidermal growth  
factor-like (LE) modules of laminin gamma1 chain harboring the  
nidogen binding site".  
RL J. Mol. Biol. 257:644-657(1996).  
RN [6].  
RP STRUCTURE BY NMR OF 824-881.  
RX MEDLINE=96196435; PubMed=8648631;  
RA Baumgartner R., Caisch M., Mayer U., Poeschl E., Huber R.,  
Timpl R., Holak T.A.;  
RT "Structure of the nidogen binding LE module of the laminin gamma1  
chain in solution.";  
RL J. Mol. Biol. 257:659-668(1996).  
RN [7].  
RP FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
CC -|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end. The gamma-1 chain is a subunit of laminin-1 (BHS laminin),  
laminin-2 (merosin), laminin-3 (S-laminin), laminin-4 (S-merosin),  
laminin-6 (K-laminin) and laminin-7 (KS-laminin).  
CC -|- SUBCELLULAR LOCATION: Extracellular.  
CC -|- TISSUE SPECIFICITY: Found in the basement membranes (major  
component).  
CC -|- DOMAIN: The alpha-helical domains I and II are thought to interact  
with other laminin chains to form a coiled coil structure.  
CC -|- DOMAIN: Domains VI and IV are globular.  
CC -|- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -|- SIMILARITY: Contains 11 laminin EGF-like domains.  
CC -|- SIMILARITY: Contains 1 laminin IV domain.  
-----  
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-----  
CC EMBL; X05211; CAA28838.1; -;  
CC EMBL; J03484; AAA39405.1; -;  
CC EMBL; J02930; AAA39408.1; -;  
CC EMBL; J03749; AAA39409.1; -;  
CC FIC; A28469; WMSB2.  
CC PDB; IKLO; 20-AUG-97.  
CC PDB; 1TLE; 12-FEB-97.  
CC MGD; MGI:99914; Lamc1.  
CC GO; GO:0005604; C:basement membrane; IDA.  
CC InterPro; IPR006209; EGF like.  
CC InterPro; IPR008212; Lam\_N2.  
CC InterPro; IPR000034; Laminin\_B.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR008211; LamNT.  
CC Pfam; PF00052; laminin\_B; 1.  
CC Pfam; PF00053; laminin\_EGF; 9.  
CC Pfam; PF00055; laminin\_Nterm; 1.  
CC PRINTS; PR00011; EGF\_LAMININ.  
CC PRODOM; PD002082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 8.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01246; LAMININ\_TYPE\_EGF; 10.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.  
FT SIGNAL 1 33  
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.  
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.  
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.  
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.  
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.  
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 503 687 LAMININ DOMAIN IV.  
FT DOMAIN 688 721 LAMININ EGF-LIKE 6.  
FT DOMAIN 722 770 LAMININ EGF-LIKE 7.  
FT DOMAIN 771 825 LAMININ EGF-LIKE 8 (NIDOGEN-BINDING).  
FT DOMAIN 826 881 LAMININ EGF-LIKE 9.  
FT DOMAIN 882 932 LAMININ EGF-LIKE 10.  
FT DOMAIN 933 980 LAMININ EGF-LIKE 11.  
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.  
FT DOMAIN 1029 1607 COILED COIL (POTENTIAL).  
FT DOMAIN 1034 1594 BY SIMILARITY.  
FT DISULFID 340 349 BY SIMILARITY.  
FT DISULFID 342 365 BY SIMILARITY.  
FT DISULFID 368 377 BY SIMILARITY.  
FT DISULFID 380 393 BY SIMILARITY.  
FT DISULFID 396 408 BY SIMILARITY.  
FT DISULFID 398 414 BY SIMILARITY.  
FT DISULFID 416 425 BY SIMILARITY.  
FT DISULFID 428 440 BY SIMILARITY.  
FT DISULFID 443 454 BY SIMILARITY.  
FT DISULFID 445 461 BY SIMILARITY.  
FT DISULFID 463 472 BY SIMILARITY.  
FT DISULFID 475 490 BY SIMILARITY.  
FT DISULFID 722 731 BY SIMILARITY.  
FT DISULFID 724 738 BY SIMILARITY.  
FT DISULFID 740 749 BY SIMILARITY.  
FT DISULFID 752 768 BY SIMILARITY.  
FT DISULFID 771 779 BY SIMILARITY.  
FT DISULFID 773 790 BY SIMILARITY.  
FT DISULFID 793 802 BY SIMILARITY.  
FT DISULFID 805 823 BY SIMILARITY.  
FT DISULFID 826 840 BY SIMILARITY.  
FT DISULFID 828 847 BY SIMILARITY.  
FT DISULFID 850 859 BY SIMILARITY.  
FT DISULFID 862 879 BY SIMILARITY.  
FT DISULFID 882 896 BY SIMILARITY.  
FT DISULFID 884 903 BY SIMILARITY.  
FT DISULFID 905 914 BY SIMILARITY.  
FT DISULFID 917 930 BY SIMILARITY.  
FT DISULFID 933 945 BY SIMILARITY.  
FT DISULFID 935 952 BY SIMILARITY.  
FT DISULFID 954 963 BY SIMILARITY.  
FT DISULFID 966 978 BY SIMILARITY.  
FT DISULFID 981 993 BY SIMILARITY.  
FT DISULFID 993 999 BY SIMILARITY.  
FT DISULFID 1001 1010 BY SIMILARITY.  
FT DISULFID 1013 1026 BY SIMILARITY.  
FT DISULFID 1029 1029 INTERCHAIN (PROBABLE).  
FT DISULFID 1032 1032 INTERCHAIN (PROBABLE).  
FT DISULFID 1598 1598 INTERCHAIN (WITH BETA-1 CHAIN).  
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1105 1105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1159 1159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	1203	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1221	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1239	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1378	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1393	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1437	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CONFLICT	216	G -> A (IN REF. 3).	
FT	CONFLICT	260	E -> D (IN REF. 2).	
FT	CONFLICT	337	S -> C (IN REF. 2).	
FT	CONFLICT	447	LR -> PS (IN REF. 2).	
FT	CONFLICT	544	D -> Y (IN REF. 2).	
FT	CONFLICT	682	T -> S (IN REF. 2).	
FT	CONFLICT	886	MISSING (IN REF. 2).	
FT	CONFLICT	1158	MISSING (IN REF. 2).	
FT	CONFLICT	1434	V -> A (IN REF. 2).	
FT	CONFLICT	1475	R -> K (IN REF. 4).	
FT	CONFLICT	1576	D -> N (IN REF. 4).	
FT	TURN	775	776	
FT	STRAND	779	781	
FT	STRAND	788	790	
FT	TURN	795	796	
FT	STRAND	797	798	
FT	TURN	800	801	
FT	STRAND	804	805	
Query Match				
Best Local Similarity 92.7%; Pred. No. 3e-295;				
Matches 1492; Conservative 61; Mismatches 54; Indels 2; Gaps 1;				
QY	1	MRGSHRAAPALPRGRWLWVLA	AAAAAAGCAAMDECTDEGGRQRCMPEFVNAAFN	60
Db	1	MTGGGAALALQPRGLWFLAVL	--AAVAGCVRAAMDECADEGGRQRCMPEFVNAAFN	58
QY	61	VTVVANTCGTPPEEYCVGTGVT	SKCHLDAGPHLOHGAALTDYNNQADTTWQS	120
Db	59	VTVVANTCGTPPEEYCVGTGVT	SKCHLDAGQOHLQHGAALTDYNNQADTTWQS	118
QY	121	QTMLAGVQVPESSINLTLHLGK	AFDIYVRLKHTSRPESFAIYKRTREDGWPYQYISG	180
Db	119	QTMLAGVQVPESSINLTLHLGK	AFDIYVRLKHTSRPESFAIYKRTREDGWPYQYISG	178
QY	181	SCENTYSKANRGFIRTGDEQAL	CTDEPDSISPTTGNVAFSTLEGRPSAYNFDSNVL	240
Db	179	SCENTYSKANRGFIRTGDEQAL	CTDEPDSISPTTGNVAFSTLEGRPSAYNFDSNVL	238
QY	241	QEWVTATDIRVTLNRLNTGDE	VFNPKVLSYVAISDFAVGGRCKNGHASECWNKEF	300
Db	239	QEWVTATDIRVTLNRLNTGDE	VFNPKVLSYVAISDFAVGGRCKNGHASECWNKEF	298
QY	301	DKLVCKNCKHNTYGVDCCKLP	PFNDPRPWRATAESASECLPCDCNRSQECYFDPPELYS	360
Db	299	DKLVCKNCKHNTYGVDCCKLP	PFNDPRPWRATAESASESLPCDCNRSQECYFDPPELYS	358
QY	361	TGHGHCTNCDNTDGAHCRER	ENPFRLGNNEACSSCHCSPVGSLSTOCDSYGRCSCKP	420
Db	359	TGHGHCTNCDNTDGAHCRER	ENPFRLGNNEACSSCHCSPVGSLSTOCDSYGRCSCKP	418
QY	421	GVMGDKCDRCQPGFHSILTA	GRPCSDPGSISDECNVETGRVCVCKDNVEGFCNCRCKPG	480
Db	419	GVMGDKCDRCQPGFHSILTA	GRPCSDPLRGSTDECNVETGRVCVCKDNVEGFCNCRCKPG	478
QY	481	FFNLESNPRGCTPCFCFHSS	VCNTAVGYSYSSITFQIDEDGWRQDGSASLEW	540
Db	479	FFNLESNPRGCTPCFCFHSS	VCNTAVGYSYVYDSSITFQIDEDGWRQDGSASLEW	538
QY	541	SSERQDIATVSDSYFFRYFI	APAKFLGKQVLSYGQNLSPFRVDRDRTLSAEDLVLEGA	600
Db	539	SSERQDIATVSDSYFFRYFI	APAKFLGKQVLSYGQNLSPFRVDRDRTLSAEDLVLEGA	598
QY	601	GLRVSVPILIAQGNYSYSET	TKVYKFLRHEATDYPWRPALTPPEFQKLNLTISIKIRGT	660
Db	599	GLRVSVPILIAQGNYSYSET	TKVYKFLRHEATDYPWRPALTPPEFQKLNLTISIKIRGT	658

QY	661	SERSAGYLDVTLASARPGVP	ATWVESCTCPVGGQFCWCLSGYVRETPNLGYPSP	720
Db	659	SERTAGYLDVTLQASARPGV	ATWVESCTCPVGGQFCWCLSGYVRETPNLGYPSP	718
QY	721	CVLACANGHSETCDPETGVC	NCNCRDNTAGPHCEKSDGYGDSGTAGTSSCQCPGCGSS	780
Db	719	CVLCTCNHSETCDPETGVC	NCNCRDNTAGPHCEKSDGYGDSGTAGTSSCQCPGCGSS	778
QY	781	CAVVPKTKVVCNCTGTGTR	CELCDDGYFGDPLGRNGPVRLCRLCCSDNIDNNAV	840
Db	779	CAIVPKTKVVCNCTGTGTR	CELCDDGYFGDPLGRNGPVRLCRLCCSDNIDNNAV	838
QY	841	NCNRLTGECLKCIYNTAGY	FCYCDRCCKDGFNPLAPNADKCKACNCPYGTWKQSSCNP	900
Db	839	NCNRLTGECLKCIYNTAGY	FCYCDRCCKDGFNPLAPNADKCKACNCPYGTWKQSSCNP	898
QY	901	VTGCECLPHVTQDGCADP	GFYNIQSGCERCCHALGSGNCGDITRTGCECQPGI	960
Db	899	VTGQCQCLPHVSGRDCGT	CPGYNIQSGCERCCHALGSGNCGDITRTGCECQPGI	958
QY	961	TGQHCERCEVNHFGFEG	CGCKPCDCHPEGSLSQCKDDGRCCEGFGVNRCDQCEENYF	1020
Db	959	TGQHCERCEVNHFGFEG	CGCKPCDCHPEGSLSQCKDDGRCCEGFGVNRCDQCEENYF	1018
QY	1021	YNRSWPGCQCPACYRLVK	DVADHRVKQLBSLIANLGTGDEMVTQDAFEDRLKEAER	1080
Db	1019	YNRSWPGCQCPACYRLVK	DVADHRVKQLBSLIANLGTGDEMVTQDAFEDRLKEAER	1078
QY	1081	EYMDLIREAGVQKVDONL	MDRLQVNNLTSSQISRLQNRNTIETGNLAEQARAHVEN	1140
Db	1079	EYMDLIREAGVQKVDONL	MDRLQVNNLTSSQISRLQNRNTIETGNLAEQARAHVEN	1138
QY	1141	TERLIEIASRELEKAKVA	ANVSITQPESTGDPNNMTLLAEAEARKLAERHKQADDIYRV	1200
Db	1139	TEQLIEIASRELEKAKVA	ANVSITQPESTGDPNNMTLLAEAEARKLAERHKQADDIYRV	1198
QY	1201	AKTANDTSTAYNLLRLT	LAGENQTAPEIEELNRYEQAKNISODLEKQARVHEAKRA	1260
Db	1199	AKTANETSAAYNLLRLT	LAGENQTAPEIEELNRYEQAKNISODLEKQARVHEAKRA	1258
QY	1261	GDKAVEIYASVAQLPDS	ETLENEANNIKVEAENLEQLIDQKLDYEDLREDMRGKELE	1320
Db	1259	GDKAVEIYASVAQLPDS	ETLENEANNIKVEAENLEQLIDQKLDYEDLREDMRGKELE	1318
QY	1321	VKNLLEKGTQEQADQLLA	RADAALAEAAKKGRTLOEANDILNNLKDQDPRVNDN	1380
Db	1319	VKNLLEKGTQEQADQLLA	RADAALAEAAKKGRTLOEANDILNNLKDQDPRVNDN	1378
QY	1381	KTAABEALRKIPAINOTI	TEANETKTEAQAALGSAADATEAKNKAHEAERIASAVQKNA	1440
Db	1379	KTAABEALRKIPAINOTI	TEANETKTEAQAALGSAADATEAKNKAHEAERIASAVQKNA	1438
QY	1441	TSTKAEAEERTFAEVTDL	DNEVNNMLKQAEAEKELKQDDADCDMMAGVSAQAQAEAE	1500
Db	1439	TSTKAEAEERTFAEVTDL	DNEVNNMLKQAEAEKELKQDDADCDMMAGVSAQAQAEAE	1498
QY	1501	INAKAKNSVTSLSIINDL	LEQLGQDQDVTDLANKLNEIEGTLLKAKDEMKSOLDKRVSD	1560
Db	1499	INAKAKNSVTSLSIINDL	LEQLGQDQDVTDLANKLNEIEGTLLKAKDEMKSOLDKRVSD	1558
QY	1561	LENEAKQEAAMIDYNRDI	EIMKDIRNLEDIRKTLPSGCFNTPFTEKP	1609
Db	1559	LESEARQEAAMIDYNRDI	EIMKDIRNLEDIRKTLPSGCFNTPFTEKP	1607

## RESULT 3

LMG3 HUMAN

ID LMG3 HUMAN

AC Q9Y6N6; STANDARD; PRT; 1587 AA.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	573	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	1587 AA;	172051 MW;	3CB6E09B5F203319 CRC64;
QY	Query Match	41.4%;	Score 3611;	DB 1; Length 1587;
QY	Best Local Similarity	43.5%;	Pred. No. 8e-127;	
QY	Matches	701;	Conservative 264;	Mismatches 578; Indels 68; Gaps 21;
QY	21	LAVIAAAAAAAAAAGCAQAADECTDGGPQPCMEFVNAAFNVTVAATNTGTPPEEYCVQT	80	
DB	10	LALLAPPAAG----	AGNGACVGDAGRPQCLPVFENAAFGRLAQASHTCGSPDPFCPHV	65
QY	81	GVTGVTSCHLCDAGOPHLOHGAFTDYNNOADTTWQSQOTMLAGVQPSINLTHLG	140	
DB	66	GAAGAGAHFCQRCDAADPQRHNASYLTDFHSQDESTWQSPSMAFGVQYPTSVNITLRLG	125	
QY	141	KAFDITVRLKFTSRPESPAIKYRTREDPGMPYQYSGSCENTYSKANRGFIRTCGDE	200	
DB	126	KAYEITVRLKFTSRPESPAIKYRSRAGPNPEYQFYASCKQYGRPEGOYLRPGEDE	185	
QY	201	QOALCTDFSDIGPLTCGNVAFETLEGRPSAYNFONSPLQEWVTATDITVTLNRLNFTG	260	
DB	186	RVAFCTSEFSDISPLSGCNVAFETLEGRPSAYNFESPGLOEWTSTELLISLORLNTFG	245	
QY	261	DEVNDRPKVLKSYYYAISDFAVGGRCKNGHASECMKNEFDFKLVGNCKHNTVGVDCCKL	320	
DB	246	DDIFKDPKVLQSYYYAIVDSFVGGRCKNGHASECGPDVAGQACRCQNTTGTDCRCL	305	
QY	321	PFNDPRWRRTAESAECILPCDNGRSOECYFPDPELYRSTGHGGHCTNCDQNTDGAHCE	380	
DB	306	PFQDPRWARCTAAAEHCLPCNCSGRSECTFDRELPRSTGHGGRCHCRDHTAGPCE	365	
QY	381	KRCNFFFLGNNEACSSCHSPGVGSLSTQDCSVGRSCPKPGVMDKDCRQCPHSLTEA	440	
DB	366	RQCNFYHWDPRMPCQPCDCQASGLHQCDDTGTCAKPTVTGWKDCRCLPEFHSLSBG	425	
QY	441	GRPCSDPSSSIDECNVETGRVCVKDNGEFCNCRCKPQFFNLSSNPRGCTPCFCGH	500	
DB	426	GRCPCTCNPAGLSDTCDPRSGRPCKENVEGNLCDCRGTFTMLQHPNPAAGSCSCFYGH	485	
QY	501	SSVCTNAVGVSYVYGISSTFQIDBDGWRAEORDGSEASLEWSSERQDIAVISDSYFPRFI	560	
DB	486	SKVCASTAQFQVHHILSDFHQGAEGWARSVGGSEHSPQWSPN----	541	
QY	561	APAKPLGQVLSYQNLFSFRVDRDRTLASDLVLEGAGLRVSVPLIAQNSYFSETT	620	
DB	542	AFGKFLGQDRSYGQPIILFTRVPPGDSPLPVQ--LRLEGTGLALS--LRHSSLSQPDAR	598	
QY	621	VKVFYFRLH---EATDYPRWPAITPFQKLLNNLTSIKIRGTYSERSAG--YLDQVTLAS	675	
DB	599	ASQCGRAQVPLQETSEDVAPPLPPPHFORLLANLTSLRLRVSPGSPAGPFLTEVRLTS	658	

Q9Y6U6 homo sapien  
Q9VRW0 drosophila  
Q8JHV6 brachydanio  
P91904 caenorhabdi  
Q8TAF8 homo sapien  
Q86788 schistocerc  
Q92429 rattus norv  
O42140 brachydanio  
O42203 brachydanio  
O57339 xenopus lae  
Q8SWY0 drosophila  
Q61965 mus musculu  
Q8NFW6 brachydanio  
Q8BPS2 bombyx mori  
Q8TAS6 homo sapien  
O44565 caenorhabdi  
Q96659 hirudo medi  
Q9N277 homo sapien  
Q91LP3 mus musculu  
O75445 homo sapien  
Q8XK1 rattus norv  
Q8K271 mus musculu  
O14637 homo sapien  
Q8C9J2 mus musculu  
Q91V90 mus musculu  
Q9ARX6 mus musculu  
Q9V725 drosophila  
O00634 homo sapien  
Q9RIA3 mus musculu

17 1485.5 17.0 1631 4 Q9Y6U6  
18 1485.5 17.0 3712 5 Q9VRW0  
19 1477.5 17.0 1827 13 Q8JHV6  
20 1394 16.0 3704 5 P91904  
21 1317 15.1 3695 4 Q8TAF8  
22 1197 13.7 1188 5 Q86788  
23 1172 13.5 604 11 Q92429  
24 1151.5 13.2 603 13 O42140  
25 1139.5 13.1 602 13 O42203  
26 1137.5 13.1 569 13 O57339  
27 1136 13.0 1026 5 Q8SWY0  
28 1131.5 13.0 464 11 Q61965  
29 1096 12.6 535 5 Q8NFW6  
30 1086.5 12.5 1069 5 Q8BPS2  
31 1071 12.3 1086 4 Q8TAS6  
32 1056 12.1 1067 5 O44565  
33 1053.5 12.1 610 5 Q96659  
34 1034 11.9 1546 4 Q9N277  
35 1031 11.8 1461 11 Q91LP3  
36 1030 11.8 1546 4 O75445  
37 979 11.2 1512 11 Q8XK1  
38 962.5 11.0 984 11 Q8K271  
39 934.5 10.7 1486 4 O14637  
40 918.5 10.5 695 11 Q8C9J2  
41 905.5 10.4 1168 11 Q91V90  
42 896 10.3 911 11 Q9ARX6  
43 879 10.1 667 5 Q9V725  
44 870 10.0 580 4 O00634  
45 870 10.0 580 11 Q9RIA3

ALIGNMENTS

RESULT 1  
Q8JHV6 PRELIMINARY; PRT; 1593 AA.  
ID Q8JHV6  
AC Q8JHV6  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Laminin gamma 1.  
GN LAMC1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22065263; PubMed=12070089;  
RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,  
RA First E.M., Stemple D.L.  
RT "Zebrafish mutants identify an essential role for laminins in  
notochord formation.";  
RL Development 129:3137-3146(2002).  
DR EMBL; AF468048; AAM61766.1;  
DR GO; GO:0005198; C:extracellular matrix; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; Lam\_N2.  
DR InterPro; IPR008212; Lam\_N2.  
DR Pfam; PF00052; laminin\_B; 1.  
DR Pfam; PF00053; laminin\_EGF; 10.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PRODOM; PDOC02082; Lam\_N2; 1.  
DR SMART; SM00180; EGF\_Lam; 11.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 7.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: May 18, 2004, 14:29:28 ; Search time 43.6478 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-14  
Perfect score: 8713  
Sequence: 1 MRGSHRAAPALPRGRWPV.....EDIRKTLPSGCFNTPSIEKP 1609  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL.25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_ricet.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteria.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6217	71.4	1593	13 Q8JHV6	Q8JHV6 brachydanio
2	4789	55.0	1007	13 Q90ZN3	Q90ZN3 gallus gall
3	3533.5	40.6	1823	5 Q8JHV6	Q8JHV6 anopheles g
4	2614.5	30.0	1190	6 Q8H2I9	Q8H2I9 equus caball
5	2612.5	30.0	1196	6 Q867A2	Q867A2 canis fami
6	1719.5	19.7	1785	13 Q8JHV7	Q8JHV7 brachydanio
7	1716	19.7	529	4 Q8N2D6	Q8N2D6 homo sapien
8	1687.5	19.4	1792	13 Q8JHV6	Q8JHV6 gallus gall
9	1652	19.0	1761	4 Q86XN2	Q86XN2 homo sapien
10	1626.5	18.7	3102	5 Q45614	Q45614 caenorhabdi
11	1580.5	18.1	1799	11 Q8R0Y0	Q8R0Y0 mus musculu
12	1566	18.0	319	4 Q96BH6	Q96BH6 homo sapien
13	1517	17.4	351	11 P97552	P97552 rattus norv
14	1506.5	17.3	2731	5 Q9VJT5	Q9VJT5 drosophila
15	1506.5	17.3	3367	5 Q9XZC9	Q9XZC9 drosophila
16	1506.5	17.3	3375	5 Q8IP51	Q8IP51 drosophila

DR	PROSITE; PS01186; EGF 2; 2.	
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 10.	
KW	Laminin_EGF-like domain	
SQ	SEQUENCE 1593 AA; 176218 MW; AS01F3A8884AA411 CRC64;	
Query Match		
Best local similarity 69.6%; Pred. No. 1.8e-252;		
Matches 1099; Conservative 213; Mismatches 268; Indels 0; Gaps 0;		
QY	30 AGCAQAAMDECTGGRRPQRCMPFVNAAFNVTVATNTCGTPPEYCVQTVGTGKSC	89
DB	14 AASHGAMDECIDDDRPQRCMPFVNAAFNVTVATNTCGSPPEFCVQTVGTGKSC	73
QY	90 HLCDAQPHLQGAFAITDYNQADTTWQSQTMAGVQPPSSINTLHLGKAFDITYR	149
DB	74 HICNAADPRHLHGAVALTDYNQVPTWQSQTMAGIQYFNSINTLHLGKSFIDITYR	133
QY	150 LKFTSPSPFAIKRTREDPMTIPYQYSGSCENTYSKANRGIIRTGGEQALCTDEF	209
DB	134 LKFTSPSPFAIKRSESDGPTPYQYSGSEKTYSKNNGFIIRTGGEQALCTDEF	193
QY	210 SDISPLTGGNVAFTLEGRPSAYNFDSNPLQEVVTAIDIRVTLNRLNTEGDFVNDPKV	269
DB	194 SDISPLTGGNVAFTLEGRPSAYNFDSNPLQEVVTAIDIRVTLNRLNTEGDFVNDPKV	253
QY	270 LKSYYYAISDFAVGRCCKNGHASECMKNEFDKLVNCKNTYGVDCCKLPFNDRPWR	329
DB	254 LKSYYYAISDFAVGRCCKNGHASECMKNEYSKLVNCKNTEGADCNCKPFINDRPWR	313
QY	330 RATAESASECLPCDNGRCSOBYDPELYRSTGHGHCITNCQDNTDGAHCERCENFFRL	369
DB	314 RATAENPNECLPCDNGKASBYDPELYRATRGHGHCRNCAADNTDGPCKERCCLANYRE	373
QY	390 GUNNEACSSCHSPVGSLSITQCDYSGRCCKGVGMDKDCRCQGFHSLTEAGRCPCSDP	449
DB	374 ASGORCLSCGNPVGSLSITQCDNTRCCKPVGVMGDKDCRCQGFHSLTEAGRCPCSNP	433
QY	450 SGIISDECNVTGRCVCKNVEGFCRCCKPGFFNLESNPRGCTPCFCFHSVYCTNAV	509
DB	434 AGSTQECVDVQRCCKENGVGFCNCKLGYFNLDPQNPQCTPCFCFQHSVYCTNAV	493
QY	510 YSVYISSTFOIDEGWRAORDGSEASLEWSSERQDIANISDSYFPRYIAPAKFLGKQ	569
DB	494 YSVHKITSTFDRDDGKQKDDSSVPVQWSPSSGSLISEDYFPIYFVAPDKFLHNQ	553
QY	570 VLSYQNLSPFSFRVDRDRTRLSAEDLVLEGAGLVSPVPLIAQNSYFSETTVKVFRLHE	629
DB	554 LLSYQNLTPFRIOHRAHARSADVDVLEGSLAVVPLIAQNSYFGEETQTTFVFLHD	613
QY	630 ATDYPWRPALTPPEFQKLLNLTSTIKRTYSGRSAGVLDVTLASARPFGVPATWES	689
DB	614 TTDYPWRPTIKHADPQKLLNLTSMIRGTYSAGSAGVLDVTLASARPFGVPTARVVEK	673
QY	690 CTCVPYGGQFCMCLSGYRBTNLPYSPCVLCACNGHSETCDPBTGVNCRDNTAGP	749
DB	674 CTCPOGYLGQHCQCQDQGRARSPRLRFRSTCERCNCNGHSDTCDPBTGMNCQHNAGL	733
QY	750 HCEKSDGYGSDTAGTSDDQPCPCPGSSCAVVPKTKVVCNCTPGTTGKRCCLCDD	809
DB	734 SCERCKDGYGSDTVSGSSDDKACPCPAGATCAVVPKTNVVCNCTPGTTGKRCCLCDD	793
QY	810 GFYGDPLGRNGVPLRCILCQSDNDTPNAGVNCNLTGCECLKCLYNTAGFYCDRCXGFF	869
DB	794 GFYGDPLGKGVPRACRACSCNNNTPNAGVNCNRESGCECLKCLYNTAGFYCDRCXGFF	853
QY	870 GNPLAPNADKCAKCNPPYGMKQSSCNPNVTGQCCLPHVTGQDCACPGFPYNTQSG	929
DB	854 GBARANVADKCKPCSKSPYGVIVDQACSVQVTCGCPCLPHVINRDCACBLGFPVNTQSG	913
QY	930 QGCERCDCALGSTNGQCDIRTGQCECQFQITGQHCERCENVHGFEGGCKPCDCHPEG	989
DB	914 KGCERCNCNPIGSTNGQCDIVSQCECQFQVGTGQHCERCENVHGFEGGCKPCDCHPEG	973

QY	990 SLSLQCKDDGRCEBREGFVGNRCDOCEENFYNRSWFGQCEPCACYPLVKDKVADHVKL	1049
DB	974 SESAQCKDDGRCHCRPGFVGSRCDCMCEENFYNRSTFGCOQCPNCYSLVRDKVNOQKQL	1033
QY	1050 QELRESLIANTGTGBMVTDOAFEDRLKEAREVNDLLREAOQVQKVDQNDLMDRLQRYNNT	1109
DB	1034 LDQLNLDLSLNTTETTSDFKAFEDRLKEAREKTIINDLLEEAQASKEVDKGLLDRLNNIKT	1093
QY	1110 LSSQISRLQNTIRNTIETGNLAEOARAHVENTERELIISARELEKAKVAAANVSVTQPE	1169
DB	1094 LNNQWNLQNTKNTVDNTGAQDARNRVRDAENLINTAREELDKAKEAISKVDIKIPTT	1153
QY	1170 TGDPNMTLLAABEAKLAERHKQEADDIVRVAKTANDTSTEAYNLLRTLAGENQTAPEI	1229
DB	1154 SGDPNMTLLAABEAKLSEKADADQIEKIAKANDTSTKAYNMLKALOGENKTSDDI	1213
QY	1230 FELNKYEQAKNI SODEKQAAARVHEEAKRAGDKAVEIYASVAQSLPDSSETLEANNI	1289
DB	1214 DELNEKYLEAKDLAKNLEKQAAKHAEAEAGNALKIYANLTSLLPPTINTKLEDDANKI	1273
QY	1290 KMEARNLEQLIDOKLQYEDLREDMRGKELEVNLLLEKGTQEQQTADQLARADAAKALA	1349
DB	1274 KKEASDLKLDKTEKTEYNDLREDLRGKETEVKLLDKGKTEQQTADQLARADAAKALA	1333
QY	1350 EBAAKKGRDITLQEANDILNLLKDFRRVNDNKTAAEALRKIPAINQITTEANEKTRAQ	1409
DB	1334 EBAAKKGRSTFQEAQDILNLLRDFDKRVNDNKTAAEDAMRRIPQINATINEANDKTRAE	1393
QY	1410 QALGSAADATAEAKNAHEERIASAVOKNATSTKAEAEERTFAEVTDLNENVMMLKQLQ	1469
DB	1394 AALGNAADAKADAKAKAEAEKIANVQKSAKYADAKAFEDTMKLDKVDKMDQLT	1453
QY	1470 EAEKELKRQDDADODMMAGMASQAQAEAEINARKAKSVTSLLSIINDLLEQLGQDIT	1529
DB	1454 AAEKELEKKAEDTDMWMSASDNADAEAGNARKAKSAVREVLNTINALLGLGNIDK	1513
QY	1530 VDLNKLNIETGLINKAKDEMVSDDLDRKVSVDLENEAKQEAAMIDYNDRIEIMKDIRNL	1589
DB	1514 VDLSKNLQDNLKADKQKAGSELDRKLKELINDAKSQEDMISDYDROIQEIIRADIANL	1573
QY	1590 EDIRKTLPGSCFNTPESEKIP 1609	
DB	1574 NDIKNTLPGCGFNTPESEKIP 1593	
RESULT 2		
Q90ZN3 PRELIMINARY; PRT; 1007 AA.		
ID	Q90ZN3	
AC	Q90ZN3	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE	Laminin gamma 1 (Fragment).	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Halfter W., Dong S., Balasubramani M., Bier M.E.;	
RT	"Aberrant histogenesis after temporary disruption of the retinal basal	
RT	lamina."	
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF373841; AAK53197.1;	
DR	GO; GO:0005578; C:extracellular matrix; IEA.	
DR	GO; GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPR006209; EGF-like.	
DR	InterPro; IPR000034; Laminin_B.	
DR	InterPro; IPR002049; Laminin_EGF.	
DR	InterPro; IPR008211; LamNT.	
DR	Pfam; PF00052; laminin B; 1.	
DR	Pfam; PF00053; laminin_EGF; 9.	

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 48.4494 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-10

Perfect score: 9758  
Sequence: 1 MGLLQVAFGLALWGTRVC.....EVRSLKDISKAVYVSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_podent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_cheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6781.5	69.5	1785	13 Q8JHV7	Q8JHV7 brachydanio
2	5434	55.7	1086	4 Q8TAS6	Q8TAS6 homo sapien
3	5323	54.6	1792	13 Q57484	Q57484 gallus gall
4	5195	53.2	984	11 Q8K271	Q8K271 mus musculus
5	5086.5	52.1	1799	11 Q8R0Y0	Q8R0Y0 mus musculus
6	4790	49.1	911	11 Q9CRX6	Q9CRX6 mus musculus
7	3813.5	39.1	1761	4 Q86XN2	Q86XN2 homo sapien
8	3743.5	38.4	1827	13 Q8JHV6	Q8JHV6 brachydanio
9	3607.5	37.0	1631	4 Q9Y6U6	Q9Y6U6 homo sapien
10	2837.5	29.1	1067	5 Q44565	Q44565 caenorhabdi
11	2271.5	23.3	1168	5 Q967S8	Q967S8 schistocerc
12	2015	20.6	761	4 Q9UHI2	Q9UHI2 homo sapien
13	1936	19.8	1026	5 Q8SWY0	Q8SWY0 drosophila
14	1832	18.8	1069	5 Q8BPS2	Q8BPS2 bombyx mori
15	1751	17.9	3704	5 P91904	P91904 caenorhabdi
16	1671	17.1	3712	5 Q9VRW0	Q9VRW0 drosophila

17	1644.5	16.9	1593	13 Q8JHV8	Q8JHV8 brachydanio
18	1636.5	16.8	1623	5 Q9U3U7	Q9U3U7 anopheles g
19	1572.5	16.1	3695	4 Q8TDF8	Q8TDF8 homo sapien
20	1531.5	15.7	1168	11 Q91V90	Q91V90 mus musculu
21	1342	13.8	1007	13 Q90ZN3	Q90ZN3 gallus gall
22	1305.5	13.4	3102	5 Q45614	Q45614 caenorhabdi
23	1243	12.7	2731	5 Q9VJT5	Q9VJT5 drosophila
24	1243	12.7	3367	5 Q9XZC9	Q9XZC9 drosophila
25	1243	12.7	3375	5 Q8TP51	Q8TP51 drosophila
26	1110.5	11.4	1546	4 Q9NS27	Q9NS27 homo sapien
27	1108.5	11.4	1546	4 Q75445	Q75445 homo sapien
28	1083	11.1	1486	4 Q14637	Q14637 homo sapien
29	1041	10.7	1461	11 Q9JLP3	Q9JLP3 mus musculu
30	1032	10.6	750	4 Q86TP7	Q86TP7 homo sapien
31	987.5	10.1	628	4 Q9HB63	Q9HB63 homo sapien
32	987.5	10.1	628	4 Q9BZP1	Q9BZP1 homo sapien
33	986.5	10.1	628	11 Q9J113	Q9J113 mus musculu
34	978.5	10.0	616	4 Q15483	Q15483 homo sapien
35	972.5	10.0	605	4 Q725B6	Q725B6 homo sapien
36	971	10.0	1512	11 Q8K3K1	Q8K3K1 rattus norv
37	875.5	9.0	1190	6 Q8HZI9	Q8HZI9 equus cabal
38	872.5	8.9	1196	6 Q867A2	Q867A2 canis famil
39	692.5	7.1	529	4 Q8N2D6	Q8N2D6 homo sapien
40	690.5	7.1	604	11 Q924Z9	Q924Z9 rattus norv
41	683.5	7.0	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi
42	683	7.0	603	13 Q42140	Q42140 brachydanio
43	680	7.0	1574	11 Q88281	Q88281 rattus norv
44	679	7.0	569	13 Q57339	Q57339 xenopus lae
45	675	6.9	602	13 Q42203	Q42203 brachydanio

#### ALIGNMENTS

RESULT 1

Q8JHV7  
ID Q8JHV7 PRELIMINARY; PRT; 1785 AA.  
AC Q8JHV7; 01-OCT-2002 (TREMREL. 22, Created)  
DT 01-OCT-2002 (TREMREL. 22, Last sequence update)  
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)  
DE Laminin beta 1.  
GN LAMB1

OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI\_TaxID=7955;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-22065263; PubMed-12070089;  
RA Parsons M.J., Follard S.M., Saude L., Feldman B., Coutinho P.,  
RA Hirst E.M., Stemple D.L.;  
RT "Zebrafish mutants identify an essential role for laminins in  
RT notochord formation.";

RL Development 129:3137-3146(2002).  
DR ENBL; A9468049; AAM61767.1;  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR002049; Laminin EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00053; laminin EGF; 13.  
DR Pfam; PF00055; laminin Nterm; 1.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR SMART; SM00136; LamNT; 1.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 10.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
KW Laminin EGF-like domain.  
SQ SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;



Db	1017	LTQSCRKVCVQNGVTVVEENCPSPGNCNCDLTSGQCLCLPNVVGQBCDQCAPTWNASGK	1076
Qy	1080	GGPCPCNCAAHGFGPSCNEFTQCOCMPGFGGRTCSCEQLFWGPDVBEACRACDCDPRGI	1139
Db	1077	GCBCDCDPCNHSFGSCNEIMGQCSCKPGFGRTCRECLEFWGNPEVKVCHACDCDPRGI	1136
Qy	1140	ETPQCDQSTGQCVCVEGVGPRCDCKTRGYSGVFFDDCTPCHOCFALWDALIGELNTRHK	1199
Db	1137	ASQCCKNVYGHCVGVGVSGPRCDTCARGTGEFFQCECHQCFAEWDILVGDLTNQTHR	1196
Qy	1200	FLEKAKALISGVIGPYRETVDSVEKKVNEIKDILAQSPAAEFLKNIGILFEEAEKLTXD	1259
Db	1197	LVQKVNTIKATGITGYPQATINNVSANSIRNILAQNPAQTPLTEIOGLLEQATMAE	1256
Qy	1260	VTEKMAQVEVKLTDTASQNSSTAGELGALQAEBSLDKTVKELAQOLERPKNSDTCGALD	1319
Db	1257	MNSNLMLTETUSEISSDNNSTDTKLKSUEAQKLEGTVDLRQVPEPKNSDIRGARA	1316
Qy	1320	SITKYFQMSLEAEKRVNASTTDPNSVTEOSALTDRVEDLMLERESPFKEQOEQARLLD	1379
Db	1317	SVTRYVEQONAEIRANASTTDFYLVNQSATLRTETEELMNQTKEEFNQRQDEFSSKLD	1376
Qy	1380	ELAGKLSLDLSAAQMTCGTTPPGAD-CSESCGGPGNCTDEGEKKCGGPGCGGLVTVAH	1438
Db	1377	NLAGQLETLULSELSEKTCGSPAGSNCADSRGGJSLCVDMSRCKGEGCGDGTLLAH	1436
Qy	1439	SAWKAMDFDRDVLGALAEVQOLSXVSEAKVRADKQNAQODVLLKTNATKERYDKSNE	1498
Db	1437	NAWQAKDPDLBIIISAMEEVDKLSXVSEAKVKADEAKNAQEVLAQTNETKKRVDSSNE	1496
Qy	1499	DARNLIKQIRNFLTSDSDLDLSIEAVANEVLKSGNASTPOOLONTLDIRREVETLSOVE	1558
Db	1497	ELRQLIKQIRDFLTQDGDLSIEAVANEVLQVQNPPTPAQLONTLDIRREVGSITDVE	1556
Qy	1559	VILQSAADIARAELLLEBAKSAKSTVDKVTADVMKLEALBEAEKAQVAEAKIKQADE	1618
Db	1557	DILNOSAADILRAESILLEGQARKAEASDVKSTAEWVKEALQHAEPRAQNSVAEALKQAAV	1616
Qy	1619	DIQGTQNLITSSETAASEETLTWASORISKLEWVZELKKAQNSGAEABYIEKVVYS	1678
Db	1617	DIKGTQDLLVSVSETSSELKLSNATRLKLESVDALLKEKALNTSISANSITEKAEIS	1676
Qy	1679	VQNQADDVKKTLUGELDERIKVYKVESLIAQKTESADARRKELLQNEAKTLIAQNSKIQ	1738
Db	1677	INALAEQLKDLJLSELDKDYSTVEELITQKAEGVAAEKRAKFLQEEARNILLQASEKIQ	1736
Qy	1739	LLBLEDLERYEDNQKLYEDKAOBLVEGEVRSLLKDISEKAVAVYSTCL	1786
Db	1737	LKUNLEKVDQNKLELQKANELVDLEKAVKELLQEIHKVTIVYSTCL	1784
RESULT 2			
Q8TAS6			
ID	Q8TAS6	PRELIMINARY;	PRT; 1086 AA.
AC	Q8TAS6;		
DT	01-JUN-2002 (TReMBLrel. 21, Created)		
DT	01-JUN-2002 (TReMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	Similar to laminin, beta 1 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_Taxid	9606;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RA	Strausberg R;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC026018; AAH26018.1; -.		
DR	GO; GO:0005198; F:structural molecule activity; IBA.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR002049; Laminin EGF.		

Q24567 drosophila  
Q16363 homo sapien  
P97927 mus musculus  
Q91172 rattus norv  
Q25092 hiruudo medi  
P21783 xenopus lae  
Q9um47 homo sapien  
Q01636 gallus gall  
P07207 drosophila  
Q06561 caenorhabdi  
Q8r490 mus musculus  
Q61982 mus musculus

34 585.5 6.0 727 1 NETA DROME  
35 565.5 5.8 1816 1 LMA4\_HUMAN  
36 559.5 5.7 1816 1 LMA4\_MOUSE  
37 537 5.5 2319 1 NTC3\_RAT  
38 532 5.5 400 1 LMB\_HIRME  
39 531 5.4 2524 1 NTC3\_XENLA  
40 527 5.4 2321 1 LMBV\_CHICK  
41 520.5 5.3 198 1 NTC3\_HUMAN  
42 511.5 5.2 2703 1 NTC3\_DROME  
43 510 5.2 3375 1 UN52\_CABEL  
44 508 5.2 539 1 NTC1\_MOUSE  
45 506 5.2 2318 1 NTC3\_MOUSE

ALIGNMENTS

RESULT 1  
LMB1\_MOUSE  
ID LMB1\_MOUSE STANDARD; PRT; 1786 AA.  
AC P02469;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin beta-1 chain precursor (laminin B1 chain).  
GN LAMB1-1 OR LAMB-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87147212; PubMed=3493487;  
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;  
RT "Sequencing of laminin B chain cDNAs reveals a  
RT multidomain protein containing cysteine-rich repeats.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).  
RN [2]  
RP SEQUENCE OF 1292-1786 FROM N.A.  
RX MEDLINE=85051302; PubMed=6209134;  
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
RT coiled-coil alpha-helix.";  
RL EMO J. 3:2355-2362(1984).  
RN [3]  
RP SEQUENCE OF 165-172; 539-547 AND 712-719.  
RX STRAIN=BALB/c; TISSUE=Endothelial cells;  
RX MEDLINE=97363207; PubMed=9219532;  
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,  
RA Sorekin T.M.;  
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of  
RT endothelium.";  
RL Eur. J. Biochem. 246:727-735(1997).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),  
CC laminin-2 (merosin), and laminin-6 (K-laminin).  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major  
CC component).  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 1 laminin IV domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its

OM protein - protein search, using sw model  
Run on: May 18, 2004, 14:26:08 ; Search time 10.1546 Seconds  
(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-10  
Perfect score: 9758  
Sequence: 1 MGLQVAFGVLWGTRVC.....EVRSLKDKSEKVAVYSTCL 1786  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9758	100.0	1786	1 LMB1_MOUSE	P02469 mus musculus
2	9144	93.7	1786	1 LMB1_HUMAN	P07942 homo sapien
3	5087.5	52.1	1801	1 LMB2_RAT	P15800 rattus norv
4	5066.5	51.9	1799	1 LMB2_MOUSE	P61292 mus musculus
5	5031.5	51.6	1798	1 LMB2_HUMAN	P55268 homo sapien
6	3859.5	39.6	1790	1 LMB1_DROME	P11046 drosophila
7	1751	17.9	3672	1 LMB2_CABEL	Q21313 caenorhabdi
8	1708	17.5	1639	1 LMB1_DROME	P15215 drosophila
9	1675	17.2	3712	1 LMA_DROME	Q00174 drosophila
10	1647	16.9	1609	1 LMG1_HUMAN	P11047 homo sapien
11	1645.5	16.9	1535	1 LMB1_CABEL	Q18823 caenorhabdi
12	1634.5	16.8	1607	1 LMG1_MOUSE	P02468 mus musculus
13	1602.5	16.4	3718	1 LMA5_MOUSE	Q61001 mus musculus
14	1575	16.1	303	1 LMB1_CHICK	Q01635 gallus gall
15	1573.5	16.1	3075	1 LMB1_HUMAN	P25391 homo sapien
16	1566.5	16.1	3695	1 LMA5_HUMAN	O15230 homo sapien
17	1555	15.9	3110	1 LMA2_HUMAN	P24043 homo sapien
18	1551.5	15.9	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1525.5	15.6	1581	1 LMG3_MOUSE	Q9r0b6 mus musculus
20	1524	15.6	3106	1 LMA2_MOUSE	Q06075 mus musculus
21	1519.5	15.6	1168	1 LMB3_MOUSE	Q61087 mus musculus
22	1513	15.5	1587	1 LMG3_HUMAN	Q9v6n6 homo sapien
23	1510	15.5	3084	1 LMA1_MOUSE	P19137 mus musculus
24	1353	13.9	3333	1 LMA3_MOUSE	Q61789 mus musculus
25	875	9.0	1191	1 LMG2_MOUSE	Q61092 mus musculus
26	862.5	8.8	1193	1 LMG2_HUMAN	Q13753 homo sapien
27	693	7.1	604	1 NET1_HUMAN	O95631 homo sapien
28	691.5	7.1	604	1 NET1_MOUSE	O09118 mus musculus
29	686	7.0	606	1 NET1_CHICK	Q09922 gallus gall
30	656	6.7	3707	1 PGBM_MOUSE	Q05793 mus musculus
31	647.5	6.6	4391	1 PGBM_HUMAN	P98160 homo sapien
32	617	6.3	612	1 UNC6_CABEL	P34710 caenorhabdi
33	608.5	6.2	581	1 NET2_CHICK	Q90923 gallus gall

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DR EMBL; M15525; AAA39407.1; ALT\_INIT.  
DR EMBL; X05212; AAA28839.1; -.  
DR PIR; A26413; MMSB1.  
DR HSP; P02468; IKLO.  
DR MGD; MG1:96743; Lambl-1.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00053; laminin\_EGF; 13.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PR00011; EGFLAMININ.  
DR SMART; SM00180; EGF\_Lam; 11.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 9.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1 21  
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.  
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.  
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.  
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.  
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.  
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).  
FT DOMAIN 541 772 LAMININ DOMAIN IV.  
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.  
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.  
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.  
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.  
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.  
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 11.  
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 12.  
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 13.  
FT DOMAIN 1179 1397 DOMAIN II.  
FT DOMAIN 1398 1430 DOMAIN ALPHA.  
FT DOMAIN 1431 1786 DOMAIN I.  
FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).  
FT DOMAIN 1368 1388 COILED COIL (POTENTIAL).  
FT DOMAIN 1448 1778 COILED COIL (POTENTIAL).  
FT DOMAIN 271 280 BY SIMILARITY.  
FT DISULFID 273 298 BY SIMILARITY.  
FT DISULFID 300 309 BY SIMILARITY.  
FT DISULFID 312 332 BY SIMILARITY.  
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FT DISULFID 1000 1009 BY SIMILARITY.  
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FT DISULFID 1105 1114 BY SIMILARITY.  
FT DISULFID 1117 1129 BY SIMILARITY.  
FT DISULFID 1132 1144 BY SIMILARITY.  
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FT DISULFID 1153 1162 BY SIMILARITY.  
FT DISULFID 1165 1176 BY SIMILARITY.  
FT DISULFID 1179 1179 INTERCHAIN (PROBABLE).  
FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).  
FT DISULFID 1785 1785 INTERCHAIN (PROBABLE).  
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).  
FT CONFLICT 1749 1749 D -> N (IN REF. 2).  
FT SEQUENCE 1786 AA; 196904 MW; 846671B7BF41A474 CRC64;

Query Match 100.0%; Score 9758; DB 1; Length 1786;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLQLVFAFGVIALWGTRVCAQEPFSGYCAEGSCYPATGDLITGRAQKLSVTSTGLHK 60  
DB 1 MGLQLVFAFGVIALWGTRVCAQEPFSGYCAEGSCYPATGDLITGRAQKLSVTSTGLHK 60  
QY 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNKLKIWQSENGVEN 120  
DB 61 PEPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTFAPNKLKIWQSENGVEN 120  
QY 121 VTIQDLLEAEFPHFLIMTFKTPPAAMLIERSSDPKWTGWYRYFAYDCESPPGISTG 180  
DB 121 VTIQDLLEAEFPHFLIMTFKTPPAAMLIERSSDPKWTGWYRYFAYDCESPPGISTG 180  
QY 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAPKIEDPYSPIQNLLKITNRIKFVKL 240  
DB 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAPKIEDPYSPIQNLLKITNRIKFVKL 240  
QY 241 HTLGNLILDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMC 300  
DB 241 HTLGNLILDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMC 300  
QY 301 RHNTKGLNCELMDPFYHDLPRPAGRNSNAKCKNCNEHSSSCHFDMAVFLATGNVSGG 360  
DB 301 RHNTKGLNCELMDPFYHDLPRPAGRNSNAKCKNCNEHSSSCHFDMAVFLATGNVSGG 360  
QY 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGTDFSVG 420  
DB 361 VCDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGTDFSVG 420  
QY 421 LIAGQCRCKLHVGERCDVCKEGFYDLISAEDPYCKSCACNPLGTIPGNGPCDSETGYCY 480  
DB 421 LIAGQCRCKLHVGERCDVCKEGFYDLISAEDPYCKSCACNPLGTIPGNGPCDSETGYCY 480

481	QY	CKBLVTGQRCDQCLPQHWSLNDLDCGRPCDCLGGLANNSSCSDSGOCSCLPHMIGROC	540
481	Db	CKBLVTGQRCDQCLPQHWSLNDLDCGRPCDCLGGLANNSSCSDSGOCSCLPHMIGROC	540
541	QY	NEVESGYFFTLDBHYIYEAEANLPGWVWVVRQYIQDRIPSWTGFVVRPVGAYLEFF	600
541	Db	NEVESGYFFTLDBHYIYEAEANLPGWVWVVRQYIQDRIPSWTGFVVRPVGAYLEFF	600
601	QY	IDNIPYSMEVEILLIRYBPQIPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVWLSLPG	660
601	Db	IDNIPYSMEYEILLIRYBPQIPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVWLSLPG	660
661	QY	SRVVLPRPVCPEKGMNVTYVRLLEPQYTAGSDVESPYTFIDSLVLMYPYCKSLDITFVG	720
661	Db	SRVVLPRPVCPEKGMNVTYVRLLEPQYTAGSDVESPYTFIDSLVLMYPYCKSLDITFVG	720
721	QY	SGDGEVINSAWETFORYRCLENSRSVYKTPMTDYCRNIIFSIISALIHQTGLACECDPQGS	780
721	Db	SGDGEVINSAWETFORYRCLENSRSVYKTPMTDYCRNIIFSIISALIHQTGLACECDPQGS	780
781	QY	LSSVCDPNGGOCOCPRNVGRTNCRCAFGFGPGNGCKPCDCHLOGSASAFCDALITGQC	840
781	Db	LSSVCDPNGGOCOCPRNVGRTNCRCAFGFGPGNGCKPCDCHLOGSASAFCDALITGQC	840
841	QY	HCFAQIYARQCDCRCLPGYWGFPSPCQPCQCNHGLDCTVTGECISCDODYTTHNCRCCLA	900
841	Db	HCFAQIYARQCDCRCLPGYWGFPSPCQPCQCNHGLDCTVTGECISCDODYTTHNCRCCLA	900
901	QY	GYGDPPIIGSDHCRPCPCPDGSDSGRQFARSCVQDPVTLOLACVCPGVIISRCDDCAS	960
901	Db	GYGDPPIIGSDHCRPCPCPDGSDSGRQFARSCVQDPVTLOLACVCPGVIISRCDDCAS	960
961	QY	GFFGNPSDFGSGCOPCOCHNIDTTPDEACDKOTGRCLKLYHTEGDHCOLQGYGYGDA	1020
961	Db	GFFGNPSDFGSGCOPCOCHNIDTTPDEACDKOTGRCLKLYHTEGDHCOLQGYGYGDA	1020
1021	QY	LRQDCRCVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTG	1080
1021	Db	LRQDCRCVCNYLGTVKEHNGSDCHCDKATGQCSCLPNVIGONCDRCAPNTWQLASGTG	1080
1081	QY	CGPCNCAAHSGPSCNEFTGQCCMPFGGRITCSEQELFWGDPDVECRACDCDPREGIE	1140
1081	Db	CGPCNCAAHSGPSCNEFTGQCCMPFGGRITCSEQELFWGDPDVECRACDCDPREGIE	1140
1141	QY	TPQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPHQCQFALMDAIIIGELTNRTHKF	1200
1141	Db	TPQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPHQCQFALMDAIIIGELTNRTHKF	1200
1201	QY	LEKAKALKISGVIGPYRETVDSEKKVNEIKDILAQSPAAPLKNIGILPEEAELTKDQV	1260
1201	Db	LEKAKALKISGVIGPYRETVDSEKKVNEIKDILAQSPAAPLKNIGILPEEAELTKDQV	1260
1261	QY	TEKMAQVEVKLTDTTASOSNSTAGELGALQAEASLDTVKVELAQLEFFIKNSDIQGALDS	1320
1261	Db	TEKMAQVEVKLTDTTASOSNSTAGELGALQAEASLDTVKVELAQLEFFIKNSDIQGALDS	1320
1321	QY	ITKYFQMSLEAEKRVNASTTDPNSTVBEQSALTDRDVEDLMLERESPFKEQOEQARLLDE	1380
1321	Db	ITKYFQMSLEAEKRVNASTTDPNSTVBEQSALTDRDVEDLMLERESPFKEQOEQARLLDE	1380
1381	QY	LAKKLQSLDLSAAAOMTCGTPPGADCSGCGGNCRITDGEKKCGGPGCGGLVTVAHSA	1440
1381	Db	LAKKLQSLDLSAAAOMTCGTPPGADCSGCGGNCRITDGEKKCGGPGCGGLVTVAHSA	1440
1441	QY	WQKAMDPRDVLALAEVEQLSKMVSPAKVRADEAKONAQDVLLKTNATKEKVDKKNEDL	1500
1441	Db	WQKAMDPRDVLALAEVEQLSKMVSPAKVRADEAKONAQDVLLKTNATKEKVDKKNEDL	1500
1501	QY	RNLTKQIRNFLETDSADLDSIEAVANEVLKSGNASTPQQLQNTLTERIRREVTLSQVEVI	1560
1501	Db	RNLTKQIRNFLETDSADLDSIEAVANEVLKSGNASTPQQLQNTLTERIRREVTLSQVEVI	1560
1561	QY	LQSSAADIAEALLLEBAKXASKSATDVKTADVMVKEALBEAEKAQVAABKAIKQADEDI	1620

Db 1561 LQSQADIAAEALLLEAKGSKSATDKVTADVMVKEALEEAKQAQAAEKAIKQADEDI 1620

Qy 1621 QGTQNLLTSIESSTAASEETLNASORIISKLERNVEELKRKAAQNSGEAEYIEKVVYSVK 1680

Db 1621 QGTQNLLTSIESSTAASEETLNASORIISKLERNVEELKRKAAQNSGEAEYIEKVVYSVK 1680

Qy 1681 QNADDDVKTKLGDGLDSKYKKVSLIAQKTEESADARKAELLQNEAKTLLAQAQNSKLQLL 1740

Db 1681 QNADDDVKTKLGDGLDSKYKKVSLIAQKTEESADARKAELLQNEAKTLLAQAQNSKLQLL 1740

Qy 1741 EDLERYEDNQKYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1786

Db 1741 EDLERYEDNQKYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 2

LMB1 HUMAN STANDARD; PRT; 1786 AA.

AC P07942;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Laminin beta-1 chain precursor (Laminin B1 chain).

GN LAMB1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=90368768; PubMed=1975589;

RA Vuolteenaho R., Chow L.T., Tryggvason K.;

RT "Structure of the human laminin B1 chain gene.";

RL J. Biol. Chem. 265:15611-15616(1990).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=87280097; PubMed=3611077;

RA Pikkariemi T., Eddy R., Fukushima Y., Byers M., Shows T.,

RA Pihlajaniemi T., Saraste M., Tryggvason K.;

RT "Human laminin B1 chain. A multidomain protein with gene (LAMB1)

RL locus in the q22 region of chromosome 7.";

RN J. Biol. Chem. 262:10454-10462(1987).

RN [3]

RN SEQUENCE OF 1276-1709 FROM N.A.

RP MEDLINE=88021029; PubMed=3661559;

RA Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,

RA Drohan W.N.;

RT "Isolation of a cDNA clone for the human laminin-B1 chain and its

RT gene localization.";

RL Am. J. Hum. Genet. 41:605-615(1987).

CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin

CC is thought to mediate the attachment, migration and organization

CC of cells into tissues during embryonic development by interacting

CC with other extracellular matrix components.

CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three

CC different polypeptide chains (alpha, beta, gamma), which are bound

CC to each other by disulfide bonds into a cross-shaped molecule

CC comprising one long and three short arms with globules at each

CC end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),

CC laminin-2 (merosin), and laminin-6 (K-laminin).

CC -I- SUBCELLULAR LOCATION: Extracellular.

CC -I- TISSUE SPECIFICITY: Found in the basement membranes (major

CC component).

CC -I- DOMAIN: The alpha-helical domains I and II are thought to interact

CC with other laminin chains to form a coiled coil structure.

CC -I- DOMAIN: Domains VI and IV are globular.

CC -I- SIMILARITY: Contains 1 laminin N-terminal domain.

CC -I- SIMILARITY: Contains 13 laminin EGF-like domains.

CC -I- SIMILARITY: Contains 1 laminin IV domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC	EMBL; M20206; AAA59487.1; -.	DR	EMBL; M20206; AAA59487.1; -.
CC	PIR; S13547; MHHU1.	DR	PIR; S13547; MHHU1.
CC	HSP; P02468; IKLO.	DR	HSP; P02468; IKLO.
CC	Genew; HGNC:6486; LAMB1.	DR	Genew; HGNC:6486; LAMB1.
CC	MIM; 150240; -.	DR	MIM; 150240; -.
CC	InterPro; IPR006209; EGF_Like.	DR	InterPro; IPR006209; EGF_Like.
CC	InterPro; IPR002049; Laminin_EGF.	DR	InterPro; IPR002049; Laminin_EGF.
CC	InterPro; IPR008211; LamNr.	DR	InterPro; IPR008211; LamNr.
CC	Pfam; PF00053; laminin_EGF; 13.	DR	Pfam; PF00053; laminin_EGF; 13.
CC	Pfam; PF00055; laminin_Nterm; 1.	DR	Pfam; PF00055; laminin_Nterm; 1.
CC	PRINTS; PR00011; EGF_LAMININ.	DR	PRINTS; PR00011; EGF_LAMININ.
CC	SMART; SMC0180; EGF_Lam; 12.	DR	SMART; SMC0180; EGF_Lam; 12.
CC	SMART; SMC0136; LamNT; 1.	DR	SMART; SMC0136; LamNT; 1.
CC	PROSITE; PS00022; EGF_1; 9.	DR	PROSITE; PS00022; EGF_1; 9.
CC	PROSITE; PS01186; EGF_2; 2.	DR	PROSITE; PS01186; EGF_2; 2.
CC	PROSITE; PS01248; LAMININ_Type_EGF; 11.	DR	PROSITE; PS01248; LAMININ_Type_EGF; 11.
CC	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.	DR	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
CC	FT CHAIN 1 21	DR	FT CHAIN 1 21
CC	FT CHAIN 22 1786	DR	FT CHAIN 22 1786
CC	FT CHAIN 271 334	DR	FT CHAIN 271 334
CC	FT CHAIN 335 397	DR	FT CHAIN 335 397
CC	FT CHAIN 398 457	DR	FT CHAIN 398 457
CC	FT CHAIN 458 509	DR	FT CHAIN 458 509
CC	FT CHAIN 510 540	DR	FT CHAIN 510 540
CC	FT CHAIN 541 771	DR	FT CHAIN 541 771
CC	FT CHAIN 773 820	DR	FT CHAIN 773 820
CC	FT CHAIN 821 866	DR	FT CHAIN 821 866
CC	FT CHAIN 867 916	DR	FT CHAIN 867 916
CC	FT CHAIN 917 975	DR	FT CHAIN 917 975
CC	FT CHAIN 976 1027	DR	FT CHAIN 976 1027
CC	FT CHAIN 1028 1083	DR	FT CHAIN 1028 1083
CC	FT CHAIN 1084 1131	DR	FT CHAIN 1084 1131
CC	FT CHAIN 1132 1178	DR	FT CHAIN 1132 1178
CC	FT CHAIN 1179 1397	DR	FT CHAIN 1179 1397
CC	FT CHAIN 1398 1430	DR	FT CHAIN 1398 1430
CC	FT CHAIN 1431 1786	DR	FT CHAIN 1431 1786
CC	FT CHAIN 1216 1315	DR	FT CHAIN 1216 1315
CC	FT CHAIN 1353 1388	DR	FT CHAIN 1353 1388
CC	FT CHAIN 1442 1781	DR	FT CHAIN 1442 1781
CC	FT CHAIN 271 280	DR	FT CHAIN 271 280
CC	FT CHAIN 273 298	DR	FT CHAIN 273 298
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CC	FT CHAIN 440 455	DR	FT CHAIN 440 455
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CC	FT CHAIN 773 803	DR	FT CHAIN 773 803
CC	FT CHAIN 806 818	DR	FT CHAIN 806 818
CC	FT CHAIN 821 833	DR	FT CHAIN 821 833
CC	FT CHAIN 833 840	DR	FT CHAIN 833 840
CC	FT CHAIN 842 851	DR	FT CHAIN 842 851
CC	FT CHAIN 854 864	DR	FT CHAIN 854 864
CC	FT CHAIN 867 876	DR	FT CHAIN 867 876
CC	FT CHAIN 869 883	DR	FT CHAIN 869 883
CC	FT CHAIN 886 895	DR	FT CHAIN 886 895
CC	FT CHAIN 898 914	DR	FT CHAIN 898 914
CC	FT CHAIN 917 933	DR	FT CHAIN 917 933
CC	FT CHAIN 919 944	DR	FT CHAIN 919 944
CC	FT CHAIN 946 955	DR	FT CHAIN 946 955

Query Match 93.7%; Score 9144; DB 1; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLQVAFAGVIALWTRVCAQEPFSGYCAAGSCYPATGDLILIGRAKLSVTCGLHK 60  
DB 1 MGLQVAFAGVIALWTRVCAQEPFSGYCAAGSCYPATGDLILIGRAKLSVTCGLHK 60  
QY 61 PEPYCVSHLQEDKCFICSDRSDYHETLNDPSHLIENVTTFAPNRLKIWQSENGVEN 120  
DB 61 PEPYCVSHLQEDKCFICSDRSDYHETLNDPSHLIENVTTFAPNRLKIWQSENGVEN 120  
QY 121 VTIQDLLEAEFPHLINTFKTPAPAMLIERSDDFGKTGWYRYFAYDCSSPPGISTG 180  
DB 121 VTIQDLLEAEFPHLINTFKTPAPAMLIERSDDFGKTGWYRYFAYDCSSPPGISTG 180  
QY 181 PMKVVDDIICDSRYSDIEPSGEVIFPALDPAFKIEDPYSPRIQNLKITNRIKEVKL 240  
DB 181 PMKVVDDIICDSRYSDIEPSGEVIFPALDPAFKIEDPYSPRIQNLKITNRIKEVKL 240  
QY 241 HTLGNLLDSRMEIREKYYAVYDMVRGNCFCYGHASECAPVDGPFNEEVEGMVHGCMC 300  
DB 241 HTLGNLLDSRMEIREKYYAVYDMVRGNCFCYGHASECAPVDGPFNEEVEGMVHGCMC 300  
QY 301 RHNTKGLNCELCMDPYHDLPRPAPGRNSNACKCNCNEHSSCHFDMAVFLATGNVSGG 360  
DB 301 RHNTKGLNCELCMDPYHDLPRPAPGRNSNACKCNCNEHSSCHFDMAVFLATGNVSGG 360  
QY 361 VCDNCOHNTMGRNCBQKPFYFQHPERDIRDPNICEPTCDPAGSENGGICDGTDFSVG 420  
DB 361 VCDNCOHNTMGRNCBQKPFYFQHPERDIRDPNICEPTCDPAGSENGGICDGTDFSVG 420  
QY 421 LIAGCRCKLHVEGRCVCKEGFVDSADPYGCKSCACNPLGTIPGNCPCDSETCYCY 480  
DB 421 LIAGCRCKLHVEGRCVCKEGFVDSADPYGCKSCACNPLGTIPGNCPCDSETCYCY 480  
QY 481 CKRLVTGRCQCLPQHWGLSNDLDCRCPDCLGGLNNSCSDSGQCSCLPHMIGRCQ 540  
DB 481 CKRLVTGRCQCLPQHWGLSNDLDCRCPDCLGGLNNSCSDSGQCSCLPHMIGRCQ 540  
QY 541 NEVEGYFTTLDHYIYAEANLPGVYVVERQYIQDRIPSWTGPQFVRPEGAYLEFF 600  
DB 541 NEVEGYFTTLDHYIYAEANLPGVYVVERQYIQDRIPSWTGPQFVRPEGAYLEFF 600  
QY 601 IDNIPSYMEYLIRYEQLPDHWKAVITVQPGKIPASSRCNGTVPDDNQVVSLSPG 660  
DB 601 IDNIPSYMEYLIRYEQLPDHWKAVITVQPGKIPASSRCNGTVPDDNQVVSLSPG 660  
QY 661 SRYVLPAPVCEKGNVTVRLELPQYTASGDSVSPYTFDSLVLMPYCKSLDIFTVGG 720  
DB 661 SRYVLPAPVCEKGNVTVRLELPQYTASGDSVSPYTFDSLVLMPYCKSLDIFTVGG 720  
QY 721 SGDEVTNSAWETFORYRCLNSRSVVKTPMTDVCNIIIFISALIHOTGLACEDPQGS 780  
DB 721 SGDEVTNSAWETFORYRCLNSRSVVKTPMTDVCNIIIFISALIHOTGLACEDPQGS 780  
QY 781 LSSVCDPNGGQCCQCPNVVGRTCNRCAPGTFGPGNGKPCDCHLQGSASAFCAITGQC 840  
DB 781 LSSVCDPNGGQCCQCPNVVGRTCNRCAPGTFGPGNGKPCDCHLQGSASAFCAITGQC 840  
QY 841 HCFQGIYARQCDRLPGYWGPFSCPCQCNHGLDCTVTGECLSQDYTTGHCERCLA 900  
DB 841 HCFQGIYARQCDRLPGYWGPFSCPCQCNHGLDCTVTGECLSQDYTTGHCERCLA 900  
QY 901 GYGGPPIIGSGDHCRPCPCPDGPDGSGRFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
DB 901 GYGGPPIIGSGDHCRPCPCPDGPDGSGRFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
QY 961 GFEGNPSDFGSGCQPCQCHNITDTPDACDXTGRCCLKLYHTEGDCQICQYGYGDA 1020  
DB 961 GFEGNPSDFGSGCQPCQCHNITDTPDACDXTGRCCLKLYHTEGDCQICQYGYGDA 1020  
QY 1021 LRQDCRCKVCNVLGTVKEHCNGSDCHCDKATGCQSCLENFVGNQNCDCRCPNTWQLASGTG 1080

DB 1021 LRQDCRCKVCNVLGTVKEHCNGSDCHCDKATGCQSCLENFVGNQNCDCRCPNTWQLASGTG 1080  
QY 1081 CQPCNCAHSPGSCNEFTGQCQCMPPGFGGRTCSCEQELFWGDDPVECRACDPCRGIE 1140  
DB 1081 CQPCNCAHSPGSCNEFTGQCQCMPPGFGGRTCSCEQELFWGDDPVECRACDPCRGIE 1140  
QY 1141 TPQOQSTGQCVCVGVGPRCDKTRGYSVGFPPDCTPCHQCFALWDALIGLITNTHKF 1200  
DB 1141 TPQOQSTGQCVCVGVGPRCDKTRGYSVGFPPDCTPCHQCFALWDALIGLITNTHKF 1200  
QY 1201 LEKAKALKISGIVGPRVETVDSVERKVEIKDILAQSPAAEPKKNIGILFEBAEKLTKDV 1260  
DB 1201 LEKAKALKISGIVGPRVETVDSVERKVEIKDILAQSPAAEPKKNIGILFEBAEKLTKDV 1260  
QY 1261 TEMAQVEVKLTDTSQSNSTAGELGALQAEASIDKTKVLAEOLEFKNSDIQALDS 1320  
DB 1261 TEMAQVEVKLTDTSQSNSTAGELGALQAEASIDKTKVLAEOLEFKNSDIQALDS 1320  
QY 1321 ITYKFOMSLAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFEQEQEQARLLDE 1380  
DB 1321 ITYKFOMSLAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFEQEQEQARLLDE 1380  
QY 1381 LAGKLOSLDLASAAQMTCTPPGADCSSECCGPNCRTPDEGKCKGCGGGLVTVHSA 1440  
DB 1381 LAGKLOSLDLASAAQMTCTPPGADCSSECCGPNCRTPDEGKCKGCGGGLVTVHSA 1440  
QY 1441 WOKAMDFDRDLASAEVQLSKMSEAKVRADEAKONADVLLKTNATKEKVDKSNEDL 1500  
DB 1441 WOKAMDFDRDLASAEVQLSKMSEAKVRADEAKONADVLLKTNATKEKVDKSNEDL 1500  
QY 1501 RNLKIQIRNFLTSDSADLDSIEAVANEVLKSNASTPOOLQNLTEDIRERVETLSQVEVI 1560  
DB 1501 RNLKIQIRNFLTSDSADLDSIEAVANEVLKSNASTPOOLQNLTEDIRERVETLSQVEVI 1560  
QY 1561 LQSAADIAEABLLLEAKRASKSATDVKTADMKVKEALEEAKQAQAAEKAKOADEI 1620  
DB 1561 LQSAADIAEABLLLEAKRASKSATDVKTADMKVKEALEEAKQAQAAEKAKOADEI 1620  
QY 1621 QGTQNLITSESETAASEETLNASQISKLERNVEELKRAAQNSEGEAEYIEKVYYSVK 1680  
DB 1621 QGTQNLITSESETAASEETLNASQISKLERNVEELKRAAQNSEGEAEYIEKVYYSVK 1680  
QY 1681 QNADYVKTLDELDELKRYKKVSLIAKTEBESADARKEALLQNEAKTLLAQNASKQLL 1740  
DB 1681 QNADYVKTLDELDELKRYKKVSLIAKTEBESADARKEALLQNEAKTLLAQNASKQLL 1740  
QY 1741 EDLERYEDNOKYLEKQAELEVRLEGEVRSLLKDISKVAIVYSTCL 1786  
DB 1741 EDLERYEDNOKYLEKQAELEVRLEGEVRSLLKDISKVAIVYSTCL 1786

## RESULT 3

LMB2 RAT

ID LMB2 RAT

AC P158Q0;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).

GN LAMB2.

OC Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=101116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89159410; PubMed=2922051;

RA Hunter D.D. Shah V., Merlie J.P., Sanes J.R.;

RT "A laminin-like adhesive protein concentrated in the synaptic cleft

of the neuromuscular junction."

RL Nature 338:229-234 (1989).





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 46.7946 Seconds

(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-12

Perfect score: 9429  
Sequence: 1 EPYIVSHLQEDKCFICDS.....EVRSLKDISEKAVYSTCL 1725

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04 : \*  
1: Geneseq1980s : \*  
2: Geneseq1990s : \*  
3: Geneseq2000s : \*  
4: Geneseq2001s : \*  
5: Geneseq2002s : \*  
6: Geneseq2003as : \*  
7: Geneseq2003bs : \*  
8: Geneseq2004s : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9429	100.0	1725	3 AAB19800	Aab19800 Mouse lam
2	9429	100.0	1725	3 AAB48451	Aab48451 Mouse lam
3	9429	100.0	1725	5 ABB81593	Abb81593 Mouse lam
4	9429	100.0	1786	3 AAB19799	Aab19799 Mouse lam
5	9429	100.0	1786	3 AAB48450	Aab48450 Mouse lam
6	9429	100.0	1786	5 ABB81592	Abb81592 Mouse lam
7	9363	99.3	1776	2 AAW50894	Aaw50894 Mouse lam
8	9307.5	98.7	1764	1 AAB291672	Aap291672 Primary a
9	8873	94.1	1765	3 AAB19798	Aab19798 Human lam
10	8873	94.1	1765	3 AAB48449	Aab48449 Human lam
11	8873	94.1	1765	5 ABB81591	Abb81591 Human lam
12	8873	94.1	1786	2 AAW50893	Aaw50893 Human lam
13	8873	94.1	1786	3 AAB16522	Aab16522 Human lam
14	8873	94.1	1786	3 AAB19797	Aab19797 Human lam
15	8873	94.1	1786	3 AAB48448	Aab48448 Human lam
16	8873	94.1	1786	4 AAB30788	Aab30788 Human ebe
17	8873	94.1	1786	5 ABB81590	Abb81590 Human lam
18	8860	94.0	1786	5 AAM48896	Aam48896 Laminin p
19	8837.5	93.7	1785	2 AAY15461	Aay15461 Human lam
20	4936	52.3	1801	7 AAW50895	Aaw50895 Rat lamin
21	4936	52.3	1801	7 ADE60383	Ade60383 Rat prote
22	4914	52.1	1799	5 AAW50359	Aaw50359 Mouse lam
23	4890	51.9	1798	2 AAW50896	Aaw50896 Human lam
24	4890	51.9	1798	2 ADE60385	Ade60385 Human Pro
25	4778	50.7	1798	5 AAU84346	Aau84346 Protein L

26	4778	50.7	1798	5 AAM50360	Aam50360 Human lam
27	3736.5	39.6	1788	4 ABB62295	Abb62295 Drosophil
28	3712.5	39.4	1761	2 AAY15457	Aay15457 Human lam
29	3616	38.3	822	5 AAM48897	Aam48897 Laminin p
30	3506.5	37.2	1670	7 ADE07851	Ade07851 Novel pro
31	2967.5	31.5	1101	7 ADE28641	Ade28641 Human NOV
32	2945.5	31.2	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2640	28.0	466	2 AAR07447	Aar07447 Human lam
34	2154	22.8	527	3 AAB58995	Aab58995 Breast an
35	1940	20.6	434	1 AAF60109	Aap60109 Human B1
36	1682.5	17.8	1639	4 ABB59807	Abb59807 Drosophil
37	1681	17.8	315	6 ABU70520	Abu70520 Human adi
38	1645	17.4	3712	4 ABB64954	Abb64954 Drosophil
39	1637.5	17.4	1572	3 AAB19806	Aab19806 Mouse lam
40	1637.5	17.4	1572	3 AAB48455	Aab48455 Mouse lam
41	1637.5	17.4	1572	5 ABB81597	Abb81597 Mouse lam
42	1637.5	17.4	1605	3 AAB19805	Aab19805 Mouse lam
43	1637.5	17.4	1605	3 AAB48454	Aab48454 Mouse lam
44	1637.5	17.4	1605	5 ABB81596	Abb81596 Mouse lam
45	1622.5	17.2	1576	3 AAB19802	Aab19802 Human lam

ALIGNMENTS

RESULT 1  
AAB19800  
ID AAB19800 standard; protein; 1725 AA.

AC AAB19800;

DT 05-MAR-2001 (first entry)

DE Mouse laminin 2 mature beta-1 chain.

KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
degenerative muscle disorder; muscular dystrophy; cell therapy.

OS Mus musculus.

PN WO200066730-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000WO-US011378.

PR 30-APR-1999; 99US-0131720P.

PR 15-JUN-1999; 99US-0139198P.

PR 12-JUL-1999; 99US-0143289P.

PR 24-SEP-1999; 99US-0155945P.

PI (UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PI Yurchenco P;

DR WPI; 2000-687537/67.

DR N-PSDB; AAA88900.

PS Claim 5; Page 226-232; 305pp; English.

CC The present sequence is that of the mouse laminin 2 beta-1 chain mature protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the

CC polynucleotides encoding them (see AAA8891-906), methods for making  
CC recombinant laminin 2, cells that express recombinant laminin 2 and  
CC methods for using purified laminin 2 for research and therapeutic  
CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX  
SQ Sequence 1725 AA;  
  
Query Match 100.0%; Score 9429; DB 3; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EPYCVSHLOEDKCFICDSRDPVHTLNPDSHLIENVVTPAPNRLKIWSENGVENV 60  
DB 1 EPYCVSHLOEDKCFICDSRDPVHTLNPDSHLIENVVTPAPNRLKIWSENGVENV 60  
  
QY 61 TIQDLAEAFHFTLHIMTFTPPAAMLIERSDFGKTGWVRYFAYDCSSPPGISTGP 120  
DB 61 TIQDLAEAFHFTLHIMTFTPPAAMLIERSDFGKTGWVRYFAYDCSSPPGISTGP 120  
  
QY 121 MKKVDDIICDSRSDIEPSTEGEVIFRALDPAPKIEDPSPRIQNLKLTNRIKFKVLH 180  
DB 121 MKKVDDIICDSRSDIEPSTEGEVIFRALDPAPKIEDPSPRIQNLKLTNRIKFKVLH 180  
  
QY 181 TLGNLILDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGMVHGCMCR 240  
DB 181 TLGNLILDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGMVHGCMCR 240  
  
QY 241 HNTVGLNCELOMPYHDLWPRPAGRNSNACKKCNNEHSSCHFDMVFLATGNVSGV 300  
DB 241 HNTVGLNCELOMPYHDLWPRPAGRNSNACKKCNNEHSSCHFDMVFLATGNVSGV 300  
  
QY 301 CDNCQHTWGRNCEQCKPFFQHPERDIRPDLNCEPCTCPAGSENGGICDGYTDFSVGL 360  
DB 301 CDNCQHTWGRNCEQCKPFFQHPERDIRPDLNCEPCTCPAGSENGGICDGYTDFSVGL 360  
  
QY 361 IAGQCRKLVHEGRCDVKEGFFYDLAEDPYGCKSCACNPLGTIPGGNPDSETGYCYC 420  
DB 361 IAGQCRKLVHEGRCDVKEGFFYDLAEDPYGCKSCACNPLGTIPGGNPDSETGYCYC 420  
  
QY 421 KRLVTGQRCQCLPQHGLSNDLGGPCDCLGGLANNSSCSGSCCLPHMIGRQCN 480  
DB 421 KRLVTGQRCQCLPQHGLSNDLGGPCDCLGGLANNSSCSGSCCLPHMIGRQCN 480  
  
QY 481 EVESGYFTTLDHYIYEAEEANLGPVVVYVERQYIQDRIPSWTGPVRYPEGAYLEFFI 540  
DB 481 EVESGYFTTLDHYIYEAEEANLGPVVVYVERQYIQDRIPSWTGPVRYPEGAYLEFFI 540  
  
QY 541 DNIYPSMEYEILIRYEPQLPDHWEKAVITVORPKIPASSRCGNTPDDNQVVSLSPGS 600  
DB 541 DNIYPSMEYEILIRYEPQLPDHWEKAVITVORPKIPASSRCGNTPDDNQVVSLSPGS 600  
  
QY 601 RYVLPAPVCEKGMNTVRLLEPQYTAGSDVESPTFIDSLVMPYCKSLDIFTVGGG 660  
DB 601 RYVLPAPVCEKGMNTVRLLEPQYTAGSDVESPTFIDSLVMPYCKSLDIFTVGGG 660  
  
QY 661 GDGEVTSAMETFORVRCLENSRSVVKTPMTDVCNRNIIIFISALIHQTGLACDCPQSSL 720  
DB 661 GDGEVTSAMETFORVRCLENSRSVVKTPMTDVCNRNIIIFISALIHQTGLACDCPQSSL 720  
  
QY 721 SSVCDPNGGQCCQCPNVVGRVTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 780  
DB 721 SSVCDPNGGQCCQCPNVVGRVTCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 780  
  
QY 781 CFQGIYARQCRCRLPGYWGFPSCQPCQCNHALDCDVTGTGECLSQDYTTGHNCERCLAG 840  
DB 781 CFQGIYARQCRCRLPGYWGFPSCQPCQCNHALDCDVTGTGECLSQDYTTGHNCERCLAG 840  
  
QY 841 YVGPPIIGSGDHPKPCPCDGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
DB 841 YVGPPIIGSGDHPKPCPCDGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900

DB 841 YVGPPIIGSGDHPKPCPCDGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
QY 901 PFGNPSDFGSCQPCQCHNIDITTDPEACDKTGRCLKLYHTEGHCHQCLQCYGYGDAL 960  
DB 901 PFGNPSDFGSCQPCQCHNIDITTDPEACDKTGRCLKLYHTEGHCHQCLQCYGYGDAL 960  
QY 961 RQDCRKCVCNYLGTGVKHECHNGSCHDKATGQCSCLPNVIGQNCDCRCPANTWQLASGTC 1020  
DB 961 RQDCRKCVCNYLGTGVKHECHNGSCHDKATGQCSCLPNVIGQNCDCRCPANTWQLASGTC 1020  
  
QY 1021 GPCNCAHSPGSCNEFTGCCQCMPPGFGRTTSECQELFWGDPDVECRACDCCDPRGIET 1080  
DB 1021 GPCNCAHSPGSCNEFTGCCQCMPPGFGRTTSECQELFWGDPDVECRACDCCDPRGIET 1080  
  
QY 1081 PQDQSTGQCVCVEGVGPRCDKCTRGYGVFPDCTPCHQCFALWDALIIIGELTNRTHKFL 1140  
DB 1081 PQDQSTGQCVCVEGVGPRCDKCTRGYGVFPDCTPCHQCFALWDALIIIGELTNRTHKFL 1140  
  
QY 1141 EKAKALKISGIVGYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTNDVT 1200  
DB 1141 EKAKALKISGIVGYRETVDSEKKNVEIKDILAQSPAAPLKNIGILFEEAEKLTNDVT 1200  
  
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDSI 1260  
DB 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQALDSI 1260  
  
QY 1261 TKYFQMSLEAEKRYNASTTDPNSTVEQSALTDRVEDLMLESPPFKQEQQEQLLDEL 1320  
DB 1261 TKYFQMSLEAEKRYNASTTDPNSTVEQSALTDRVEDLMLESPPFKQEQQEQLLDEL 1320  
  
QY 1321 AGKQLSLDLASAAQWTCGTPPGADCSSECGGPNCRDTEGEKKCGGPGCGGLVTVSAWS 1380  
DB 1321 AGKQLSLDLASAAQWTCGTPPGADCSSECGGPNCRDTEGEKKCGGPGCGGLVTVSAWS 1380  
  
QY 1381 QKAMDPRDVLASALAEVQLSKMVESEAKVRADAKQNAQVLLKTNATKEDKVNEDLR 1440  
DB 1381 QKAMDPRDVLASALAEVQLSKMVESEAKVRADAKQNAQVLLKTNATKEDKVNEDLR 1440  
  
QY 1441 NLIKQIRNFLTEDGADLDSIEAVANEVLKSGNASTPQQLQNLITDIERVETLSQVEVIL 1500  
DB 1441 NLIKQIRNFLTEDGADLDSIEAVANEVLKSGNASTPQQLQNLITDIERVETLSQVEVIL 1500  
  
QY 1501 QQSAADIARABELLEAEKRAKSKATDVKVTADWVKEALEAEKAAQVAEAKIQADEDIQ 1560  
DB 1501 QQSAADIARABELLEAEKRAKSKATDVKVTADWVKEALEAEKAAQVAEAKIQADEDIQ 1560  
  
QY 1561 GTQNLLTTSISETAASEETLTNASORISKLENNVEELKRAAQNSEAEYIEKVVYSVKQ 1620  
DB 1561 GTQNLLTTSISETAASEETLTNASORISKLENNVEELKRAAQNSEAEYIEKVVYSVKQ 1620  
  
QY 1621 NADDDVKKTLDELDEKYYKKVESLIAQKTESADARRKAEELLQNEAKTLLAQNSKLQLE 1680  
DB 1621 NADDDVKKTLDELDEKYYKKVESLIAQKTESADARRKAEELLQNEAKTLLAQNSKLQLE 1680  
  
QY 1681 DLERKYEDNQKYLEDKAQELVRLSEVRSLLKDISEKVAVYSTCL 1725  
DB 1681 DLERKYEDNQKYLEDKAQELVRLSEVRSLLKDISEKVAVYSTCL 1725

RESULT 2  
AAB48451  
ID AAB48451 standard; protein; 1725 AA.  
XX  
AC AAB48451;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 20.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX

OS Mus musculus.  
PN WO200066732-A2.  
XX  
ED 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX  
PF 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX  
PA (BIOS-) BIOSTRATUM INC.  
XX  
XX Kortessmaa J, Tryggvason K;  
PI N-PSDB; AAC83712.  
DR WPI; 2000-687539/67.  
XX N-PSDB; AAC83712.  
XX  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 189-194; 245pp; English.  
XX  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration.  
XX  
XX Sequence 1725 AA;  
XX  
XX Query Match 100.0%; Score 9429; DB 3; Length 1725;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 EPYCIVSHLOEDKCFICDSRDPYHETLNPDHSHLIENVVTTFAPNRLKIMWQSENGV 60  
DB 1 EPYCIVSHLOEDKCFICDSRDPYHETLNPDHSHLIENVVTTFAPNRLKIMWQSENGV 60  
QY 61 TIQLDLEAEFHTLIMTKTFRPAAMLIERSDFGKTGWYRYFAYDCSSFFGISTGP 120  
DB 61 TIQLDLEAEFHTLIMTKTFRPAAMLIERSDFGKTGWYRYFAYDCSSFFGISTGP 120  
QY 121 MKKVDDIICDSRYSDIESTGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKFKVLH 180  
DB 121 MKKVDDIICDSRYSDIESTGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKFKVLH 180  
QY 181 TLGDNLDSRMEIREKYYAVYVDMVRGNCFCYGHASECAPVDGVNEVEGMVHGCMCR 240  
DB 181 TLGDNLDSRMEIREKYYAVYVDMVRGNCFCYGHASECAPVDGVNEVEGMVHGCMCR 240  
QY 241 HNTKGLNCELAMD FVHDLFWPAEGRNSNACKKNCNHSCHDFDAVFLATGNVSGV 300  
DB 241 HNTKGLNCELAMD FVHDLFWPAEGRNSNACKKNCNHSCHDFDAVFLATGNVSGV 300  
QY 301 CNDCHNTMGRNCEOCKPFYFQHPDRDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 301 CNDCHNTMGRNCEOCKPFYFQHPDRDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
QY 361 IAGQCRCKLHVEGERCDYCKSGFYDLSAEDPYGCKSCACNPLGTIPGNCDSSETGYCYC 420

DB 361 IAGQCRCKLHVEGERCDYCKSGFYDLSAEDPYGCKSCACNPLGTIPGNCDSSETGYCYC 420  
QY 421 KELVTGQRCDQCLPQHGLSNDLDGCRPCDCDGLGALNNSCEDSGQSCCLPHMIGRQCN 480  
DB 421 KELVTGQRCDQCLPQHGLSNDLDGCRPCDCDGLGALNNSCEDSGQSCCLPHMIGRQCN 480  
QY 481 EYESGYFTTLDHYTYEABEANI.GRGVWVVERQYTDRIIPSWTGTGFGVVRVPEGAVLEPFI 540  
DB 481 EYESGYFTTLDHYTYEABEANI.GRGVWVVERQYTDRIIPSWTGTGFGVVRVPEGAVLEPFI 540  
QY 541 DNIPYSMEYEIILIRVEPOLPDHWEKAVITVQPGKIPASSRCGNTVPDDDNVWSLSPGS 600  
DB 541 DNIPYSMEYEIILIRVEPOLPDHWEKAVITVQPGKIPASSRCGNTVPDDDNVWSLSPGS 600  
QY 601 RYVVLPRPVCFEKGMYTVRLLEPOYTASGSDVESPYTFIDSLVLMFYCKSLDIDITVGS 660  
DB 601 RYVVLPRPVCFEKGMYTVRLLEPOYTASGSDVESPYTFIDSLVLMFYCKSLDIDITVGS 660  
QY 661 GDGEVTSNASETQRYRCLNERSVVKTPMTDVCNIIIFSISALIHQTGLACECPQGS 720  
DB 661 GDGEVTSNASETQRYRCLNERSVVKTPMTDVCNIIIFSISALIHQTGLACECPQGS 720  
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNCXPCDCHLOGSASAFCDATIGQCH 780  
DB 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTGFGPNCXPCDCHLOGSASAFCDATIGQCH 780  
QY 781 CFQGIYAROCDCRCLPGYMGFPSCQCCNGHALDCDVTGTECLSCQDYTTGHCNCRCLAG 840  
DB 781 CFQGIYAROCDCRCLPGYMGFPSCQCCNGHALDCDVTGTECLSCQDYTTGHCNCRCLAG 840  
QY 841 YTGDPPIIGSDHCRPCPCPDGSGRQFARSQYQDPVTLQLACVCDPGVIGRCDCCAG 900  
DB 841 YTGDPPIIGSDHCRPCPCPDGSGRQFARSQYQDPVTLQLACVCDPGVIGRCDCCAG 900  
QY 901 FEGNPSDFGSCQPCQCHNIIITDPEACDXTGTCLKLYHTEGDHCLCOYGYVGDAL 960  
DB 901 FEGNPSDFGSCQPCQCHNIIITDPEACDXTGTCLKLYHTEGDHCLCOYGYVGDAL 960  
QY 961 RODCRKVCNLYGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWOLASGTGC 1020  
DB 961 RODCRKVCNLYGTVKEHCNGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWOLASGTGC 1020  
QY 1021 GRNCNNAHSFGSCNEFTGQCCQCPGFGGRGTRCSQELFWGDDPVECRACDCDPRGLET 1080  
DB 1021 GRNCNNAHSFGSCNEFTGQCCQCPGFGGRGTRCSQELFWGDDPVECRACDCDPRGLET 1080  
QY 1081 PQCDQSTGQCVCEGVGEGPRCDKTRGYSGVFPDCTPCHQCFCFALMDAIIIGELTNTRKFL 1140  
DB 1081 PQCDQSTGQCVCEGVGEGPRCDKTRGYSGVFPDCTPCHQCFCFALMDAIIIGELTNTRKFL 1140  
QY 1141 EKAKALKISGVIGPYRETVDVSEKKNVETKDIQAAPAEPLKNIGILFEEAEKLTQDVT 1200  
DB 1141 EKAKALKISGVIGPYRETVDVSEKKNVETKDIQAAPAEPLKNIGILFEEAEKLTQDVT 1200  
QY 1201 EKMAQVEVLTDITASOSNSTAGELQALQAEASLSKTVKELAEQLEFIKNSIQGALDSI 1260  
DB 1201 EKMAQVEVLTDITASOSNSTAGELQALQAEASLSKTVKELAEQLEFIKNSIQGALDSI 1260  
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVDEMLERESPFKEQOEQARLLDEL 1320  
DB 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVDEMLERESPFKEQOEQARLLDEL 1320  
QY 1321 AGKLOSLDLSAAQWTCGTPPGADCSSECGGPNCRDTEGEKKCGGPGCGGLVTVHAWSAM 1380  
DB 1321 AGKLOSLDLSAAQWTCGTPPGADCSSECGGPNCRDTEGEKKCGGPGCGGLVTVHAWSAM 1380  
QY 1381 QKAMDPRDVLASALAEVEQLSKWSEAKVRADEAKQADVLKTNATKEKVDKSNEDLR 1440  
DB 1381 QKAMDPRDVLASALAEVEQLSKWSEAKVRADEAKQADVLKTNATKEKVDKSNEDLR 1440  
QY 1441 NLIKQIRNFLTSDSADLSIEAVANEVLKSGNASTPQOLQNLTEIDIRREVETLSQVEVIL 1500  
DB 1441 NLIKQIRNFLTSDSADLSIEAVANEVLKSGNASTPQOLQNLTEIDIRREVETLSQVEVIL 1500

QY 1501 QQAADIAIARAELELEBAKASKSATDVKTADVMKEALBEAKQAQVAEKAIAKQADEDIQ 1560  
DB 1501 QQAADIAIARAELELEBAKASKSATDVKTADVMKEALBEAKQAQVAEKAIAKQADEDIQ 1560  
QY 1561 GTQNLITSESETAASEETITNASORISKLERNVEELK3KAAQNSGEAEYIEKVYVSKQ 1620  
DB 1561 GTQNLITSESETAASEETITNASORISKLERNVEELK3KAAQNSGEAEYIEKVYVSKQ 1620  
QY 1621 NADVVKTLDGELDEKVKVESLIAQTBESADARKABELLQNEAKTLIAQNSKLQLE 1680  
DB 1621 NADVVKTLDGELDEKVKVESLIAQTBESADARKABELLQNEAKTLIAQNSKLQLE 1680  
QY 1681 DLERKVEDNOKYLEDQAQLVRLEGEVRSLLKDISEKVAVYSTCL 1725  
DB 1681 DLERKVEDNOKYLEDQAQLVRLEGEVRSLLKDISEKVAVYSTCL 1725

## RESULT 3

ABB81593  
ID ABB81593 standard; protein; 1725 AA.

XX ABB81593;

DT 19-SBP-2002 (first entry)

DE Mouse laminin 10 second chain protein sequence SEQ ID NO:12.

XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.

XX Mus musculus.

XX WO200250111-A2.

XX 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

DR N-PSDB; ABQ72911.

XX New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for

PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 153-158; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a second chain protein of laminin 10, from the present  
CC invention

XX Sequence 1725 AA;

Query Match

100.0%; Score 9429; DB 5; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSLHIENVVTTFAPNRLKIWQSENGVENV 60  
DB 1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSLHIENVVTTFAPNRLKIWQSENGVENV 60  
QY 61 TIQDLIAEAPHFTLIMFTKTPRPAAMLIERSDFGKTGWGVYFAYDCSSPPGISTGP 120  
DB 61 TIQDLIAEAPHFTLIMFTKTPRPAAMLIERSDFGKTGWGVYFAYDCSSPPGISTGP 120  
QY 121 MKYVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRAIKFKVLH 180  
DB 121 MKYVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKITNLRAIKFKVLH 180  
QY 181 TLGNLLDSRMEIREKYYAYVDMVVGNCFCYGHASECAPVDGVNVEEVMVGHGCMCR 240  
DB 181 TLGNLLDSRMEIREKYYAYVDMVVGNCFCYGHASECAPVDGVNVEEVMVGHGCMCR 240  
QY 241 HNTKGLNCELMDPYHDLPMWPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300  
DB 241 HNTKGLNCELMDPYHDLPMWPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300  
QY 301 CDNCQNTMGRNCEQKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 301 CDNCQNTMGRNCEQKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGL 360  
QY 361 IAGQCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420  
DB 361 IAGQCRKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420  
QY 421 KRLVTGQRCDQCLPQHWGLSNDLGCRCPCDCLGGALNNSCEDSDGQCSCLPMHIGRQC 480  
DB 421 KRLVTGQRCDQCLPQHWGLSNDLGCRCPCDCLGGALNNSCEDSDGQCSCLPMHIGRQC 480  
QY 481 EVESGYFTTLDHYIYEABEANLPGVWVVERQVIOIRIPSWTGPGRVVRPEGAYLEFFI 540  
DB 481 EVESGYFTTLDHYIYEABEANLPGVWVVERQVIOIRIPSWTGPGRVVRPEGAYLEFFI 540  
QY 541 DNIPIYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNVTVPDDNQVVSLSPGS 600  
DB 541 DNIPIYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRCGNVTVPDDNQVVSLSPGS 600  
QY 601 RYVVLPRPVCPEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGS 660  
DB 601 RYVVLPRPVCPEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGS 660  
QY 661 GDGEVITNSAWETFORVRCLENSRSVVKTPMTDVCRNIIFISALIHOTGLACECDPQSL 720  
DB 661 GDGEVITNSAWETFORVRCLENSRSVVKTPMTDVCRNIIFISALIHOTGLACECDPQSL 720  
QY 721 SSVCDPNGGQCCRPNVVGRTCNRCAPGTFGPNCKPCDCHLQGSASAFCDAITGQCH 780  
DB 721 SSVCDPNGGQCCRPNVVGRTCNRCAPGTFGPNCKPCDCHLQGSASAFCDAITGQCH 780  
QY 781 CFQGIYARQCDRCCLPFGYWGFPSCQPCQCNHGLDCTVTGCECLSCQYTTGHNCERCLAG 840  
DB 781 CFQGIYARQCDRCCLPFGYWGFPSCQPCQCNHGLDCTVTGCECLSCQYTTGHNCERCLAG 840  
QY 841 YGPIITGSDGHCPCPCPDGSGRQFARSCQDPVTLOLACVCDPGLYIGSRCDCCASG 900  
DB 841 YGPIITGSDGHCPCPCPDGSGRQFARSCQDPVTLOLACVCDPGLYIGSRCDCCASG 900  
QY 901 PFGNPSDFGSGCQPCQCHNIDTTDPEACDKTGRCLKLYHTBEGDHCQLCQYGYGDAL 960  
DB 901 PFGNPSDFGSGCQPCQCHNIDTTDPEACDKTGRCLKLYHTBEGDHCQLCQYGYGDAL 960  
QY 961 QDCRKCVCNVLGTVXHCNGSDCHCDKATGQCSCLENVIGONCDRCAPNTWQLASGTGC 1020  
DB 961 QDCRKCVCNVLGTVXHCNGSDCHCDKATGQCSCLENVIGONCDRCAPNTWQLASGTGC 1020  
QY 1021 GPCNCAHSPGSCNEFTGQCQCMPPGGRGTSECOLEFWGDDPDVECRACDDPGRGRET 1080

Db 1021 GPCNCAHSGFSGCNFTGQCQCMPFGGRTCSQBELFWGDDPDVECRACDCDPRGIET 1080  
Qy 1081 POCDOSTGCVCEGVGPRCKCTRGYSVFPDCTPCHQCQFALMDAIIIGELTNRTHKFL 1140  
Db 1081 POCDOSTGCVCEGVGPRCKCTRGYSVFPDCTPCHQCQFALMDAIIIGELTNRTHKFL 1140  
Qy 1141 EKAKALKSGVIGPRTVDSVEKKNEIKDILAQSPAAEPKNIIGILFBAEAKLTKDVT 1200  
Db 1141 EKAKALKSGVIGPRTVDSVEKKNEIKDILAQSPAAEPKNIIGILFBAEAKLTKDVT 1200  
Qy 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLQKTVKELAEQLEFIKNSDIQALDSI 1260  
Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLQKTVKELAEQLEFIKNSDIQALDSI 1260  
Qy 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLERESPFKQCBQAEARLLDEL 1320  
Db 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLERESPFKQCBQAEARLLDEL 1320  
Qy 1321 AGKLOSLDLASAAQMTCTGPPGACDSESCGPGNCTDEGEKKCGGPGGLTVVAHSAW 1380  
Db 1321 AGKLOSLDLASAAQMTCTGPPGACDSESCGPGNCTDEGEKKCGGPGGLTVVAHSAW 1380  
Qy 1381 QKAMPFDRDVLASALAEVQLSKQVSEAKVRADAKQNAQDVLLKTNATKVKDKSNEDLR 1440  
Db 1381 QKAMPFDRDVLASALAEVQLSKQVSEAKVRADAKQNAQDVLLKTNATKVKDKSNEDLR 1440  
Qy 1441 NLIKOIRNFLTSDSADLSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQEVIL 1500  
Db 1441 NLIKOIRNFLTSDSADLSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQEVIL 1500  
Qy 1501 QQSAADIAEALLLEAKSAKSATDVKTADVMKEALEEAFKAQVAAEKAQKQADEIDQ 1560  
Db 1501 QQSAADIAEALLLEAKSAKSATDVKTADVMKEALEEAFKAQVAAEKAQKQADEIDQ 1560  
Qy 1561 GTQNLITSTESTASAEETLTNASORISKLEBNVEELKRAQNSGEAEYIEKVYYSVKQ 1620  
Db 1561 GTQNLITSTESTASAEETLTNASORISKLEBNVEELKRAQNSGEAEYIEKVYYSVKQ 1620  
Qy 1621 NADDVKKTLGDGLDEKYYKVESLIAQKTEESADARRKAEELLQNEAKTLTAAQNSKLQLE 1680  
Db 1621 NADDVKKTLGDGLDEKYYKVESLIAQKTEESADARRKAEELLQNEAKTLTAAQNSKLQLE 1680  
Qy 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
Db 1681 DLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
  
RESULT 4  
AAB19799  
ID AAB19799 standard; protein; 1786 AA.  
XX AC AAB:9799;  
XX DT 05-MAR-2001 (first entry)  
XX DE Mouse laminin 2 beta-1 chain.  
XX KW Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
XX KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX OS Mus musculus.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..21  
XX FT /label= Signal\_peptide 22..1786  
XX FT Protein /label= Mature\_protein  
XX WO2000066730-A2.  
XX PN 09-NOV-2000.  
XX PD  
XX PF 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-01311720P.  
PR 15-JUN-1999; 99US-01391989P.  
PR 12-JUL-1999; 99US-01433899P.  
PR 24-SEP-1999; 99US-0155945P.  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
FA Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88899.  
DR Purified laminin 2 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 212-218; 305pp; English.  
PS The present sequence is that of the beta-1 chain of mouse laminin 2.  
CC Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
CC (100 kDa) chains. It is thought to be specifically required for  
CC stabilizing myotubes during skeletal muscle development, and for  
CC preventing apoptosis. Genetic defects in human laminin 2 structure or  
CC expression are associated with a major type of congenital muscular  
CC dystrophy. Laminin 2 is also thought to be important in Schwann  
CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
CC polynucleotides encoding them (see AAA88891-906), methods for making  
CC recombinant laminin 2. Cells that express recombinant laminin 2, and  
CC methods for using purified laminin 2 for research and therapeutic  
CC purposes including peripheral nerve regeneration, treatment of  
CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
CC attachment and migration, ex vivo cell therapy, improving the take of  
CC grafts, improving the biocompatibility of medical devices and preparing  
CC improved culture devices and media  
XX SQ Sequence 1786 AA;  
  
Query Match 100.0%; Score 9429; DB 3; Length 1786;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EPTCVSHLQEDKKCFICDSRDPYHETLNPDSHLINVTTPAPNRLKIWQSENGENV 60  
Db 62 EPTCVSHLQEDKKCFICDSRDPYHETLNPDSHLINVTTPAPNRLKIWQSENGENV 121  
  
Qy 61 TIQDLAEAFHFTLMTKTRPAAMLIERSSDFGTGWVRYPAYDCESPFGISTGP 120  
Db 122 TIQDLAEAFHFTLMTKTRPAAMLIERSSDFGTGWVRYPAYDCESPFGISTGP 181  
  
Qy 121 MKKVDIIICDSRYSDIEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKITNRIKFKVLH 180  
Db 182 MKKVDIIICDSRYSDIEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKITNRIKFKVLH 241  
  
Qy 181 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGVHGHCMCR 240  
Db 242 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGVHGHCMCR 301  
  
Qy 241 HNTKGLNCELMDFYHDLFWPRAEGNSNACKKCNHSSSSCHSDFMAVFLATGNVSGV 300  
Db 302 HNTKGLNCELMDFYHDLFWPRAEGNSNACKKCNHSSSSCHSDFMAVFLATGNVSGV 361  
  
Qy 301 CDNCQNTWGNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
Db 362 CDNCQNTWGNCEQCKPFYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421  
  
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLASADPYGCKSCACNPLGTIPGNCPCDSETCYCYC 420  
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLASADPYGCKSCACNPLGTIPGNCPCDSETCYCYC 481  
  
Qy 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDIDLGALNNNSCEDSGQCSCLPHMTGRQCN 480

482 KRLVTGQRCCQLPQHGLNSLDGCRPCDLDGGALNNNSCSDSCQCSCLPHMIGRQC 541  
481 EVESGYFTTLDHYIYEAEBANLPGVWVVEROYI QDRIPSWTGPVVRVPGAVLEFFI 540  
542 EVESGYFTTLDHYIYEAEBANLPGVWVVEROYI QDRIPSWTGPVVRVPGAVLEFFI 601  
541 DNTPYSMEXBILTRYEPOLPDHWEKAVITVORPKIPASSRCGNTVPPDDNQVSLSPGS 600  
602 DNTPYSMEXBILTRYEPOLPDHWEKAVITVORPKIPASSRCGNTVPPDDNQVSLSPGS 661  
601 RYVVLPRPVCFEKGMNVTVLELPPQYTAGSDVESPTTIDSLVLMFYCKSLDITFVGS 660  
662 RYVVLPRPVCFEKGMNVTVLELPPQYTAGSDVESPTTIDSLVLMFYCKSLDITFVGS 721  
661 GGEVNTSAWETTORVRLCNSVSVKTPMTDVCRNIIIFSISALIHOTGLACECPQGS 720  
722 GGEVNTSAWETTORVRLCNSVSVKTPMTDVCRNIIIFSISALIHOTGLACECPQGS 781  
721 SSVCDPNGGQOCQRPNVVGTNCRKAPGTFPGFNGKPCDCHLQGSASAFCDALITGOCH 780  
782 SSVCDPNGGQOCQRPNVVGTNCRKAPGTFPGFNGKPCDCHLQGSASAFCDALITGOCH 841  
781 CFQGIYARQCDRLPLGFWGPPSCQPCQNGHALDCTVTGECLSQCDYTTGHCNRCERCLAG 840  
842 CFQGIYARQCDRLPLGFWGPPSCQPCQNGHALDCTVTGECLSQCDYTTGHCNRCERCLAG 901  
841 YGDPPIIGSDGHCRCPCPCPDGSPGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAG 900  
902 YGDPPIIGSDGHCRCPCPCPDGSPGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAG 961  
901 FFGNPSDFGSCQPCQCHNIDTTDEACDKOTGRCLKCLYHTEGHCQLCQYGYGDAL 960  
962 FFGNPSDFGSCQPCQCHNIDTTDEACDKOTGRCLKCLYHTEGHCQLCQYGYGDAL 1021  
961 RQCRKVCNVLGTVEKHNGSCHCDKATGQSCCLPNVIGQNCDCRCAPTWQLASGTGC 1020  
1022 RQCRKVCNVLGTVEKHNGSCHCDKATGQSCCLPNVIGQNCDCRCAPTWQLASGTGC 1081  
1021 GPCNCAAHSGFSCNEFTQCQCMFGGRTCEQQLFWGDPVVECRACDCDPRGIFT 1080  
1082 GPCNCAAHSGFSCNEFTQCQCMFGGRTCEQQLFWGDPVVECRACDCDPRGIFT 1141  
1081 PQDQSTGQCVVEGVGPRCDKTRGYSVFPDCTPCHQCFALMDAIIIGELTNTRHKL 1140  
1142 PQDQSTGQCVVEGVGPRCDKTRGYSVFPDCTPCHQCFALMDAIIIGELTNTRHKL 1201  
1141 EKAKALISGVIQYRETVDVSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQV 1200  
1202 EKAKALISGVIQYRETVDVSEKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQV 1261  
1201 EKVAQVEVKLTDTASOSNSTAGELGALQABAEKLTQVXELAEQLEFFIKNSDIQGALDSI 1260  
1262 EKVAQVEVKLTDTASOSNSTAGELGALQABAEKLTQVXELAEQLEFFIKNSDIQGALDSI 1321  
1261 TKYFQMSLEAEKRVNASTTDPNSTVQSAITRDRVEDLMLERESPFKEQEQEARLLDEL 1320  
1322 TKYFQMSLEAEKRVNASTTDPNSTVQSAITRDRVEDLMLERESPFKEQEQEARLLDEL 1381  
1321 AGKLQSLDLGAAQMTCTGTPFGADCSSECGGPNCRITDEGEKCKGCGGGLVVAHSAW 1380  
1382 AGKLQSLDLGAAQMTCTGTPFGADCSSECGGPNCRITDEGEKCKGCGGGLVVAHSAW 1441  
1381 QKAWDFRDLVLAALAEVQLSKMVSSEKVPADAKQNAQDVLKTNATKEKVDKSNEDR 1440  
1442 QKAWDFRDLVLAALAEVQLSKMVSSEKVPADAKQNAQDVLKTNATKEKVDKSNEDR 1501  
1441 NLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQQLQNLITDIREVETLSQVEVIL 1500  
1502 NLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQQLQNLITDIREVETLSQVEVIL 1561  
1501 QQSAADTARAELELLLEAEKASKATDVKTADVMKVALEAEKAAQVAEKAIKQADEDTQ 1560  
1562 QQSAADTARAELELLLEAEKASKATDVKTADVMKVALEAEKAAQVAEKAIKQADEDTQ 1621

QY 1561 GTONLLTSIBSETAASSETLTNASQRTSKLERNVEELKRAAQNGBAEYIEKVYVSVKQ 1620  
Db 1622 GTONLLTSIBSETAASSETLTNASQRTSKLERNVEELKRAAQNGBAEYIEKVYVSVKQ 1691  
QY 1621 NADDVKTKTLDGELDEKVKVESLIAQKTESADARRKAEKLLQNEAKTLLAQANSKLOLLE 1680  
Db 1682 NADDVKTKTLDGELDEKVKVESLIAQKTESADARRKAEKLLQNEAKTLLAQANSKLOLLE 1741  
QY 1691 DLERYEDNQYLEDKQAELVRLGEVRSLLKQISEKVAVYSTCL 1725  
Db 1742 DLERYEDNQYLEDKQAELVRLGEVRSLLKQISEKVAVYSTCL 1786

RESULT 5  
AAB48450  
ID AAB48450 standard; protein; 1786 AA.  
XX  
AC AAB48450;  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX  
OS Mus musculus.  
XX  
PN WO200066732-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX  
PA (BIOS-) BIOTRATUM INC.  
XX  
XX Kortessmaa J, Tryggvason K;  
PI  
XX  
XX WPI; 2000-687539/67.  
DR N-PSDB; AAC83711.  
XX  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX  
PS Claim 5; Page 176-182; 245pp; English.  
XX  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
XX family of heterotrimeric glycoproteins that function via binding  
XX interactions with neighbouring cell receptors and by forming laminin  
XX networks. They are signalling molecules which influence cellular  
XX function. Laminin 8 is useful for treating injuries to tissue of  
XX mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
XX treating injuries to vascular tissue, promoting cell attachment and  
XX migration, ex vivo cell therapy, improving the biocompatibility of  
XX medical devices, and preparing improved cell culture devices and media.  
XX Laminin 8 is also useful for promoting re-endothelialisation at the site  
XX of vascular injuries, improving the take of grafts, improving the  
XX biocompatibility of medical devices, treating neural injuries (neural  
XX regeneration), regulating angiogenesis, and promoting cell attachment and  
XX migration

Sequence 1786 AA;  
Query Match 100.0%; Score 9429; DB 3; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	EPYCIIVSHLQEDKKCFICSDRDPYHETLNPSHLLIENVVTTFAFNRLKIMWQSENGVENV	60
Db	62	EPYCIIVSHLQEDKKCFICSDRDPYHETLNPSHLLIENVVTTFAFNRLKIMWQSENGVENV	121
Qy	61	TIQLDLAEFHTHLIMTFKTPRPAAMLIERSSDPGKTGWYRYPADYDCSSFFGISTGP	120
Db	122	TIQLDLAEFHTHLIMTFKTPRPAAMLIERSSDPGKTGWYRYPADYDCSSFFGISTGP	181
Qy	121	MKKVDDIICDSRYSIEPSTEGEVIFFRALDPAFKIEDPYSRIQNLKITNLRKFKVKLH	180
Db	182	MKKVDDIICDSRYSIEPSTEGEVIFFRALDPAFKIEDPYSRIQNLKITNLRKFKVKLH	241
Qy	181	TLGDNLDSRMEIRKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGWHGCMCR	240
Db	242	TLGDNLDSRMEIRKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGWHGCMCR	301
Qy	241	HNTKGLNCELQMDFYHDLPPWRPAEGRNSNACKNCNEHSSCHDFMAVFLATGNVSGV	300
Db	302	HNTKGLNCELQMDFYHDLPPWRPAEGRNSNACKNCNEHSSCHDFMAVFLATGNVSGV	361
Qy	301	CDNCQHTMGRNCEOCKPPYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	360
Db	362	CDNCQHTMGRNCEOCKPPYFOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	421
Qy	361	IAGQCRCKLVHGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNCPDSETGYCYC	420
Db	422	IAGQCRCKLVHGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGGNCPDSETGYCYC	481
Qy	421	KELVGTQRCDCQLPQHWSLNDLDCRCPDCLGGALANNSCEDSGQCSCLPHMIGRCN	480
Db	482	KELVGTQRCDCQLPQHWSLNDLDCRCPDCLGGALANNSCEDSGQCSCLPHMIGRCN	541
Qy	481	EYVESGYFTLLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGTGFRVPEGAYLEFFI	540
Db	542	EYVESGYFTLLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGTGFRVPEGAYLEFFI	601
Qy	541	DNIPYSMEYELLIRYBPOLPDHWEKAVITVQPPGKIPASSRCGNTVPDDDNQVLSLSPGS	600
Db	602	DNIPYSMEYELLIRYBPOLPDHWEKAVITVQPPGKIPASSRCGNTVPDDDNQVLSLSPGS	661
Qy	601	RYVLPVPVCFEKGMYTVRLLEPQYTAGSDVESPYPFTIDSLVLMPYCKSLDIFTVGS	660
Db	662	RYVLPVPVCFEKGMYTVRLLEPQYTAGSDVESPYPFTIDSLVLMPYCKSLDIFTVGS	721
Qy	661	GDGEVNTSAWETFORVRCLENSRVVKTPTMTDVCNMIIFSIISALIHOTGLACECDPQSL	720
Db	722	GDGEVNTSAWETFORVRCLENSRVVKTPTMTDVCNMIIFSIISALIHOTGLACECDPQSL	781
Qy	721	SSVCDPNGGQCQCRPNVVGRTNCRCAPGTFGPGNGCKPCDCHLOQSASAFCDAITGQCH	780
Db	782	SSVCDPNGGQCQCRPNVVGRTNCRCAPGTFGPGNGCKPCDCHLOQSASAFCDAITGQCH	841
Qy	781	CFQGIYARQCDRLCPYWGFPSCQCCQNGHALDCDVTGECSCDQYTTGHCRCCLAG	840
Db	842	CFQGIYARQCDRLCPYWGFPSCQCCQNGHALDCDVTGECSCDQYTTGHCRCCLAG	901
Qy	841	YIGDPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG	900
Db	902	YIGDPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTTLQACVCDPGYIGSRCDDCASG	961
Qy	901	FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKLYHTEGDHCOLCOYGYGDAL	960
Db	962	FFGNPSDFGSCQPCQCHNIDTTDPEACDKDTGRCLKLYHTEGDHCOLCOYGYGDAL	1021
Qy	961	RQCRKVCNLYGTVEHNGSDCHCDKATGQCSCLPNVIGQNCRCRCPNTWQLASGTGC	1020
Db	1022	RQCRKVCNLYGTVEHNGSDCHCDKATGQCSCLPNVIGQNCRCRCPNTWQLASGTGC	1081
Qy	1021	GPCNCAHAFSGPSCNEFTGQCCQMPFGGRTCSCEQELFWGDDPVECRACDCDPRGIET	1080
Db	1082	GPCNCAHAFSGPSCNEFTGQCCQMPFGGRTCSCEQELFWGDDPVECRACDCDPRGIET	1141

RESULT 6

ABB81592

ID ABB81592 standard; protein; 1786 AA.

XX ABB81592;

AC ABB81592;

DT 19-SEP-2002 (first entry)

XX Mouse laminin 10 second chain protein sequence SEQ ID NO:10.

XX Laminin alpha 5; laminin 10; vulneterary; cell growth; differentiation;  
tissue repair development; laminin; healing; vascular tissue;  
re-endothelialisation; vascular injury; cell attachment; cell stasis;  
proliferation; migration.

OS Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Protein /label= signal

XX /label= laminin\_10\_second\_chain

XX WO200250111-A2.

XX 27-JUN-2002.

XX



PF 21-DEC-2001; 2001WO-US051035.  
 XX 21-DEC-2000; 2000US-02574499.  
 PR 28-MAR-2001; 2001US-0279282P.  
 PR 13-NOV-2001; 2001US-00279282.  
 XX  
 PA (BIOS-) BIOSTRATUM INC.  
 XX  
 XX Trygsvaen K, Doi M, Thyboll J;  
 PI WPI; 2002-557650/59.  
 DR N-PSDB; ABQ72910.  
 XX  
 PT New human laminin-10 proteins, useful for accelerating the healing of  
 PT vascular tissue, improving the biocompatibility of grafts, or for  
 PT promoting re-endothelialization at the site of vascular injuries.  
 XX  
 PS Claim 9; Page 140-145; 231pp; English.  
 XX  
 XX The present invention describes human laminin alpha 5. Also described is  
 CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are  
 CC useful in maintaining cell/tissue phenotype as well as promoting cell  
 CC growth and differentiation in tissue repair development. Specifically,  
 CC laminin 10 can be used for accelerating the healing injuries of vascular  
 CC tissue, improving the biocompatibility of grafts useful for treating such  
 CC injuries, for promoting re-endothelialisation at the site of vascular  
 CC injuries, and promote cell attachment and subsequent cell stasis,  
 CC proliferation, differentiation, and/or migration. The present sequence  
 CC encodes a second chain protein of laminin 10, from the present invention  
 XX  
 XX Sequence 1786 AA;  
 SQ

Query Match 100.08; Score 9429; DB 5; Length 1786;  
 Best Local Similarity 100.08; Pred. No. 0;  
 Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENY 60  
 DB 62 EPYCVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENY 121  
 QY 61 TIQDLEAFHFTLIMFTKTPRAAMLIERSDFGKTGWYRYFAYDCSSPPGISTGP 120  
 DB 122 TIQDLEAFHFTLIMFTKTPRAAMLIERSDFGKTGWYRYFAYDCSSPPGISTGP 181  
 QY 121 MKKVDDIICDSRYSDIEPSTEGEYIFRALDPAPKIEDPYSPRIQNLKITNRIKFKVLH 180  
 DB 182 MKKVDDIICDSRYSDIEPSTEGEYIFRALDPAPKIEDPYSPRIQNLKITNRIKFKVLH 241  
 QY 181 TLGDNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVGVNVEEGVMWHGCMCR 240  
 DB 242 TLGDNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVGVNVEEGVMWHGCMCR 301  
 QY 241 HNTKGLNCELQMDFYHDLPMRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 300  
 DB 302 HNTKGLNCELQMDFYHDLPMRPAEGRNSNACKKNCNEHSSSCHFDMAVFLATGNVSGGV 361  
 QY 301 CNDCHNTWGNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
 DB 362 CNDCHNTWGNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 421  
 QY 361 JAGQCRCKLHVGEGRCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 420  
 DB 422 JAGQCRCKLHVGEGRCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCYC 481  
 QY 421 KELVTGQRCDQCLPOHWGLSNDLQGRPCDDCLGGALNNSCSDSCQCSCLPHMIGRCQN 480  
 DB 482 KELVTGQRCDQCLPOHWGLSNDLQGRPCDDCLGGALNNSCSDSCQCSCLPHMIGRCQN 541  
 QY 481 EVESGYFFTTLDHYIYEAEEANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEPFI 540  
 DB 542 EVESGYFFTTLDHYIYEAEEANLPGVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEPFI 601  
 QY 541 DNI PYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCQNTVPDDDDNQVVSLSPGS 600

DB 602 DNI PYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCQNTVPDDDDNQVVSLSPGS 661  
 QY 601 RYVVLPRPVCFEKGMYTVLELPQYTASGSDVESPVTFIDSLVLMYPYCKSLDIFTVGGS 660  
 DB 662 RYVVLPRPVCFEKGMYTVLELPQYTASGSDVESPVTFIDSLVLMYPYCKSLDIFTVGGS 721  
 QY 661 GDGEVTSAMETFORYLENRSRVSVMTPMDYVCRNIIFISALIHQTGLACSDPQGS 720  
 DB 722 GDGEVTSAMETFORYLENRSRVSVMTPMDYVCRNIIFISALIHQTGLACSDPQGS 781  
 QY 721 SSVCDPNGGQCCRPNVVGRTCNRCAPGTGFGPCKPCDCHLQGSASAFCDATGQCH 780  
 DB 782 SSVCDPNGGQCCRPNVVGRTCNRCAPGTGFGPCKPCDCHLQGSASAFCDATGQCH 841  
 QY 781 CFQGIYARQDRCLPGWHPFSCQPCQCNHALDCTVTGECLSQDQYTTGHNCECLAG 840  
 DB 842 CFQGIYARQDRCLPGWHPFSCQPCQCNHALDCTVTGECLSQDQYTTGHNCECLAG 901  
 QY 841 YYGPIIISGSDHCRPCPCPDGDSGRQFARSQYQDPVTQLQACVCDPGVIGSRCDCCASG 900  
 DB 902 YYGPIIISGSDHCRPCPCPDGDSGRQFARSQYQDPVTQLQACVCDPGVIGSRCDCCASG 961  
 QY 901 FFGNPSDFGSGSQPCQCHNIDTTPDPCADKDTGRCLKCLYHTEGHQCLCOGYGYGDAL 960  
 DB 962 FFGNPSDFGSGSQPCQCHNIDTTPDPCADKDTGRCLKCLYHTEGHQCLCOGYGYGDAL 1021  
 QY 961 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPIWQLASGTGC 1020  
 DB 1022 RQDCRKVCNVLGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPIWQLASGTGC 1081  
 QY 1021 GPCNCAHSGFSGSCHEFTQCCQCMFPGGRTCSCEQELFWGDDPVECRACDDPRGJET 1080  
 DB 1082 GPCNCAHSGFSGSCHEFTQCCQCMFPGGRTCSCEQELFWGDDPVECRACDDPRGJET 1141  
 QY 1081 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVPPDCTPCHQCPCALMDAIIGELTNRTHKFL 1140  
 DB 1142 PQCDQSTGQCVCEGVEGPRCDKTRGYSGVPPDCTPCHQCPCALMDAIIGELTNRTHKFL 1201  
 QY 1141 EKAKALKISGIVGYRETVDSEKKNWEIKDILAQSPAEPKNGILFEEAEKLTQDVT 1200  
 DB 1202 EKAKALKISGIVGYRETVDSEKKNWEIKDILAQSPAEPKNGILFEEAEKLTQDVT 1261  
 QY 1201 EKQAQVEVKLTDTASQSNSTAGELGALQAEASLQKTVKELAEQLEFFIKNSDIQALDSI 1260  
 DB 1262 EKQAQVEVKLTDTASQSNSTAGELGALQAEASLQKTVKELAEQLEFFIKNSDIQALDSI 1321  
 QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLESPPKEQOEQARLLDEL 1320  
 DB 1322 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLESPPKEQOEQARLLDEL 1381  
 QY 1321 AGKLQSLDLASAAQMTCTGTPPGADCSSESCGGPNCRCTDEGEKKCGGPGCGGLVTVHAWS 1380  
 DB 1382 AGKLQSLDLASAAQMTCTGTPPGADCSSESCGGPNCRCTDEGEKKCGGPGCGGLVTVHAWS 1441  
 QY 1381 QKAWDPDRVLSALAEVQLSKMVSEAKYRAEAKQADVLKTNATKVKYDKNEDLR 1440  
 DB 1442 QKAWDPDRVLSALAEVQLSKMVSEAKYRAEAKQADVLKTNATKVKYDKNEDLR 1501  
 QY 1441 NLIKQIRNFLTSDSADLSIEAVANVLKSGNASTPQQLQNTLDIRERVETLSQVEVIL 1500  
 DB 1502 NLIKQIRNFLTSDSADLSIEAVANVLKSGNASTPQQLQNTLDIRERVETLSQVEVIL 1561  
 QY 1501 QQSAADTARAEALLLEAEKASKASATDKVTADMVKEALEEAEKAAVAEKAQKQADEIDQ 1560  
 DB 1562 QQSAADTARAEALLLEAEKASKASATDKVTADMVKEALEEAEKAAVAEKAQKQADEIDQ 1621  
 QY 1561 GTQNLITSIESETAASEETLTNASQRIKLERNVLEKKAQNSGEAFYIEKVVYSVKQ 1620  
 DB 1622 GTQNLITSIESETAASEETLTNASQRIKLERNVLEKKAQNSGEAFYIEKVVYSVKQ 1681  
 QY 1621 NADDVKTKLDELDEKVKVESILIAQKTEESADARKKELLQNEAKTLLAQANSKLQLE 1680

Db 1582 NADDVKTLDGELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLLAQANSKLQLE 1741  
Qy 1681 DLEKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1725  
Db 1742 DLEKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 7  
AAW50894  
ID AAW50894 standard; protein; 1776 AA.  
XX AC AAW50894;  
XX DT 07-DEC-1998 (first entry)  
XX DE Mouse laminin B1 chain.  
XX Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
KW therapy.  
XX Mus sp.  
OS WO9815179-A1.  
XX PN 16-APR-1998.  
XX PD 08-OCT-1997; 97WO-US018145.  
XX PF 08-OCT-1996; 96US-0027981P.  
XX PR (UNTW ) UNIV WASHINGTON.  
XX PA Castillo G, Snow AD;  
XX PI WPI; 1998-240534/21.  
XX DR Use of laminin and fragments - for developing products for use in the  
XX diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
XX CJD.  
XX PS Claim 15; Page 90-93; 132pp; English.  
XX This is the amino acid sequence of the mouse laminin B1 chain. The  
XX primary object of the invention is to use laminin, laminin-derived  
XX protein fragments and/or laminin-derived polypeptides as potent  
XX inhibitors of amyloid formation, deposition, accumulation and/or  
XX persistence in Alzheimer's disease and other amyloidoses. The laminin  
XX products (see AAW50898-99) may include mouse or human laminin A or A1  
XX chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
XX chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
XX binding domain of the laminin A chain. A claimed method for treating an  
XX amyloid disease comprises administering a polypeptide having a  
XX conformational similarity to a fragment of a laminin protein. A method  
XX for diagnosing an amyloid disease involves determining levels of laminin  
XX in a sample. Production of laminin or its fourth globular repeat in vivo  
XX provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
XX products and methods can be used for the diagnosis, prognosis, monitoring  
XX and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
XX and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
XX (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
XX associated with chronic inflammation, various forms of malignancy and  
XX Familial Mediterranean Fever (AA amyloid or inflammation-association  
XX amyloidosis), the amyloidosis associated with multiple myeloma and other  
XX B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
XX II diabetes (amylin or islet amyloid), the amyloidosis associated with  
XX prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler  
XX syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis

CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
CC transthyretin amyloid), and the amyloidosis associated with endocrine  
CC tumours such as medullary carcinoma of the thyroid (variant of  
CC procalcitonin)  
XX  
SQ Sequence 1776 AA;  
Query Match 99.3%; Score 9363; DB 2; Length 1776;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1715; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
Qy 1 EPYCIVSHLOEDKQKFCIDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSEGVENV 60  
Db 62 EPYCIVSHLOEDKQKFCIDSRDPYHETLNPDSHLIENVTTFAPNRLKIWQSEGVENV 121  
Qy 61 TIQDLDEAEFHFTHLIMTEKTFERPAAMLIERSDFKGTWGVYRYFAYDCESFPFGISTGP 120  
Db 122 TIQDLDEAEFHFTHLIMTEKTFERPAAMLIERSDFKGTWGVYRYFAYDCESFPFGISTGP 181  
Qy 121 MKKVDDIIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPSPRIQNLKLTNLRIRKFKVLUH 180  
Db 182 MKKVDDIIICDSRYSDIEPSTEGEVIFFRALDPAFKIEDPSPRIQNLKLTNLRIRKFKVLUH 241  
Qy 181 TLGDNLDSRMEIREKYIYAVYDMVVRGNCFCVGHASECAPVDGVNVEEVGVMVGHCMCR 240  
Db 242 TLGDNLDSRMEIREKYIYAVYDMVVRGNCFCVGHASECAPVDGVNVEEVGVMVGHCMCR 301  
Qy 241 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGV 300  
Db 302 HNTKGLNCELMDFYHDLPRPAEGRNSNACKKCNNEHSSCHFDMAVFLATGNVSGV 361  
Qy 301 CDNCOHNTWGRNCEOCKPFYFQHPREDIRDPNLCEPCTCDPAGESNGGI CDGYTDFSVGL 360  
Db 362 CDNCOHNTWGRNCEOCKPFYFQHPREDIRDPNLCEPCTCDPAGESNGGI CDGYTDFSVGL 421  
Qy 361 IAGQCRCKLHVEGERCDVCKEGFYDLSABDPYCKSCACNPLGTIPGPNPCDSETGYCYC 420  
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSABDPYCKSCACNPLGTIPGPNPCDSETGYCYC 481  
Qy 421 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSDSCSCCLPHMIGRQCN 480  
Db 482 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGGALNNSCSDSCSCCLPHMIGRQCN 541  
Qy 481 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 540  
Db 542 EVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVPEGAYLEFFI 601  
Qy 541 DNIPYSMEYELIRYEPOLPDHWEKAVITVORPGKITPASSRCGNTVPDDNQVVSLSPGS 600  
Db 602 DNIPYSMEYELIRYEPOLPDHWEKAVITVORPGKITPASSRCGNTVPDDNQVVSLSPGS 661  
Qy 601 RYVVLPRPVCFEKGMYTVRLPQVYTAGSDVSPYTFIDSLVLMYPYCKSLDIFTVGG 660  
Db 662 RYVVLPRPVCFEKGMYTVRLPQVYTAGSDVSPYTFIDSLVLMYPYCKSLDIFTVGG 721  
Qy 661 GDGEVNTSAWETFORVRCLENSRVKPTMTDVCNRIIFISALIHQTLGACDCDPOGSL 720  
Db 722 GDGEVNTSAWETFORVRCLENSRVKPTMTDVCNRIIFISALIHQTLGACDCDPOGSL 781  
Qy 721 SSVCDPNNGGOCCEPNVVGRTNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 780  
Db 782 SSVCDPNNGGOCCEPNVVGRTNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 841  
Qy 781 CFQGIYARQCDRCLPGYWGFPSPQPCQCNHGLDCDVTGTECLSCDQYTTGHCNRCCLAG 840  
Db 842 CFQGIYARQCDRCLPGYWGFPSPQPCQCNHGLDCDVTGTECLSCDQYTTGHCNRCCLAG 901  
Qy 841 YGDPPIIGSGDHCKPCPCPPGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
Db 902 YGDPPIIGSGDHCKPCPCPPGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 961

QY 901 FFGNPSDFGSGCQPCOCHHNIITDTPACDKDTGTRCLKLYHTEDGHQCLQOQVGYGDAL 960  
 Db 962 FFGNPSDFGSGCQPCOCHHNIITDTPACDKDTGTRCLKLYHTEDGHQCLQOQVGYGDAL 1021  
 QY 961 RODCRKVCNLYGTVEKHGNSDCHDKATGQCSCLPNVIGONCDRCAPNTWOLASGTGC 1020  
 Db 1022 RODCRKVCNLYGTVEKHGNSDCHDKATGQCSCLPNVIGONCDRCAPNTWOLASGTGC 1081  
 QY 1021 GPCNCNAHSPGSPSNEFTGQCCQMPFGGRTSCQELFWGDPDVECRACDCDPRGIET 1080  
 Db 1082 GPCNCNAHSPGSPSNEFTGQCCQMPFGGRTSCQELFWGDPDVECRACDCDPRGIET 1141  
 QY 1081 POCDOSTGQCVGVGEGPRCDKTRGYSGVFPDCTPCHQCQFALWDALIGELTNTHKFL 1140  
 Db 1142 POCDOSTGQCVGVGEGPRCDKTRGYSGVFPDCTPCHQCQFALWDALIGELTNTHKFL 1201  
 QY 1141 ERKALKISGVIGPYRETVDVSEKKNVIEIKDILAQSPAAEPLKNGILFEEAEKLTQDVT 1200  
 Db 1202 ERKALKISGVIGPYRETVDVSEKKNVIEIKDILAQSPAAEPLKNGILFEEAEKLTQDVT 1261  
 QY 1201 ERKAOVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGLDSI 1260  
 Db 1262 ERKAOVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQGLDSI 1321  
 QY 1261 TRYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQOEQARLLDEL 1320  
 Db 1322 TRYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQOEQARLLDEL 1381  
 QY 1321 AGKLQSLDLSAAQWTCGTPPGADCSSECGGNCRTDGEKKCGGCGGLVTVASAW 1380  
 Db 1382 AGKLQSLDLSAAQWTCGTPPGADCSSECGGNCRTDGEKKCGGCGGLVTVASAW 1441  
 QY 1381 QXAMPDRDVLGALAEVQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440  
 Db 1442 QXAMPDRDVLGALAEVQLSKWVSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501  
 QY 1441 NLIKQIRNFLTSDADLSIEAVANVLKSGNASTPQOLNLTEDIRVETISQVEVIL 1500  
 Db 1502 NLIKQIRNFLTSDADLSIEAVANVLKSGNASTPQOLNLTEDIRVETISQVEVIL 1561  
 QY 1501 QQSAADIAPAEALLBEAKRASKSATDVKVTADMKVKEALEEAKQAQVAEAKIAQOEDIQ 1560  
 Db 1562 QQSAADIAPAEALLBEAKRASKSATDVKVTADMKVKEALEEAKQAQVAEAKIAQOEDIQ 1621  
 QY 1561 GTQNLLTSTESATASEETLTNASORISKLEARNVEELKRAQNSGAEVIEKVVYSVKQ 1620  
 Db 1622 GTQNLLTSTESATASEETLTNASORISKLEARNVEELKRAQNSGAEVIEKVVYSVK- 1680  
 QY 1621 NADDVKTLTGELDEKYYKVESLIAQKTESADARRKAELQNEAKTLAQANSKLQLE 1680  
 Db 1681 ---DVKKTLDGELDEKYYKVESLIAQKTESADARRKAELQNEAKTLAQANSKLQLE 1737  
 QY 1681 DLERYEDNOKYLEDKAQELVRLEGEVRSILKDISEKVA 1719  
 Db 1738 DLERYEDNOKYLEDKAQELVRLEGEVRSILKDISEKVA 1776

## RESULT 8

AAP91672

ID AAP91672 standard; protein; 1764 AA.

AC AAP91672;

XX

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 29-JUN-1990 (first entry)

XX

DE

XX Primary amino acid sequence of B1 chain of laminin.

KW

KW Laminin B1 chain fragment; heparin; prosthetic devices;

KW cell culture substrates; cell adhesion promoter; nerve regeneration;

KW wound healing; implant acceptance; cell attachment; metastasis inhibitor.

XX

OS Mus musculus.  
 OS Synthetic.  
 PH Key  
 FT Peptide  
 FT Peptide  
 FT Peptide  
 XX Location/Qualifiers  
 PN 641..860  
 XX /note= "designated F9"  
 XX 1171..1188  
 XX /note= "designated F13"  
 XX WO8901493-A.  
 PD 23-FEB-1989.  
 XX 87US-00087157.  
 PF 19-AUG-1987;  
 XX 87US-00087157.  
 PR 19-AUG-1987;  
 XX (MINU ) MINNESOTA UNIVERSITY.  
 PA Charonis A, Furcht LT;  
 XX WPI; 1989-068855/09.  
 XX New laminin B1 chain polypeptide(s) - for promoting heparin binding and cell adhesion.  
 PS Disclosure; Page ?; 42pp; English.  
 CC The new polypeptides have an amino acid sequence corresp. to a laminin B1 chain fragment having specific binding capacity for heparin. Specifically mentioned are the two polypeptides F9 and F13 (see FT). The polypeptides may be used to promote binding of heparin to synthetic substrates and promote cell adhesion, eg endothelial, melanoma, fibrosarcoma, glioma and pheochromocytoma cells. They may be useful for assisting nerve regeneration, promoting wound healing, implant acceptance, cell attachment to culture substrates and inhibiting metastasis of malignant cells. They may be pred. by conventional Merrifield solid-phase synthesis. Also claimed are prosthetic devices and cell culture substrates coated with the new polypeptides. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)  
 SQ Sequence 1764 AA;

Query Match 98.78; Score 9307.5; DB 1; Length 1764;  
 Seat Local Similarity 99.08; Pred. No. 0;  
 Matches 1707; Conservative 4; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 EPYCIIVSHLOEDKCKFCICDSRDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENV 60  
 Db 41 EPYCIIVSHLOEDKCKFCICDSRDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENV 100  
 QY 61 TIQLDLAEAFHFTLIMTFKTERPAAMLIERSSDFGKTGWVRYPAYDCSESPFGISTGP 120  
 Db 101 TIQLDLAEAFHFTLIMTFKTERPAAMLIERSSDFGKTGWVRYPAYDCSESPFGISTGP 160  
 QY 121 MKYVDDIICDSRYSDIEPSTEGEVI FRALDPAPFKIEDPYSRIQNLKITNRIKFKVLH 180  
 Db 161 MKYVDDIICDSRYSDIEPSTEGEVI FRALDPAPFKIEDPYSRIQNLKITNRIKFKVLH 220  
 QY 181 TLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNVEEYGVHGHCMCR 240  
 Db 221 TLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNVEEYGVHGHCMCR 280  
 QY 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNHEHSSSCHFDMAVFLATGNVSGGV 300  
 Db 281 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNHEHSSSCHFDMAVFLATGNVSGGV 340  
 QY 301 CDNCQHNMTGRNCEQKPFYFQHPERDIDRPNLCEPCTCDPAGSENGGICDGYTTPSVGL 360  
 Db 341 CDNCQHNMTGRNCEQKPFYFQHPERDIDRPNLCEPCTCDPAGSENGGICDGYTTPSVGL 400  
 QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSABDPYCKSKACNPLGTTPGNGNFCDSBTGYCYC 420

401	Db	IAQCRCKLHVBERCDVCKBGFDTLSABDPYCKGKSCACNPLGTPPGNCPDSESYCYC	460
421	Qy	KRLVTGORCDQLCPQHWGLSNDLDCRCPDCDLGGALNNCSBEDSQCSCLPHMIGRCN	480
461	Db	KRLVTGORCDQLCPQHWGLSNDLDCRCPDCDLGGALNNCSBEDSQCSCLPHMIGRCN	520
481	Qy	EVBESHYFTTLHYIYEAEANLPGVVVERQYIQDRIPSWTGCFVAVPBGAYLEPFI	540
521	Db	EVBESHYFTTLHYIYEAEANLPGVVVERQYIQDRIPSWTGCFVAVPBGAYLEPFI	580
541	Qy	DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCCNTVPDDDNQVSSLSPGS	600
581	Db	DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCCNTVPDDDNQVSSLSPGS	640
601	Qy	RYVVLPRPVCFKGMNYTVRLELPQYTAGSDVESPYTFIDSILVLMPYCKSLDIFVTGGS	660
641	Db	RYVVLPRPVCFKGMNYTVRLELPQYTAGSDVESPYTFIDSILVLMPYCKSLDIFVTGGS	700
661	Qy	GDGEVNSAWETFORVRCLENSSVKVTMTDVCRNIIIFSIISALIHOTGLACECDPQGSIL	720
701	Db	GDGEVNSAWETFORVRCLENSSVKVTMTDVCRNIIIFSIISALIHOTGLACECDPQGSIL	760
721	Qy	SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFPGFNGCKPCDCHLOGSASAFCDAITGQCH	780
761	Db	SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFPGFNGCKPCDCHLOGSASAFCDAITGQCH	820
781	Qy	CFOGIYARQCDRCLPGYWGFPSPCQPCOCHNGHALDCDVTGECILSCDYTGHCNCRCLAG	840
821	Db	CFOGIYARQCDRCLPGYWGFPSPCQPCOCHNGHALDCDVTGECILSCDYTGHCNCRCLAG	880
841	Qy	YGDPIIGSDGHRPCPCPDGPDGSRGFARSCYQDPVTQLACVCDPGYIGSRCDPCASG	900
881	Db	YGDPIIGSDGHRPCPCPDGPDGSRGFARSCYQDPVTQLACVCDPGYIGSRCDPCASG	940
901	Qy	FFGNPSDFGSGCQPCQCHNIDTTDPEACDKOTGRCLKLYHTGEGHCOLCOGYGYGDAL	960
941	Db	FFGNPSDFGSGCQPCQCHNIDTTDPEACDKOTGRCLKLYHTGEGHCOLCOGYGYGDAL	1000
961	Qy	RQDCRKVCVNYLGTIVKEHNGSDCHCDKATGCQSCLPNVIGQNCDCAPNTWLASGTGC	1020
1001	Db	RQDCRKVCVNYLGTIVKEHNGSDCHCDKATGCQSCLPNVIGQNCDCAPNTWLASGTGC	1060
1021	Qy	GPCNCAAHFPGSPCNFTGCQCMPPGFGRTGTCSECOELFWGDDVECRACDCCPRGIET	1080
1061	Db	GPCNCAAHFPGSPCNFTGCQCMPPGFGRTGTCSECOELFWGDDVECRACDCCPRGIET	1120
1081	Qy	PQCDQSTGCQCVBGGVGBRCDKCTRGYSGVFPDPCTPCHOCFALWDAIIGELNTRTHKFL	1140
1121	Db	PQCDQSTGCQCVBGGVGBRCDKCTRGYSGVFPDPCTPCHOCFALWDAIIGELNTRTHKFL	1180
1141	Qy	EKAKALISGIVGIPRYRTVDSVERKVNIEKDIIAQSPPAAPLKNIGILFBEAEKLTQDVT	1200
1181	Db	EKAKALISGIVGIPRYRTVDSVERKVNIEKDIIAQSPPAAPLKNIGILFBEAEKLTQDVT	1240
1201	Qy	EKMAQVEVKLTDTTASQNSTAGELGALQAEASLSDTKVLAEOLEFIKNSDTCGALDSI	1260
1241	Db	EKMAQVEVKLTDTTASQNGHAGELGALQAEASLSDTKVLAEOLEFIKNSDTCGALDSI	1300
1261	Qy	TKYFOMSLAEKRVNASTTDPNSVTEQSALTDRVEDLMLERSPFKEQEEQEARLLDEL	1320
1301	Db	TKYFOMSLAEKRVNASTTDPNSVTEQSALTDRVEDLMLERSPFKEQEEQEARLLDEL	1360
1321	Qy	AGKLOSLDLASAAQMTGTPPGADCSSECCGPNCRDTDEBKCGGPGCGGLVTVHAWS	1380
1361	Db	AGKLOSLDLASAAQMTGTPPGADCSSECCGPNCRDTDEBKCGGPGCGGLVTVHAWS	1420
1381	Qy	QKAMDPRFDVLSALAEVEQLSKVWSEAKVRADEAKQNAQVLLKTNATKVKDKSNEDLR	1440
1421	Db	QKAMDPRFDVLSALAEVEQLSKVWSEAKVRADEAKQNAQVLLKTNATKVKDKSNEDLR	1480
1441	Qy	NLIKQIRNFLTEDSADLDSIEBAVANEVLKSNASTPOOLQNLITDIERVETLISQVEVIL	1500
1481	Db	NLIKQIRNFLTEDSADLDSIEBAVANEVLKSNASTPOOLQNLITDIERVETLISQVEVIL	1540

QY	1501	QOQAADIAAEALLLEAEKPKASATDVKVTADMVKEALEEAEKAKQAAAEKAIKQADEDIQ	1560
Db	1541	QOQAADIAAEALLLEAEKPKASATDVKVTADMVKEALEEAEKAKQAAAEKAIKQADEDIQ	1600
QY	1561	GTQNLLTSIETSETPAASEETLTNASORISIKLERNVVELKPKAAQNSGEABYIEKVVYSVKQ	1620
Db	1601	GTQNLLTSIETSETPAASEETLTNASORISIKLERNVVELKPKAAQNSGEABYIEKVVYSVKQ	1660
QY	1621	NADVVKTLTGELDEKVKVKSLLIAQKTESADARKKAEELLQNEAKTLLAQANSKIQELLE	1680
Db	1661	NADVVKTLTGELD-KYKVKVESLLIAQKTESADARKKAEELLQNEAKTLLAQANSKIQELLE	1719
QY	1681	DLERKYEDNQKYLEDKAQLVRLGEVRSLLDKISEKVAIVYSTCL	1725
Db	1720	DLERKYEDNQKYLEDKAQLVRLGEVRSLLDKISEKVAIVYSTCL	1764
RESULT 9			
AA	19798	standard; protein; 1765 AA.	
XX	AA	19798;	
AC	AA	19798;	
XX	XX	05-MAR-2001 (first entry)	
DT	DT	Human laminin 2 mature beta-1 chain.	
DE	DE	Human laminin 2 mature beta-1 chain.	
XX	XX	Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;	
KW	KW	degenerative muscle disorder; muscular dystrophy; cell therapy.	
XX	XX	Homo sapiens.	
OS	OS	WO2000066730-A2.	
XX	XX	09-NOV-2000.	
PD	PD	28-APR-2000; 2000WO-US011378.	
XX	XX	30-APR-1999; 99US-0131720P.	
PR	PR	15-JUN-1999; 99US-0139198P.	
PR	PR	12-JUL-1999; 99US-0143289P.	
PR	PR	24-SEP-1999; 99US-0155945P.	
XX	XX	(UNVE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.	
PA	PA	Yurchenco P;	
FI	FI	WPI; 2000-687537/67.	
DR	DR	N-PSDB; AAA88898.	
XX	XX	Purified laminin 2 protein, useful for research and therapeutic purposes	
PT	PT	including peripheral nerve regeneration, treatment of degenerative muscle	
PT	PT	disorders, angiogenesis regulation, and ex vivo cell therapy.	
XX	XX	Claim 5; Page 199-204; 305pp; English.	
XX	XX	The present sequence is that of the human laminin 2 beta-1 chain mature	
CC	CC	protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and	
CC	CC	gamma-1 (100 kDa) chains. It is thought to be specifically required for	
CC	CC	stabilizing myotubes during skeletal muscle development, and for	
CC	CC	preventing apoptosis. Genetic defects in its structure or expression are	
CC	CC	associated with a major type of congenital muscular dystrophy. Laminin 2	
CC	CC	is also thought to be important in Schwann cell/basal lamina	
CC	CC	interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-	
CC	CC	1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding	
CC	CC	them (see AAA8891-906), methods for making recombinant laminin 2, cells	
CC	CC	that express recombinant laminin 2, and methods for using purified	
CC	CC	laminin 2 for research and therapeutic purposes including peripheral	
CC	CC	nerve regeneration, treatment of degenerative muscle disorders,	
CC	CC	angiogenesis regulation, promoting cell attachment and migration, ex vivo	
CC	CC	cell therapy, improving the take of grafts, improving the	
CC	CC	biocompatibility of medical devices and preparing improved culture	

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CC devices and media
XX Query Match 94.1%; Score 8873; DB 3; Length 1765;
SQ Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCVISHLOEDKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 60
DB 41 EPYCVISHLOEDKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 100
QY 61 TIQDLLEABFPHLTHLIMTKTPPAAMLIERSSDFGKTWGVYRYFAYDCESFPGISGTP 120
DB 101 TIQDLLEABFPHLTHLIMTKTPPAAMLIERSSDFGKTWGVYRYFAYDCESFPGISGTP 160
QY 121 MKKVDDIICDSRYSDDIEPSTEGEVIIFRALDPAFKIEDPYSRIQNLKLTNRIKFKVLH 180
DB 161 MKKVDDIICDSRYSDDIEPSTEGEVIIFRALDPAFKIEDPYSRIQNLKLTNRIKFKVLH 220
QY 181 TLGDNLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNNEEVEGMVHGCMCR 240
DB 221 TLGDNLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNNEEVEGMVHGCMCR 280
QY 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNCEHSSCHFDMAVFLATGNVSGGV 300
DB 281 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNCEHSSCHFDMAVFLATGNVSGGV 340
QY 301 CDNCQHTWGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
DB 341 CDNCQHTWGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 400
QY 361 IAGQCRKLVHGERCDVCKEGBYDLSAEDPYGCKSCACNPLGTPPGNCPDSEYGYCYC 420
DB 401 IAGQCRKLVHGERCDVCKEGBYDLSAEDPYGCKSCACNPLGTPPGNCPDSEYGYCYC 460
QY 421 KRLVTGRCDCQCLPQHWGLSNDLDGRCPCDCLGGALNNSCEDSGQCSCLPHMIGROCN 480
DB 461 KRLVTGRCDCQCLPQHWGLSNDLDGRCPCDCLGGALNNSCEDSGQCSCLPHMIGROCN 520
QY 481 EVESGYFTTLDHYIEAEFANLPGVGVVVERQYIQDRIPSWTGTGFVRVPSGAYLEPFI 540
DB 521 EVESGYFTTLDHYIEAEFANLPGVGVVVERQYIQDRIPSWTGTGFVRVPSGAYLEPFI 580
QY 541 DNIPIYSNEYILLIRYEPOLPDHWEKAVITVORPGKIPASSRCQNTVPDDNQNVSLSPGS 600
DB 581 DNIPIYSNEYILLIRYEPOLPDHWEKAVITVORPGKIPASSRCQNTVPDDNQNVSLSPGS 640
QY 601 RYVVLPRPVCFEKGMNTYVLELFPQYTAGSDYVESPYTFIDSLVLMYPYCKSLDIFTVGGS 660
DB 641 RYVVLPRPVCFEKGMNTYVLELFPQYTAGSDYVESPYTFIDSLVLMYPYCKSLDIFTVGGS 700
QY 661 GDGEVTVNSAWETTORVRCLENSRVKTPMTDYCRNIIIFSIISALIHOTGLACECDPQGS 720
DB 701 GDGEVTVNSAWETTORVRCLENSRVKTPMTDYCRNIIIFSIISALIHOTGLACECDPQGS 760
QY 721 SSVCDPNGGQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITGQCH 780
DB 761 SSVCDPNGGQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSVNAFCNPTVGTQCH 820
QY 781 CFQGIYARQCDRLCPGYWGFPPSCQPCQCNCHALDCTVTGECUSQDQYTTGHCNCRCLAG 840
DB 821 CFQGIYARQCDRLCPGYWGFPPSCQPCQCNCHALDCTVTGECUSQDQYTTGHCNCRCLAG 880
QY 841 YGDPPIIGSDGHCPCPCPGPSGRGFARSSCYQDPVTIQLACVCDPVGIGSRCDPCASG 900
DB 881 YGDPPIIGSDGHCPCPCPGPSGRGFARSSCYQDPVTIQLACVCDPVGIGSRCDPCASG 940
QY 901 FFGNPSDFGSCQPCQCHNIDTTPDPAKDKOTGRCLKLYHTEGHCQLCQGYGQDAL 960
DB 941 YFGNPSDFGSCQPCQCHNIDTTPDPAKDKOTGRCLKLYHTEGHCQLCQGYGQDAL 1000
QY 961 RQDCRKVCVNYLGTVEHCHGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWTWLAGSGTGC 1020
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DB 1001 RQDCRKVCVNYLGTVEHCHGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWTWLAGSGTGC 1060
QY 1021 GPCNCAAHSGFSGSCNEFTGQCCOMPFGGRTCSQEQLFWGDPDVECRACDCDPRGIET 1080
DB 1061 DPCNCAAHSGFSGSCNEFTGQCCOMPFGGRTCSQEQLFWGDPDVECRACDCDPRGIET 1120
QY 1081 PQCDQSTGQCVGVGVEGPRCDKTRGYSGVFPDCTPCHQCFALMDAIIGELNTRTHKFL 1140
DB 1121 PQCDQSTGQCVGVGVEGPRCDKTRGYSGVFPDCTPCHQCFALMDAIIGELNTRTHKFL 1180
QY 1141 EKAKALKISGIVGYRETVDSVEKKNEIKDIIAQSPAAPAEPLKNIIGLFEAEKLTQDVT 1200
DB 1181 EKAKALKISGIVGYRETVDSVEKKNEIKDIIAQSPAAPAEPLKNIIGLFEAEKLTQDVT 1240
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQABAEASLDKTVKELAEQLPFIKNSDIQALDSI 1260
DB 1241 EKMAQVEVKLTDTASQSNSTAGELGALQABAEASLDKTVKELAEQLPFIKNSDIQALDSI 1300
QY 1261 TKTFQMSLEAEKRVNASTTDPNSTVEQSALTTRORVEDMLERESPKEQOEEOEARLLDEL 1320
DB 1301 TKTFQMSLEAEKRVNASTTDPNSTVEQSALTTRORVEDMLERESPKEQOEEOEARLLDEL 1360
QY 1321 AGKLOSLDLGAAAOQTCGTPPGADCSSECGGPNCRDEGEKCGPGGCGGLVTVAHSAW 1380
DB 1361 AGKLOSLDLGAAAOQTCGTPPGADCSSECGGPNCRDEGEKCGPGGCGGLVTVAHSAW 1420
QY 1381 QKAMDFRDVLSALAEVEQLSKMVSEAKVRADAKQNAQDVLLKTNATKEKVDKSNEDLR 1440
DB 1421 QKAMDFRDVLSALAEVEQLSKMVSEAKVRADAKQNAQDVLLKTNATKEKVDKSNEDLR 1480
QY 1441 NLIQKIRNEFTEDSADLDSIEAVANEVLKSGNASTPOQLQNLTERIRERVELTISOVEVIL 1500
DB 1481 NLIQKIRNEFTEDSADLDSIEAVANEVLKSGNASTPOQLQNLTERIRERVELTISOVEVIL 1540
QY 1501 QQSAAADARAEELLLEAEAKRASKSATDVKTADVMVKALEAEAEKAAQVAAEKAIQOADEDIQ 1560
DB 1541 QQSAAADARAEELLLEAEAKRASKSATDVKTADVMVKALEAEAEKAAQVAAEKAIQOADEDIQ 1600
QY 1561 GTQNLTSISEETAASSETLTNASORISKLERNVVELKRAAQNCSGEAEYIEKVVTYSVKQ 1620
DB 1601 GTQNLTSISEETAASSETLTNASORISKLERNVVELKRAAQNCSGEAEYIEKVVTYSVKQ 1660
QY 1621 NADDVKTLDELDEKYEKVESLIAQKTESADARRKAEKALLQNEAKTLLAQANSKLQLE 1680
DB 1661 NADDVKTLDELDEKYEKVESLIAQKTESADARRKAEKALLQNEAKTLLAQANSKLQLE 1720
QY 1681 DLERKYEDNQYLEDKAEQELVRLEGEVRSLLKDISKQVAVYSTCL 1725
DB 1721 DLERKYEDNQYLEDKAEQELVRLEGEVRSLLKDISKQVAVYSTCL 1765
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## RESULT 10

AAB48449

ID AAB48449 standard; protein: 1765 AA.

XX AAB48449;

XX AC AAB48449;

XX DT 02-MAR-2001 (first entry)

XX XX Human laminin 8 polypeptide, SEQ ID NO: 16.

XX XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
XX XX antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
XX XX vascular tissue injury; neural injury; angiogenesis regulation.

OS Homo sapiens.

XX WO200066732-A2.

XX PD 09-NOV-2000.

XX XX 28-APR-2000; 2000WO-US011543.

XX 30-APR-1999; , 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
PI N-PSDB; AAC83710.  
XX WPI; 2000-687539/67.  
DR N-PSDB; AAC83710.  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 163-168; 245pp; English.  
PS The present sequence is a laminin 8 polypeptide chain. Laminins are a  
XX family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
XX migration  
XX Sequence 1765 AA;  
Query Match 94.1%; Score 8873; DB 3; Length 1765;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;  
QY 1 EPYCVSHLQEDKKCFICSDRDPYHETLNPDSLHLENNVTTAPNRLKIWQSENGVENV 60  
DB 41 EPYCVSHLQEDKKCFICNSQDPYHETLNPDSLHLENNVTTAPNRLKIWQSENGVENV 100  
QY 61 TTQLDEAFHFHLLIMTKTRPAAMLIERSDFGKWTGVYRAYDCESFPFGISTGP 120  
DB 101 TTQLDEAFHFHLLIMTKTRPAAMLIERSDFGKWTGVYRAYDCESFPFGISTGP 160  
QY 121 MKKVDDIIICDSRYSDIEPSTEGEVIIPALDPFAKIEDPYSPIQNLKITNLRIFVKLH 180  
DB 161 MKKVDDIIICDSRYSDIEPSTEGEVIIPALDPFAKIEDPYSPIQNLKITNLRIFVKLH 220  
QY 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGHWCHMCWR 240  
DB 221 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGHWCHMCWR 280  
QY 241 HNTKGLNCELMDFYHDLPRPAGRNSNACKKCNKNEHSSCHFDMAYFLATGNVSGV 300  
DB 281 HNTKGLNCELMDFYHDLPRPAGRNSNACKKCNKNEHSSCHFDMAYFLATGNVSGV 340  
QY 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTFVSGL 360  
DB 341 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 400  
QY 361 IAGCCCKLHVEGERCDVCKEGFYDLASADPYGCKSCACNPLGTIPGGNPDSETGYCYC 420  
DB 401 IAGCCCKLHVEGERCDVCKEGFYDLUSSDPFGCKSCACNPLGTIPGGNPDSETGYCHYC 460  
QY 421 KRLVTGRCQDQCILPQHWGLNSNDLGGCRPCDCLGGALNNSCSBDSQCCSCLPHMIGRQCN 480  
DB 461 KRLVTGRCQDQCILPQHWGLNSNDLGGCRPCDCLGGALNNSCPAESQCCSCLPHMIGRQCN 520  
QY 481 EVESGYFTTLDHYIYEAEANLPGVVVVERQYIQDIRIPSWTGTGPFVRVPEGAYLEFFI 540

DB 521 EPEPGYVFATLDHYLYEAEANLPGVSVISVERQYIQDIRIPSWTGTGPFVRVPEGAYLEFFI 580  
QY 541 DNIPYSMEYELLIRYEPQLPDHWEKAVITVQRGKIPASSRCQNTVPDDDNQVVSLSPGS 600  
DB 581 DNIPYSMEYDILIRYEPQLPDHWEKAVITVQRGKIPASSRCQNTVPDDDNQVVSLSPGS 640  
QY 601 RYVVLPRPVCFEKGMNYTVRLELPQYTAGSDSVESPYTFIDSLVLMYPYCKSLDIFTVGGS 660  
DB 641 RYVVLPRPVCFEKGMNYTVRLELPQYTAGSDSVESPYTFIDSLVLMYPYCKSLDIFTVGGS 700  
QY 661 GDGEVNTSAWETFORVRCLENSSVVKTDMTDCVCRNIIFSISALIHOTGLACEDPQGL 720  
DB 701 GDGVNTNSAWETFORVRCLENSSVVKTDMTDCVCRNIIFSISALLHQTGLACEDPQGL 760  
QY 721 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSASAFDAITGQCH 780  
DB 761 SSVCDPNGGQCQCRPNVVGRTCNRCAPGTFGFGNGCKPCDCHLQGSVNAFCNPVTGQCH 820  
QY 781 CFIGIYARQCDRCCLPGWGPSPQCCQNGHALDCTVTGCECLSCODYTGHNCERCLAG 840  
DB 821 CFIGIYARQCDRCCLPGWGPSPQCCQNGHALDCTVTGCECLSCODYTGHNCERCLAG 880  
QY 841 YGDPPIIGSDHCRPCPCPDGPGSGRQPARSCYQDPVTQLACVCDPVGIGSRCDDCASG 900  
DB 881 YGDPPIIGSDHCRPCPCPDGPGSGRQPARSCYQDPVTQLACVCDPVGIGSRCDDCASG 940  
QY 901 FFGNPSDFGSCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGHQCLQCYVYGDAL 960  
DB 941 YFGNPSDFGSCQPCQCHNIDITDPEACDKTGRCLKCLYHTEGHQCFRGYVYGDAL 1000  
QY 961 RQCRKVCNLYGTVEHNGNSDCHDKATGQCSCLPNVIGQNCDCRCAPNWOLASGTGC 1020  
DB 1001 RQCRKVCNLYGTVEHNGNSDCHDKATGQCSCLPNVIGQNCDCRCAPNWOLASGTGC 1060  
QY 1021 GPCNCAHNSFGPSCNEFTQCCQCMFPGGRTTCEQELFWGDPDVECRACDCCDPRIET 1080  
DB 1061 GPCNCAHNSFGPSCNEFTQCCQCMFPGGRTTCEQELFWGDPDVECRACDCCDPRIET 1120  
QY 1081 PQDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTCHOCFALWDAIIGELTNRHFKPL 1140  
DB 1121 PQDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTCHOCFALWDAIIGELTNRHFKPL 1180  
QY 1141 EKAKALISGVIQPYRTVDSEVKVNEIKDILAQSPAAPAEPLKNIIGILPEAEKLTQDVT 1200  
DB 1181 EKAKALISGVIQPYRTVDSEVKVNEIKDILAQSPAAPAEPLKNIIGILPEAEKLTQDVT 1240  
QY 1201 EKMAQVVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLBEIKNSDIQGLDLSI 1260  
DB 1241 EMMAQVVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLBEIKNSDIQGLDLSI 1300  
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRORVEDLMLERESPFKEQEQEQLLDEL 1320  
DB 1301 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRORVEDLMLERESPFKEQEQEQLLDEL 1360  
QY 1321 AGKLQSLDLGAAQMTCTGTPFGADCSSECGGNCRDTDEGKKGCGGPGCGGLVTVVAHSAW 1380  
DB 1361 AGKLQSLDLGAAQMTCTGTPFGADCSSECGGNCRDTDEGKKGCGGPGCGGLVTVVAHSAW 1420  
QY 1381 QKANDFQDVLALAEVQLSKVSEAKVRADAKQNAQDVLKTNATKVKDKSNECLR 1440  
DB 1421 QKANDFQDVLALAEVQLSKVSEAKVRADAKQNAQDVLKTNATKVKDKSNECLR 1480  
QY 1441 NLIKQIRNFLETDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRREVETISQVEVIL 1500  
DB 1481 NLIKQIRNFLETDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRREVETISQVEVIL 1540  
QY 1501 QOSAADTARAEILLIEAKRASKATDVKTADVMVKEALEAEAKQAAAEKAIKQADEIDQ 1560  
DB 1541 QOSAADTARAEILLIEAKRASKATDVKTADVMVKEALEAEAKQAAAEKAIKQADEIDQ 1600  
QY 1561 QTONLLTSISETAASBETLTNASQRISKLERNVVELKRAAQNSGAEVIEKVVYSVKQ 1620

Db 1601 GTQNLTSIESETAASEETLPNASORISELERNVEELKKAQNSGEAEYIEKVVTWKQ 1660  
 QY 1621 NADDVAKTLDGELDEKYKVESLIQKTEESADARRKAEELLQNEAKTLLAQAQSKLOLLE 1680  
 Db 1661 SAEDVAKTLDGELDEKYKVENLIQKTEESADARRKAEMLQNEAKTLLAQAQSKUQLK 1720  
 QY 1681 DLKRYEDNQKLEDKAQLVLEGEVRSLLKDISEKVAVYSTCL 1725  
 Db 1721 DLKRYEDNQRYLEDKAQLARLEGEVRSLLKDISQKAVYSTCL 1765

RESULT 11  
 ABB81591  
 ID ABB81591 standard; protein; 1765 AA.  
 XX ABB81591;  
 AC ABB81591;  
 XX 19-SEP-2002 (first entry)  
 DT Human laminin 10 second chain protein sequence SEQ ID NO:8.  
 XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
 KW tissue repair development; laminin; healing; vascular tissue;  
 KW re-endothelialisation; laminin injury; cell attachment; cell stasis;  
 KW proliferation; migration.  
 XX Homo sapiens.  
 OS  
 XX WO2002050111-A2.  
 PN 27-JUN-2002.  
 XX 21-DEC-2001; 2001WO-US051035.  
 XX 21-DEC-2000; 2000US-0257449P.  
 PR 28-MAR-2001; 2001US-0279282P.  
 PR 13-NOV-2001; 2001US-00279282.  
 XX (BIO-) BIOSTRATUM INC.  
 XX  
 XX Trygvaason K, Doi M, Thyboll J;  
 XX WPI; 2002-557650/59.  
 DR N-PSDB; ABQ72909.  
 XX  
 XX New human laminin-10 proteins, useful for accelerating the healing of  
 PT vascular tissue, improving the biocompatibility of grafts, or for  
 PT promoting re-endothelialization at the site of vascular injuries.  
 XX  
 XX Claim 9; Page 126-132; 231pp; English.  
 XX  
 XX The present invention describes human laminin alpha 5. Also described is  
 CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
 CC useful in maintaining cell/tissue phenotype as well as promoting cell  
 CC growth and differentiation in tissue repair development. Specifically,  
 CC laminin 10 can be used for accelerating the healing injuries of vascular  
 CC tissue, improving the biocompatibility of grafts useful for treating such  
 CC injuries, for promoting re-endothelialisation at the site of vascular  
 CC injuries, and promote cell attachment and subsequent cell stasis,  
 CC proliferation, differentiation, and/or migration. The present sequence  
 CC represents a second chain protein of laminin 10, from the present  
 CC invention  
 XX  
 XX Sequence 1765 AA;  
 SQ

Query Match 94.1%; Score 8873; DB 5; Length 1765;  
 Best Local Similarity 92.9%; Pred. No. 0;  
 Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EBYCVSHLOEDKCKFCIDSDPHETLNPDSHLIENVTTFAPNRLKIWQSENGVY 60  
 Db 41 EBYCVSHLOEDKCKFCIDSDPHETLNPDSHLIENVTTFAPNRLKIWQSENGVY 100

QY 61 TIQLDLBAEFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCESSEPGISTGP 120  
 Db 101 TIQLDLBAEFHFTLIMTFKTRPAAMLIERSSDFGKTGWVRYFAYDCESSEPGISTGP 160  
 QY 121 MKVDVDDICDSRYSDIEPSTEVEVI FRALDPAFKIEDPSPRIQNLKLTNLRAIKFKVLH 180  
 Db 161 MKVDVDDICDSRYSDIEPSTEVEVI FRALDPAFKIEDPSPRIQNLKLTNLRAIKFKVLH 220  
 QY 181 TLGDNLDSRMEIREKYVYVDMVVRGNCFCYGHASECAPVDGVNEVEVGMVHGCMCR 240  
 Db 221 TLGDNLDSRMEIREKYVYVDMVVRGNCFCYGHASECAPVDGVNEVEVGMVHGCMCR 280  
 QY 241 HNTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGGV 300  
 Db 281 HNTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNNEHSSSCHDFMAVFLATGNVSGGV 340  
 QY 301 CDNCOHTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGL 360  
 Db 341 CDNCOHTMGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGL 400  
 QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420  
 Db 401 IAGQCRCKLHVEGERCDVCKEGFYDLAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 460  
 QY 421 KELVTGQRCDQCLPQHWGLSNLDLDCRPFCDCLGGALNNSCSBDSGCSCLPHMIGRQCN 480  
 Db 461 KELVTGQRCDQCLPQHWGLSNLDLDCRPFCDCLGGALNNSCSBDSGCSCLPHMIGRQCN 520  
 QY 481 EYSGYIFTTLDHYIYEAEBANLPGVYVVERQYIQDRIPSWTGPVVRPEGAYLEPTI 540  
 Db 521 EYSGYIFTTLDHYIYEAEBANLPGVYVVERQYIQDRIPSWTGPVVRPEGAYLEPTI 580  
 QY 541 DNIPIYSMEYELIRYEPQLPDHWEKAVITVQRPGKITPASSRCGNTVPDDDNQVVSLSPGS 600  
 Db 581 DNIPIYSMEYELIRYEPQLPDHWEKAVITVQRPGKITPASSRCGNTVPDDDNQVVSLSPGS 640  
 QY 601 RYVVLPRPVCEKGMNTVRLLEIPOYTASGSDVESYPTFIDSLVLMYPYCKSLDIFTVGGS 660  
 Db 641 RYVVLPRPVCEKGMNTVRLLEIPOYTASGSDVESYPTFIDSLVLMYPYCKSLDIFTVGGS 700  
 QY 661 GDGEVTSAMETFORVRCLENSRSVVKTPMTDTCRNIIFISALIHQTGLACECDPQGS 720  
 Db 701 GDGEVTSAMETFORVRCLENSRSVVKTPMTDTCRNIIFISALIHQTGLACECDPQGS 760  
 QY 721 SSVCDPNGGQOCHPNVVGRTNRCAPGTGFGPNCKCDCHLQGSASFDAITGQCH 780  
 Db 761 SSVCDPNGGQOCHPNVVGRTNRCAPGTGFGPNCKCDCHLQGSASFDAITGQCH 820  
 QY 781 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCDVTGECCLSCODYTTHNCERCLAG 840  
 Db 821 CFQGIYARQCDRCLPGYWGFPSCQPCQCNHGLDCDVTGECCLSCODYTTHNCERCLAG 880  
 QY 841 YGDPFIISGDHCHPCPCPGPDSGRQFARSCYQDPVTLQACVCPGVIGSRCDCCAG 900  
 Db 881 YGDPFIISGDHCHPCPCPGPDSGRQFARSCYQDPVTLQACVCPGVIGSRCDCCAG 940  
 QY 901 FFGNPSFGSGSCQPCQCHNIDITDPEACDKOTGRCLKLYHTEGDHCHLQCYGYGDA 960  
 Db 941 YFGNPSFGSGSCQPCQCHNIDITDPEACDKOTGRCLKLYHTEGDHCHLQCYGYGDA 1000  
 QY 961 RQDCKVCNLYGTVXEHCHNGSDCHDKATGQSCCLPNVIGQNCDCRCAENTWOLASGTC 1020  
 Db 1001 RQDCKVCNLYGTVXEHCHNGSDCHDKATGQSCCLPNVIGQNCDCRCAENTWOLASGTC 1060  
 QY 1021 GPCNCAAHSGFSGSCNEFTQCCQCMFPGGRTCSCEQLFWGDPDVECRACDPRGIET 1080  
 Db 1061 GPCNCAAHSGFSGSCNEFTQCCQCMFPGGRTCSCEQLFWGDPDVECRACDPRGIET 1120  
 QY 1081 PQDQOSTGQCVGVEGVEGPECDKCTRGYSVGPEDCTCPCHQCFALNDALITETNTHKPL 1140  
 Db 1121 PQDQOSTGQCVGVEGVEGPECDKCTRGYSVGPEDCTCPCHQCFALNDALITETNTHKPL 1180  
 QY 1141 EKAKALXISGIVGYRETVDVSVEKKVNEIKDILAOQSPAAEPLKNTGILPEAEKUTKDV 1200



Db 1181 EKAALKLSGIVGPIRETVDSEVRKVEIKDILAQSPAAPLKNIGNLFEEAEKLIKDV 1240  
Qy 1201 EKMAQVEVLTDTASQSNSTAGELGALQAEBSLDTXWELAEOLBFIKNSDIOGALDSI 1260  
Db 1241 EMMAQVEVLTSDTTSQSNSTAKELDSLQTEAESLDTNFKELAEOLBFIKNSDINGALDSI 1300  
Qy 1261 TKYFQMSLEAEKRVNASTTDFNSVTQESALPDRVEDLMLERESFPFKQOQBEQARLDEL 1320  
Db 1301 TKYFQMSLEAEKRVNASTTDFNSVTQESALPDRVEDLMLERESFPFKQOQBEQARLDEL 1360  
Qy 1321 AGKLQSLDLASAAQMTCTPPGACDSESECGGPNCRIDEGKKCGGPGCGGLVTVVAHSAW 1380  
Db 1361 AGKLQSLDLASAAQMTCTPPGACDSESECGGPNCRIDEGKKCGGPGCGGLVTVVAHSAW 1420  
Qy 1381 QKAMPDFDVLASAEVQLSKWSEAKVRADEAKQADVLLKTNATKEKVDKNSDLR 1440  
Db 1421 QKAMPDFDVLASAEVQLSKWSEAKVRADEAKQADVLLKTNATKEKVDKNSDLR 1480  
Qy 1441 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTDIERVETLSQVEVIL 1500  
Db 1481 NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTDIERVETLSQVEVIL 1540  
Qy 1501 QSAADIARAELLBEAEKASATDVKVTADWKEALEAEKQVAAEKAKQADESDIQ 1560  
Db 1541 QSAADIARAELLBEAEKASATDVKVTADWKEALEAEKQVAAEKAKQADESDIQ 1600  
Qy 1561 GTQNLLTSESSTAASEETLNASORISKLERNVEELKRAKQNSGEAEYIEKVYVYVKQ 1620  
Db 1601 GTQNLLTSESSTAASEETLNASORISKLERNVEELKRAKQNSGEAEYIEKVYVYVKQ 1660  
Qy 1621 NADDVKKTLDBELDKYKVESLIAQKTESADARRKAEILLQNEAKTLLAQAANSKLQILLE 1680  
Db 1661 SAEDVKKTLDBELDKYKVESLIAQKTESADARRKAEILLQNEAKTLLAQAANSKLQILLE 1720  
Qy 1681 DLERYEDNOKYLEDAQELVRLGEVRSLLKDISEKVAVYSTCL 1725  
Db 1721 DLERYEDNOKYLEDAQELVRLGEVRSLLKDISEKVAVYSTCL 1765

RESULT 12

AAW50893  
ID AAW50893 standard; protein; 1786 AA.  
XX  
AC AAW50893;  
XX  
DT 07-DEC-1998 (first entry)  
DE Human laminin B1 chain.  
XX Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9815179-A1.  
PN  
PD 16-APR-1998.  
XX  
PF 08-OCT-1997; 97WO-US018145.  
XX  
PR 08-OCT-1996; 96US-0027981P.  
XX  
PA (UNIV ) UNIV WASHINGTON.  
XX Castillo G, Snow AD;  
PX

WPI; 1998-240534/21.  
XX Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CUD.  
XX  
PS Claim 15; Page 86-89; 132pp; English.

XX This is the amino acid sequence of the human laminin B1 chain. The  
CC primary object of the invention is to use laminin, laminin-derived  
CC protein fragments and/or laminin-derived polypeptides as potent  
CC inhibitors of amyloid formation, deposition, accumulation and/or  
CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
CC products (see AAW50898-98) may include mouse or human laminin A or A1  
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
CC binding domain of the laminin A chain. A claimed method for treating an  
CC amyloid disease comprises administering a polypeptide having a  
CC conformational similarity to a fragment of a laminin protein. A method  
CC for diagnosing an amyloid disease involves determining levels of laminin  
CC in a sample. Production of laminin or its fourth globular repeat in vivo  
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
CC products and methods can be used for the diagnosis, prognosis, monitoring  
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
CC associated with chronic inflammation, various forms of malignancy and  
CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
CC prion diseases including Creutzfeldt-Jacob disease, Gertsmann-Straussler  
CC syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis  
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
CC transthyretin amyloid), and the amyloidosis associated with endocrine  
CC tumours such as medullary carcinoma of the thyroid (variant of  
CC procalcitonin)

Sequence 1786 AA;

Query Match 94.1%; Score 8873; DB 2; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;  
Qy 1 EPYCIIVSHLOEDKKCFICDSRDPYHETLAPDPSHLIENVTTPAPNRLKIWQSENGVENV 60  
Db 62 EPYCIIVSHLOEDKKCFICNSQDPYHETLAPDPSHLIENVTTPAPNRLKIWQSENGVENV 121  
Qy 61 TIQLDLEAEFPHFTHLIMTFKTPAPAMLIERSDFDKTGWVRYFYAYDCESSPPGISTGP 120  
Db 122 TIQLDLEAEFPHFTHLIMTFKTPAPAMLIERSDFDKTGWVRYFYAYDCESSPPGISTGP 181  
Qy 121 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAPKIEDPYSRIONLKITNLRIKFKVLH 180  
Db 182 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAPKIEDPYSRIONLKITNLRIKFKVLH 241  
Qy 181 TLGNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVEGVHGHCMCR 240  
Db 242 TLGNLLDSRMEIREKYVYAVYDMVVRGNCFCYGHASECAPVDGVNVEEVEGVHGHCMCR 301  
Qy 241 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSSCHFDMAVFLATNGVSGGV 300  
Db 302 HNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSSCHFDMAVFLATNGVSGGV 361  
Qy 301 CDNCQHTNMGENCECKPFVFOHPERDIRDPNLCEBCTCDPAGSENGGICDGYTDFSVGL 360  
Db 362 CDNCQHTNMGENCECKPFVFOHPERDIRDPNLCEBCTCDPAGSENGGICDGYTDFSVGL 421  
Qy 361 IAGQCCKLHVEGERCDVCKEGFYDLASDPYCKSCACNPLGTIPGNGPCDSETCYCYC 420  
Db 422 IAGQCCKLHVEGERCDVCKEGFYDLASDPYCKSCACNPLGTIPGNGPCDSETCYCYC 481

QY	421	KRLVTGORCQCLPQHWGLSNDLDGCRPCDCDILGGALNNSCSDSQCSCLPMHIGRCQN	480
DB	482	KRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCDILGGALNNSCFABSGQCSCRPHMIGRCQN	541
QY	481	EVSQGYFTTLDHYIYEAEANLPGVVVVERQYIQDIRIPSWTGPQFVRVPEGAYLEFFI	540
DB	542	EVSPGYIYFATLDHYIYEAEANLPGVSVIYERQYIQDIRIPSWTGAQFVRVPEGAYLEFFI	601
QY	541	DNIPYSMEYILIRYEPQLPDHWEKAVITYORPGKIPASSRCQNTVPDDDNQVVSLSPGS	600
DB	602	DNIPYSMEYDILIRYEPQLPDHWEKAVITYORPGRIPTSSRCQNTIPDDDNQVVSLSPGS	661
QY	601	RYVVLPRPVCFEKGMYTVLELPOYNTASGSDVESPYTFIDSILVLMYPYCKSLDIFTVGGS	660
DB	662	RYVVLPRPVCFEKGNTVTVLELPOYNTSSSDSDVESPYTLLDSILVLMYPYCKSLDIFTVGGS	721
QY	661	GDGEVNTNSAWETFORYFCLNSRSVVKTPMTDVCVCRNIIFISALIIHQTLGACSDCPQGS	720
DB	722	GDGVVNTNSAWETFORYFCLNSRSVVKTPMTDVCVCRNIIFISALLHQTLGACSDCPQGS	781
QY	721	SSVCDPNGGQCCRPNVVGRVTCNRCAPTGTFGPGNGCKPCDCHLQSGASAFCDATIGQCH	780
DB	782	SSVCDPNGGQCCRPNVVGRVTCNRCAPTGTFGPGSGCKPCECHLQSVNAFCNPVTIGQCH	841
QY	781	CFQGIYARQCDRCLUPGYWGFPSQPCQCNCGHALDLDIVTGECLSCDQYTTGHNCERCLAG	840
DB	842	CFQGVYARQCDRCLUPGHWFPSQPCQCNCGHADDQDPVTGECLNCQDQYTWGHNCRCLAG	901
QY	841	YYGDP11GSGDHCRPCPCPDGSDGRQFARSQYDQPVTLQACVCDPGYIGSRCDCCASG	900
DB	902	YYGDP11GSGDHCRPCPCPDGSDGRQFARSQYDQPVTLQACVCDPGYIGSRCDCCASG	961
QY	901	FFGNPSDFGSGCQPCQCHNIDTTDPBACDKDGTGRCLKCLYHTEGDHCLQCYGYVGDAL	960
DB	962	YFGNPSEVGGSCQPCQCHNIDTTDPBACDKETGRCLKCLYHTEGEHCQCFRGYGYGDAL	1021
QY	961	RQDCRKVCNVLTGVTKBCHNGSDCHCKATQGCSCPLNVIQONCDRCAPNTWQLASGTC	1020
DB	1022	RQDCRKVCNVLTGVQBCHNGSDCQCKATQGCCLCLFNVIQONCDRCAPNTWQLASGTC	1081
QY	1021	GPCNCAHSPGSCNFTGQCCQNPFGGRTGSECQELFWGDDVCECRACDQCPRGIE	1080
DB	1082	DPCNCAHSPGSCNFTGQCCQNPFGGRTGSECQELFWGDPDVECRACDQCPRGIE	1141
QY	1081	PQCDQSTGQCVGVGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDIAIIGELNTRTHKFL	1140
DB	1142	PQCDQSTGQCVGVGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIAELNTRTHRFL	1201
QY	1141	EKAKALKISGVIGYRFTVDSVEKKNVEIKDILAQSPAAEPKNIGILFEEAKLTKDVT	1200
DB	1202	EKAKALKISGVIGYRFTVDSVERKVSEIKDILAQSPAAEPKNIGILFEEAKLTKDVT	1261
QY	1201	EKMAQVEKLTDTTASQNSTAGELGALQABAESLDKTVKELAEQLEIFKNSDIQGALDSI	1260
DB	1262	EMMAQVEKLTSDTTQSNSSTAKELDSLSQTEAESLDNTVKELAEQLEIFKNSDIRGALDSI	1321
QY	1361	TKYFQMSLEABKRVNASTDTPNSVTVEQSALTRDRVEDLMLERESPFFKEQEEQEARLLDEL	1320
DB	1322	TKYFQMSLEABERVNASTTEPNSTVEQSALMRDVEDVMMERESQFKEQEEQEARLLDEL	1381
QY	1321	AGKLQSLDLSAAAOVTCGTPPGADCISSECCGPNCRCTDEGEKKGCGPGCGGLVTVAHSAW	1380
DB	1382	AGKLQSLDLSAAAEVTCGTPPGASCSETECCGPNCRCTDEGEKKGCGPGCGGLVTVAHNAW	1441
QY	1391	QKAMDFDRDVLALAEVBOLSKWYSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDLR	1440
DB	1442	QKAMDLQDQVLALAEVBOLSKWYSEAKLRADEAKQSAEDILLTKTNATKEKMDKSNELR	1501
QY	1441	NLIKQIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL	1500
DB	1502	NLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTEDIRERVETLSQVEVIL	1561

Qy	1501	QQSAAIDIAREILLERAKKASKATDVKVTADWVKALEREAKQAQVAEKAIKQADEDIQ	1556
Db	1562	QHSAAIDIAREMLLEAKKASKATDVKVTADWVKALEREAKQAQVAEKAIKQADEDIQ	1621
Qy	1561	GTQNLLTSTSEETAAGSEETLTNTASQRISKLERVVELKKAQNSGEAEYIEKVVYSVKQ	1620
Db	1622	GTQNLLTSTSEETAAGSEETLTFNASQRISSELRVVELKKAQNSGEAEYIEKVVYSVKQ	1681
Qy	1621	NADVVKTLDELDEKVKKVESLIAOKTSESADARRKAEALLQNEAKTLAQANSKLQLE	1680
Db	1682	SAEDVKTLDELDEKVKKVENLIAKTTESADARRKAEALLQNEAKTLAQANSKLQLLK	1741
Qy	1681	DLERKVEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVVAYYSTCL	1725
Db	1742	DLERKVEDNQRYLEDKAQELARLEGEVRSLLKDISEKVVAYYSTCL	1786
RESULT 32			
AAB16522			
ID	AA16522	standard; protein; 1786 AA.	
XX	XX		
AC	AC	AAB16522;	
XX	XX		
DT	DT	27-OCT-2000 (first entry)	
XX	XX		
DE	DE	Human laminin protein sequence.	
XX	XX		
KW	KW	Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;	
KW	KW	endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;	
KW	KW	psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;	
KW	KW	cerebral collateral; arteriovenous malformation; rubecosis; cancer;	
KW	KW	diabetic retinopathy; arthritis; wound healing; peptic ulcer;	
KW	KW	Helicobacter related disease; fracture; cat scratch fever.	
OS	OS	Hom sapiens.	
XX	XX		
FN	FN	WO2000032631-A2.	
PD	PD	08-JUN-2000.	
PF	PF	06-DEC-1999; 99WO-US028897.	
XX	XX		
PR	PR	04-DEC-1998; 98US-00206059.	
XX	XX		
PA	PA	(ENTR-) ENTREMED INC.	
FI	FI	Macdonald NJ, Sim KL;	
XX	XX		
DR	DR	WPI; 2000-412290/35.	
XX	XX		
PT	PT	New angiogenesis-inhibiting protein receptors, useful in methods for	
PT	PT	treating diseases and processes that are mediated by angiogenesis, such	
PT	PT	as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.	
XX	XX		
PS	PS	Claim 1; Fig 6A; 100pp; English.	
XX	XX		
CC	CC	This invention relates to angiogenesis-inhibiting protein receptors, and	
CC	CC	the DNA sequences encoding them. Angiogenesis is the generation of new	
CC	CC	blood vessels into a tissue, and normally occurs in wound healing, foetal	
CC	CC	and embryonal development and the formation of the corpus luteum,	
CC	CC	endometrium and placenta. Angiostatin is a protein (see AAB16450 and	
CC	CC	AA168202) involved in angiogenesis, and has an amino acid sequence	
CC	CC	similar to that of a plasminogen fragment (see murine plasminogen	
CC	CC	AA16490). Angiostatin has the ability to inhibit angiogenesis.	
CC	CC	Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and	
CC	CC	AA168203). Sequences AAA68242 and AAB16522 represent coding and protein	
CC	CC	sequences of human laminin. Laminin is an angiostatin binding protein,	
CC	CC	and some of the peptides of the invention share homology with regions of	
CC	CC	laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the	
CC	CC	angiogenesis-inhibiting protein receptor fragments of the invention. The	
CC	CC	peptides bind either angiostatin or endostatin and can be used in methods	
CC	CC	for treating diseases and processes that are mediated by angiogenesis,	
CC	CC	such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis,	

CC	Crohn's disease, cerebral collaterals, arteriovenous malformations, rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers, Helicobacter related diseases, fractures, placentaion and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628241 encode the peptides of the invention	XX
SQ	Sequence 1786 AA;	
Query Match	94.1%; Score 8873; DB 3; Length 1786;	
Best Local Similarity	92.9%; Pred. No. 0;	
Matches 1602; Conservative	71; Mismatches 52; Indels 0; Gaps 0;	
QY	1 EYCVIVSHQEDKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60	
DB	62 EYCVIVSHQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 121	
QY	61 TIQLDLAEAFHFTLIMTKTPRPAAMLIERSDFGKTGWVRYFAYDCEASFPGISTGP 120	
DB	122 TIQLDLAEAFHFTLIMTKTPRPAAMLIERSDFGKTGWVRYFAYDCEASFPGISTGP 181	
QY	121 MKKVDIIICDSRYSDIEPSTEGEVIIPRALDPAPKIEDPYSPRIQNLKILNRIKFKVLH 180	
DB	182 MKKVDIIICDSRYSDIEPSTEGEVIIPRALDPAPKIEDPYSPRIQNLKILNRIKFKVLH 241	
QY	181 TLGDNLDSRMEIREKYYAVVDMVVRGNCFCVGHASECAPVDGVNEEVGVHGHCMCR 240	
DB	242 TLGDNLDSRMEIREKYYAVVDMVVRGNCFCVGHASECAPVDGVNEEVGVHGHCMCR 301	
QY	241 HNTKGLNLCMDFYHDLFWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGVNSGV 300	
DB	302 HNTKGLNLCMDFYHDLFWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGVNSGV 361	
QY	301 CONCHNTWGRCEOCKPYFQHPERDIEDPNLCPECTCDPAGSENGGICDGYTDFSVGL 360	
DB	362 CDDCHNTWGRCEOCKPYFQHPERDIEDPNLCPECTCDPAGSENGGICDGYTDFSVGL 421	
QY	361 IAGQCRCKLHVEGERCDVCKEGDYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 420	
DB	422 IAGQCRCKLHVEGERCDVCKEGDYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYC 481	
QY	421 KRLVTQORCDQCLPQHWGLSNDLDGRCPCDCLGGALNNSCEDSGOCSCLPHMTGROCN 480	
DB	482 KRLVTQCHCDQCLPQHWGLSNDLDGRCPCDCLGGALNNSCEDSGOCSCLPHMTGROCN 541	
QY	481 EYSGYVFTLTHYIYEAEANLPGVWVVRQYIQDRIPSWTGTFVRVPEGAYLEPFI 540	
DB	542 EYSGYVFTLTHYIYEAEANLPGVWVVRQYIQDRIPSWTGTFVRVPEGAYLEPFI 601	
QY	541 DNTPYMEYELLIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVDDDNQVSLSPGS 600	
DB	602 DNTPYMEYELLIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTVDDDNQVSLSPGS 661	
QY	601 RYVVLPRPVCFKGMVYVLELPQYTAGSDVESPYTFIDSLVLMPCSKLDIFTVGS 660	
DB	662 RYVVLPRPVCFKGMVYVLELPQYTAGSDVESPYTFIDSLVLMPCSKLDIFTVGS 721	
QY	661 GDGEVINSAWETFORYRCLNENSSVVKTPMTDVCNRIIFPSIALIHQTGLACECPQGS 720	
DB	722 GDGEVINSAWETFORYRCLNENSSVVKTPMTDVCNRIIFPSIALIHQTGLACECPQGS 781	
QY	721 SSVCDNNGGQCCRPNVWGTCNRCAPGTFGFGNCKPCDCHLQSSASAFCDATIGQCH 780	
DB	782 SSVCDNNGGQCCRPNVWGTCNRCAPGTFGFGNCKPCDCHLQSSASAFCDATIGQCH 841	
QY	781 CFQGIYARQCDRLPLGWGFPSCQPCQCNHGLDCTVTGECLSQDQYTTGNHCERCLAG 840	
DB	842 CFQGIYARQCDRLPLGWGFPSCQPCQCNHGLDCTVTGECLSQDQYTTGNHCERCLAG 901	
QY	841 YGDPPIIGSDHCRPCPCDGPDSGFQFARSQYQDPVTQLQACVCPGVIYGRCDCCAG 900	
DB	902 YGDPPIIGSDHCRPCPCDGPDSGFQFARSQYQDPVTQLQACVCPGVIYGRCDCCAG 961	
QY	901 FFGNPSDFGSGSCQPCQCHNIDITDPEACDKDTGRCLKLYHTEGHDHCLQCYGYGDAL 960	

Db	962 YFGNPSEVGSSCQPCQCHNIDITDPEACDKDTGRCLKLYHTEGHDHCLQCYGYGDAL 1021	
QY	961 RQCRKVCVNYLGTVKEHCHNGSDCHDKATQGCSCLPNVIGQNCDCAPNTWOLASGTGC 1020	
DB	1022 RQCRKVCVNYLGTVKEHCHNGSDCHDKATQGCSCLPNVIGQNCDCAPNTWOLASGTGC 1081	
QY	1021 GPCNCAHNSFGPSCNEFTQCQCOCMPGFGERTCEQELFWGDPDVECRACDCDPRGIET 1080	
DB	1082 DPCNCAHNSFGPSCNEFTQCQCOCMPGFGERTCEQELFWGDPDVECRACDCDPRGIET 1141	
QY	1081 PQCDQSTGQCVCVGVGVGPRCDKCTRIGYGVFPDCTPCHQCFCALWDALIGELNTRTHKFL 1140	
DB	1142 PQCDQSTGQCVCVGVGVGPRCDKCTRIGYGVFPDCTPCHQCFCALWDALIGELNTRTHKFL 1201	
QY	1141 EKAKALKISGVIQPYRBTVDSEKKNKNEIKDIIIAQSPAAEPKNIIGLFEAEKLTQDVT 1200	
DB	1202 EKAKALKISGVIQPYRBTVDSEKKNKNEIKDIIIAQSPAAEPKNIIGLFEAEKLTQDVT 1261	
QY	1201 EKMAQVEVLTDTASQSNSTAGELGALQAEASISLDTKVELARQLEFIKNSDIQGALDSI 1260	
DB	1262 EKMAQVEVLTDTASQSNSTAGELGALQAEASISLDTKVELARQLEFIKNSDIQGALDSI 1321	
QY	1261 TKYFQMSLEAEKRVNASTTDPNSTVPOSALTRDRVEDLMLESPPKEQOEEOARLLDEL 1320	
DB	1322 TKYFQMSLEAEKRVNASTTDPNSTVPOSALTRDRVEDLMLESPPKEQOEEOARLLDEL 1381	
QY	1321 AGKLSLDLSAAQMTCTGTPPGADCSBEGCGNCRCTDEGEKCGGPGCGGLVTVAHSAW 1380	
DB	1382 AGKLSLDLSAAQMTCTGTPPGADCSBEGCGNCRCTDEGEKCGGPGCGGLVTVAHSAW 1441	
QY	1381 QKAMDFDRDVLALAEVEQLSKMVSEAKVRADSEAKQNAQDVLKTNATKVKDKSNEDLR 1440	
DB	1442 QKAMDFDRDVLALAEVEQLSKMVSEAKVRADSEAKQNAQDVLKTNATKVKDKSNEELR 1501	
QY	1441 NLIQIENFLTESADLDSIEAVANVILKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1500	
DB	1502 NLIQIENFLTESADLDSIEAVANVILKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1561	
QY	1501 QQSAADIAAEELILEAEKASKSATDVKVTADVMVKEALEAEKAKQAQAEKAIQADEDIQ 1560	
DB	1562 QQSAADIAAEELILEAEKASKSATDVKVTADVMVKEALEAEKAKQAQAEKAIQADEDIQ 1621	
QY	1561 GTQNLITSISETHAASETLTNASQISKLERNVEELKRAAONSGEAEVIEKVVYTVKQ 1620	
DB	1622 GTQNLITSISETHAASETLTNASQISKLERNVEELKRAAONSGEAEVIEKVVYTVKQ 1681	
QY	1621 NADVKTKTLDGELDEKVKVKSLEIAQKTESADARRKAEELIQNEAKTLAQANSKLQLE 1680	
DB	1682 SAEDVKTKTLDGELDEKVKVKSLEIAQKTESADARRKAEELIQNEAKTLAQANSKLQLE 1741	
QY	1681 DLERYEDNQYLEDKAEQELVRLEGEVRSLLKDISEKAVYSTCL 1725	
DB	1742 DLERYEDNQYLEDKAEQELVRLEGEVRSLLKDISEKAVYSTCL 1786	
RESULT 14		
AAB19797	standard; protein; 1786 AA.	
ID	AAB19797	
XX	AC	AAB19797;
XX	AC	AAB19797;
XX	DT	05-MAR-2001 (first entry)
XX	XX	Human laminin 2 beta-1 chain.
DE	XX	Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;
XX	KW	degenerative muscle disorder; muscular dystrophy; cell therapy.
XX	OS	Hom sapiens.
XX	XX	Key
XX	XX	Location/Qualifiers
XX	XX	1. .21
XX	XX	Peptide

FT	Protein	/label= Signal_peptide 22..1786 /label= Mature_protein
FX	WO2000066730-A2.	
XX		
XX	09-NOV-2000.	
PD		
PP	28-APR-2000; 200OWO-US011378.	
PF		
PR	30-APR-1999; 99US-0131720P.	
PR	15-JUN-1999; 99US-0139138P.	
PR	12-JUL-1999; 99US-0143289P.	
PR	24-SEP-1999; 99US-0155945P.	
XX		
PA	(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.	
PI	Yurchenco P;	
XX		
XX	WPI; 2000-687537/67.	
DR	N-PSDB; AAA88897.	
XX		
PT	Purified laminin 2 protein, useful for research and therapeutic purposes	
PT	including peripheral nerve regeneration, treatment of degenerative muscle	
PT	disorders, angiogenesis regulation, and ex vivo cell therapy.	
XX		
PS	Claim 5; Page 186-191; 305pp; English.	
XX		
CC	The present sequence is that of the beta-1 chain of human laminin 2.	
CC	Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1	
CC	(100 kDa) chains. It is thought to be specifically required for	
CC	stabilizing myotubes during skeletal muscle development, and for	
CC	preventing apoptosis. Genetic defects in its structure or expression are	
CC	associated with a major type of congenital muscular dystrophy. Laminin 2	
CC	is also thought to be important in Schwann cell/basal lamina	
CC	interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-	
CC	1 chain polypeptides (see AAB:9791-806) and the polynucleotides encoding	
CC	them (see AAB:9891-906), methods for making recombinant laminin 2, cells	
CC	that express recombinant laminin 2, and methods for using purified	
CC	laminin 2 for research and therapeutic purposes including peripheral	
CC	nerve regeneration, treatment of degenerative muscle disorders,	
CC	angiogenesis regulation, promoting cell attachment and migration, ex vivo	
CC	cell therapy, improving the take of grafts, improving the	
CC	biocompatibility of medical devices and preparing improved culture	
CC	devices and media	
XX		
SQ	Sequence 1786 AA;	
	Query Match 94.1%; Score 8873; DB 3; Length 1786;	
	Best Local Similarity 92.9%; Pred. No. 0;	
	Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0	
Qy	1 EPCYVSHLOEKKFCICDSRDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 60	
Db	62 EPCYVSHLOEKKFCICDSRDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 121	
Qy	61 TIQLDLEAFHFTHLIMTFKTPRPAAMLIERSSPFGKTGWYRYFAYDCSSPFGISTGP 120	
Db	122 TIQLDLEAFHFTHLIMTFKTPRPAAMLIERSSPFGKTGWYRYFAYDCSSPFGISTGP 181	
Qy	121 MKKVDDIIICDSYSDIEPSTEGEVFRALDPAFKLIEPSPRIQNLKIITNLRIKFKVLH 180	
Db	182 MKKVDDIIICDSYSDIEPSTEGEVFRALDPAFKLIEPSPRIQNLKIITNLRIKFKVLH 241	
Qy	181 TLGNLLDRMEIREKYVAVYDMVVRGNCFCYGHASECAPDGVGNEVEGVHGHCMCR 240	
Db	242 TLGNLLDRMEIREKYVAVYDMVVRGNCFCYGHASECAPDGVGNEVEGVHGHCMCR 300	
Qy	241 HNTKGLNCELCMDFYHDLRPAEGRNSNAKCKNCNCHSHSSCHFDNAVFLATGNVSGGV 300	
Db	302 HNTKGLNCELCMDFYHDLRPAEGRNSNAKCKNCNCHSHSISCHFDNAVFLATGNVSGGV 361	
Qy	301 CDMCNHTWGRNCFCKPFFVFOHPRDIRDPNLICPTCTCDPAGSENGGICDGYTDFSVGL 360	

Db 1442 QKAMDLDQDVLASAEVEQLSKMVSEAKLRADEAKQSAEDILKTNATKEMDKSNEBLR 1501  
QY 1441 NLKQIRNFETSDADLDSIEAVANVLYKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1500  
Db 1502 NLKQIRNFUTQSDADLDSIEAVANVLYKXEMESTPQOLQNLTEDIRERVESLSQVEVIL 1561  
QY 1501 QQSAADTARAEILLLEAKRASKSATDVKTADVMVKEALEBAEAKQAAEKAIAQADEDIQ 1560  
Db 1562 QHSAADTARAEMLLEAKRASKSATDVKTADVMVKEALEBAEAKQAAEKAIAQADEDIQ 1621  
QY 1561 GTQNLITSIESETAASETITNASORISKLERNVEELKRAQNSGEAEYIEKVYVSVKQ 1620  
Db 1622 GTQNLITSIESETAASETIFNASCRISLERNVEELKRAQNSGEAEYIEKVYTVKQ 1681  
QY 1621 NADVVKTKDGLDEKDYKVKVESLIAQKTESADARRKAELOLQNEAKTLLAQANSKLQLE 1680  
Db 1682 SAEDVVKTKDGLDEKDYKVKVENLIAKTESADARRKAELOLQNEAKTLLAQANSKLQLLK 1741  
QY 1681 DLERKYEDNQYLEDKQAEQVRLGEVRSLLKDISEKVAVYSTCL 1725  
Db 1742 DLERKYEDNQYLEDKQAEQVRLGEVRSLLKDISQKVAVYSTCL 1786

RESULT 15  
AAB48448  
ID AAB48448 standard; protein; 1786 AA.

XX AAB48448;  
XX 02-MAR-2001 (first entry)  
XX Human laminin 8 polypeptide, SEQ ID NO: 14.  
XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX Homo sapiens.

OS WO2000066732-A2.  
FN 09-NOV-2000.  
PD 28-APR-2000; 2000WO-US011543.  
PF 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
PI WPI; 2000-587539/67.  
XX N-PSDB; AAC83709.  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 150-155; 245pp; English.

XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site

CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration  
XX Sequence 1786 AA;  
SQ Query Match 94.1%; Score 8873; DB 3; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;  
QY 1 EYCVIVSHLOBDKKCFICDSRDPVHETLNPDSHLEIENVVTFAPNRLKIWNQSENGVENV 60  
Db 62 EYCVIVSHLOBDKKCFICNSQDPYHETLNPDSHLEIENVVTFAPNRLKIWNQSENGVENV 121  
QY 61 TTLDLEAEFFTHLIMTFKFRPAAMLIERSSPGKTGWVRYFAYDCESSFPQISTGP 120  
Db 122 TTLDLEAEFFTHLIMTFKFRPAAMLIERSSPGKTGWVRYFAYDCESSFPQISTGP 181  
QY 121 MKKVDDIIICDSRYSDIEPSTGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLH 180  
Db 182 MKKVDDIIICDSRYSDIEPSTGEVIFRALDPAFKIEDPSPRIQNLKLTNLRIFVKLH 241  
QY 181 TLGDNLDSRMEIREKYYAVYDMVVRGNCYCHASCAPVDGVNEEVGWHGCHCVR 240  
Db 242 TLGDNLDSRMEIREKYYAVYDMVVRGNCYCHASCAPVDGVNEEVGWHGCHCVR 301  
QY 241 HNTKGLNCELMDFYHDLFWPRAEGRNSNACKNCNEHSSCHDFMAVFLATGNVSGV 300  
Db 302 HNTKGLNCELMDFYHDLFWPRAEGRNSNACKNCNEHSSCHDFMAVFLATGNVSGV 361  
QY 301 CMCQHTWGRNCEOCKPPYFOHPERDIRDNMLCEPCTCDPAGSENGICDGYTDFSVGL 360  
Db 362 CMCQHTWGRNCEOCKPPYFOHPERDIRDNMLCEPCTCDPAGSENGICDGYTDFSVGL 421  
QY 361 IAGQCRKLVHGERCDVCKEGFYDLSDAEDPYGCKSCACNPLGTIPGNGPCDSEGYCYC 420  
Db 422 IAGQCRKLVHGERCDVCKEGFYDLSDAEDPYGCKSCACNPLGTIPGNGPCDSEGYCYC 481  
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDCRCDLGGALANSCSDSGQSCCLPHMIGRQCN 480  
Db 482 KRLVTGQRCDQCLPQHWGLSNDLDCRCDLGGALANSCSDSGQSCCLPHMIGRQCN 541  
QY 481 EYESGYFTLDHYLYEAEANLPGVWVVERQYIQDRIPSWTQPGFVVRVPGAYLEFFI 540  
Db 542 EYESGYFTLDHYLYEAEANLPGVWVVERQYIQDRIPSWTQPGFVVRVPGAYLEFFI 601  
QY 541 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVWSLSPGS 600  
Db 602 DNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVWSLSPGS 661  
QY 601 RYVVLPRPVCPEKGMNYTVRLELPQYTAGSDVEGSPYTFIDSLVLMPYCKSLDIFTVGS 660  
Db 662 RYVVLPRPVCPEKGMNYTVRLELPQYTAGSDVEGSPYTFIDSLVLMPYCKSLDIFTVGS 721  
QY 661 GDGEVTSNAWETFORVRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSL 720  
Db 722 GDGEVTSNAWETFORVRCLENSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQSL 781  
QY 721 SSVCDPNGGQCCRPNNVORTNRCAPGTFGPGNCKPCDCHLQGSASAFCDAITGQCH 780  
Db 782 SSVCDPNGGQCCRPNNVORTNRCAPGTFGPGNCKPCDCHLQGSASAFCDAITGQCH 841  
QY 781 CFQGIYARQCDRLCPGYWGFPPSCQPCQCNHGLDCDVTGTGECSCQDYYTGHNCERCLAG 840  
Db 842 CFQGIYARQCDRLCPGYWGFPPSCQPCQCNHGLDCDVTGTGECSCQDYYTGHNCERCLAG 901  
QY 841 YGDEPTIGSDHCRPCPCPDGPDGSGRQFARSCVDQPVTLQACVCDPGVIGSRCDCCAG 900  
Db 902 YGDEPTIGSDHCRPCPCPDGPDGSGRQFARSCVDQPVTLQACVCDPGVIGSRCDCCAG 961  
QY 901 FFGNPSDFGSCQPCQCHNIDTDEACDKDTGRCLKCLYHTEGDHCLQCVGYGDAAL 960

Db 962 YGPNSEVGGSCQPCCQHNNIDTTPDPAKDKETGRCLKLYHTEGHCQFCRFGYYGDAL 1021  
QY 961 RQDCKVCNVLGTVEKHCNGSDCHCDKATQCCLPNVIGQNCDCRCPNTWQLASGTGC 1020  
Db 1022 RQDCKVCNVLGTVEKHCNGSDCQCDKATQCCLPNVIGQNCDCRCPNTWQLASGTGC 1081  
QY 1021 GPCNNAHSPGSCNVEBTGQCCQCPGFGGRTCSQCQLFWGDDPVECRACDCDPRGIET 1080  
Db 1082 DFCNNAHSPGSCNVEBTGQCCQCPGFGGRTCSQCQLFWGDDPVECRACDCDPRGIET 1141  
QY 1081 POCDOSTGQCVVEGVGPRCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1140  
Db 1142 POCDOSTGQCVVEGVGPRCDKTRGYSGVFPDCTPCHQCFALWDALIGELTNRTHKFL 1201  
QY 1141 EXAKALKISGVIGPYRETVDSVEKKNELKDIQAAPAEPLKNGILFEEAEKLIKDV 1200  
Db 1202 EXAKALKISGVIGPYRETVDSVEKKNELKDIQAAPAEPLKNGILFEEAEKLIKDV 1261  
QY 1201 EKMAQVEVKLTDTASQNSSTAGELQAEABSLDKTVKELAEQLEFIKNSDIOGALDSI 1260  
Db 1262 EKMAQVEVKLTDTASQNSSTAGELQAEABSLDKTVKELAEQLEFIKNSDIOGALDSI 1321  
QY 1261 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLERESPFKEQOEQARLLDEL 1320  
Db 1322 TKYFQMSLEAEKRVNASTDPNSTVEQSALTRDRVEDLMLERESPFKEQOEQARLLDEL 1381  
QY 1321 AGKIQSLDLSAAQMTCTGPPGADCSSECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1380  
Db 1382 AGKIQSLDLSAAQMTCTGPPGADCSSECGGPNCRCTDEGEKKCGGPGCGGLVTVAHSAW 1441  
QY 1381 QKAMDPRDVL SALAEVEQLSKVSEAKVRADAEAKQADVLKTNATKEKVDKSNEDLR 1440  
Db 1442 QKAMDPRDVL SALAEVEQLSKVSEAKVRADAEAKQADVLKTNATKEKVDKSNEDLR 1501  
QY 1441 NLTKQIRNLTEDSADLSIEAVANEVLKSGNASTPOOLONLTEDIRERVETLSQVEVIL 1500  
Db 1502 NLTKQIRNLTEDSADLSIEAVANEVLKSGNASTPOOLONLTEDIRERVETLSQVEVIL 1561  
QY 1501 QCSAADIAAEALLLEAEKASKSATDVKTADWVKEALEEAEKAOVAAEKAIKQADEDIQ 1560  
Db 1562 QCSAADIAAEALLLEAEKASKSATDVKTADWVKEALEEAEKAOVAAEKAIKQADEDIQ 1621  
QY 1561 GTQNLITSIESETAASEETLFWASQRISELERNEVELKEKAQNSGEAEYIEKVYVVKQ 1620  
Db 1622 GTQNLITSIESETAASEETLFWASQRISELERNEVELKEKAQNSGEAEYIEKVYVVKQ 1681  
QY 1621 NADDVKTLTGELDEKYKKVESLIAQKTEESADARRKAEKLLQNEAKTLQAQNSKLQLE 1680  
Db 1682 NADDVKTLTGELDEKYKKVESLIAQKTEESADARRKAEKLLQNEAKTLQAQNSKLQLE 1741  
QY 1681 DLERKYEDNQYLEDKAEQLVRLEGEVRSLIKDISEKVAVYSTCL 1725  
Db 1742 DLERKYEDNQYLEDKAEQLVRLEGEVRSLIKDISEKVAVYSTCL 1786

Search completed: May 18, 2004, 14:42:12  
Job time : 52.8946 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 13.0493 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-12  
Perfect score: 9429  
Sequence: 1 EPCYIVSHLQEDKKCFICDS.....EVRSLKDISEKVAIVTSTCL 1725

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9429	100.0	1725	4	US-09-562-702A-20
2	9429	100.0	1725	4	US-09-561-818A-20
3	9429	100.0	1786	4	US-09-562-702A-18
4	9429	100.0	1786	4	US-09-561-818A-18
5	8873	94.1	1765	4	US-09-562-702A-16
6	8873	94.1	1765	4	US-09-561-818A-16
7	8873	94.1	1786	4	US-09-562-702A-14
8	8873	94.1	1786	4	US-09-561-818A-14
9	8873	94.1	1786	4	US-09-561-709B-9
10	5489	58.2	1196	1	US-08-144-121-4
11	5489	58.2	1196	2	US-08-735-893-4
12	4914	52.1	1799	4	US-09-845-583A-6
13	4783	50.7	1798	4	US-09-561-709B-11
14	4778	50.7	1798	4	US-09-845-583A-8
15	3712.5	39.4	1761	4	US-09-561-709B-1
16	2967.5	31.5	1101	4	US-09-561-709B-5
17	2808	29.8	1342	4	US-09-561-709B-13
18	1637.5	17.4	1572	4	US-09-562-702A-32
19	1637.5	17.4	1572	4	US-09-561-818A-28
20	1637.5	17.4	1605	4	US-09-562-702A-30
21	1637.5	17.4	1605	4	US-09-561-818A-26
22	1622.5	17.2	1576	4	US-09-562-702A-24
23	1622.5	17.2	1576	4	US-09-561-818A-24
24	1622.5	17.2	1584	4	US-09-562-702A-28
25	1622.5	17.2	1609	4	US-09-562-702A-22
26	1622.5	17.2	1609	4	US-09-561-818A-22
27	1622.5	17.2	1617	4	US-09-562-702A-26

28	1619	17.2	271	1	US-08-152-019A-28	Sequence 28, Appl
29	1584	16.8	3635	4	US-09-845-583A-2	Sequence 2, Appl
30	1584	16.4	279	1	US-08-152-019A-29	Sequence 29, Appl
31	1542	16.4	278	2	US-08-460-309-13	Sequence 13, Appl
32	1542	16.4	278	2	US-08-125-077-13	Sequence 13, Appl
33	1534	16.3	3075	2	US-08-460-309-5	Sequence 5, Appl
34	1534	16.3	3075	2	US-08-125-077-5	Sequence 5, Appl
35	1533	16.3	3111	2	US-08-460-309-4	Sequence 4, Appl
36	1533	16.3	3111	2	US-08-125-077-4	Sequence 4, Appl
37	1527.5	16.2	3088	4	US-09-562-702A-8	Sequence 8, Appl
38	1527.5	16.2	3089	4	US-09-562-702A-4	Sequence 2, Appl
39	1527.5	16.2	3110	4	US-09-562-702A-2	Sequence 2, Appl
40	1527.5	16.2	3110	4	US-09-562-702A-6	Sequence 6, Appl
41	1527.5	16.2	3110	4	US-09-561-709B-7	Sequence 7, Appl
42	1497.5	15.9	3084	4	US-09-562-702A-12	Sequence 12, Appl
43	1497.5	15.9	3106	4	US-09-562-702A-10	Sequence 10, Appl
44	1484	15.7	1587	4	US-09-845-583A-10	Sequence 10, Appl
45	1484	15.7	1587	4	US-09-561-709B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-562-702A-20  
; Sequence 20, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-20

Query Match	100.0%	Score 9429;	DB 4;	Length 1725;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1725;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	EPCYIVSHLQEDKKCFICDSRDPYHTLNPDSHLIENVTTFAPNRLKIWQSENGVNV	60	
Db	1	EPCYIVSHLQEDKKCFICDSRDPYHTLNPDSHLIENVTTFAPNRLKIWQSENGVNV	60	
Qy	61	TIQDLEAEFHETHLMTFKTPAAMLIERSDFGTGVTGVRIFYAYDCSSPPGISTGP	120	
Db	61	TIQDLEAEFHETHLMTFKTPAAMLIERSDFGTGVTGVRIFYAYDCSSPPGISTGP	120	
Qy	121	MKKYVDDIICDSRYSDEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKITNLRIKFKVLH	180	
Db	121	MKKYVDDIICDSRYSDEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKITNLRIKFKVLH	180	
Qy	181	TLGNDLLDSMETREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMCR	240	
Db	181	TLGNDLLDSMETREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMCR	240	
Qy	241	HNKGLNCELMDYFHYDLNWRPAEGRNSNACKKCNCHNEHSSSCHFDNAVPLATGNVSGGV	300	
Db	241	HNKGLNCELMDYFHYDLNWRPAEGRNSNACKKCNCHNEHSSSCHFDNAVPLATGNVSGGV	300	



QY 301 CDNCQHTMGRCQCKPFFQHPERDIRDNLCEPCTCDPAGSENGICDGTDFSVGL 360  
DB 301 CDNCQHTMGRCQCKPFFQHPERDIRDNLCEPCTCDPAGSENGICDGTDFSVGL 360  
QY 361 IAGQCRKXHVGEBCDVKCEGFFDLSAEDPYGCKSCACNPLGTIPGPNPCDSETCYC 420  
DB 361 IAGQCRKXHVGEBCDVKCEGFFDLSAEDPYGCKSCACNPLGTIPGPNPCDSETCYC 420  
QY 421 KRLVTGQCDQCLFQHWGLSNDLDCRCPDCCDLGGALNNSCSDSCQSCCLPHMIGRCN 480  
DB 421 KRLVTGQCDQCLFQHWGLSNDLDCRCPDCCDLGGALNNSCSDSCQSCCLPHMIGRCN 480  
QY 481 EVESGYFTLLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540  
DB 481 EVESGYFTLLDHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFFI 540  
QY 541 DNIPIYSMEYELIYEPOLPDHWEKAVITVORPKIPASSRCNTVPDDNQVLSLSPG 600  
DB 541 DNIPIYSMEYELIYEPOLPDHWEKAVITVORPKIPASSRCNTVPDDNQVLSLSPG 600  
QY 601 RYVVLPRPVCPEKGMNVTVRLELQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGGS 660  
DB 601 RYVVLPRPVCPEKGMNVTVRLELQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGGS 660  
QY 661 GDGEVTSNATWETQRYRCLNRSVWTKMTDVCNRIIFISALIHQTLGACECDPQSL 720  
DB 661 GDGEVTSNATWETQRYRCLNRSVWTKMTDVCNRIIFISALIHQTLGACECDPQSL 720  
QY 721 SSVCDPNSGQCCQCPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASFADAITGQCH 780  
DB 721 SSVCDPNSGQCCQCPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASFADAITGQCH 780  
QY 781 CFQGIYARQDRCLPGYGFPSQPCQCNHALDCDVTGECSCDQYTGHCNCRCLAG 840  
DB 781 CFQGIYARQDRCLPGYGFPSQPCQCNHALDCDVTGECSCDQYTGHCNCRCLAG 840  
QY 841 YGDPPIIGSGDHCRPCPCDGPDSGRQFARSCYQDPVTLQACVCPGPGYIGSRCDCCAS 900  
DB 841 YGDPPIIGSGDHCRPCPCDGPDSGRQFARSCYQDPVTLQACVCPGPGYIGSRCDCCAS 900  
QY 901 PFGNPSDFGSGCQCHNITDTPACDKDGRCLKCLYHTEGHDHCOLCOYGYGDAL 960  
DB 901 PFGNPSDFGSGCQCHNITDTPACDKDGRCLKCLYHTEGHDHCOLCOYGYGDAL 960  
QY 961 RQDRCKVCNVLGTVKEHCHGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQASGTGC 1020  
DB 961 RQDRCKVCNVLGTVKEHCHGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQASGTGC 1020  
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DB 1021 GPCNCAHSGPSCNBTGQCQCMFGGRTCSECKLFWGDPDYECRACDCDPRGIET 1080  
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DB 1081 PQDQSTQCVCVGVGEGPRCDKTRGYSGVFPDCTPCHQCFALMDAIIIGELTNRTHKPL 1140  
QY 1141 EKAKALISGVIQYRVTVDVSVEKKNIEKDILAQSPAAEPLKNGILFEAEKTKQVT 1200  
DB 1141 EKAKALISGVIQYRVTVDVSVEKKNIEKDILAQSPAAEPLKNGILFEAEKTKQVT 1200  
QY 1201 EKMAQVEVLTDTASQSNSTAGELGALQAEASLDKTVKELABQLEFIKNSDIQALDSI 1260  
DB 1201 EKMAQVEVLTDTASQSNSTAGELGALQAEASLDKTVKELABQLEFIKNSDIQALDSI 1260  
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DB 1321 AGKLOSLDLASAAQMTCTPPGADCSSECGGNCRTRDEGKCGGPGGGLVTVHAHSAW 1380  
QY 1381 QKAMDFDRDVLASALAEVQLSKMVSEAKVDEAKQNAQDVLTKTNAKTKYDKVKNEDLR 1440

DB 1381 QKAMDFDRDVLASALAEVQLSKMVSEAKVDEAKQNAQDVLTKTNAKTKYDKVKNEDLR 1440  
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DB 1441 NLIQIINFUTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500  
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DB 1501 QOSMAADTARAEILLLEAKRASKSATDKVTADVMVKALEAEAKAQAARAKAIKQADEDIQ 1560  
QY 1561 GTQNLITSIESETAASEETLTNASQRIKSLERNVEBELKKAQNSGEAEYIEKVVYSVKQ 1620  
DB 1561 GTQNLITSIESETAASEETLTNASQRIKSLERNVEBELKKAQNSGEAEYIEKVVYSVKQ 1620  
QY 1621 NADDVKTKLDELDEKVKVESLIIAOKTESADARPAKELLQNEAKTLAQAANSKLQLE 1680  
DB 1621 NADDVKTKLDELDEKVKVESLIIAOKTESADARPAKELLQNEAKTLAQAANSKLQLE 1680  
QY 1681 DLERKYEDNQYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1725  
DB 1681 DLERKYEDNQYLEDKAQELVRLGEVRSLLKDISEKVAVYSTCL 1725

## RESULT 2

US-09-561-818A-20  
; Sequence 20, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tyvggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-20

Query Match 100.0%; Score 9429; DB 4; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCIYSHLOEKCKTCDSRDPYHETLAPDASHLIENVVTTAPNRLKIWQSENGVENV 60  
DB 1 EPYCIYSHLOEKCKTCDSRDPYHETLAPDASHLIENVVTTAPNRLKIWQSENGVENV 60  
QY 61 TIQDLAEAFHFTHLIMTFKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPGISGTP 120  
DB 61 TIQDLAEAFHFTHLIMTFKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPGISGTP 120  
QY 121 MKKVDDIICDSRYSDEPSTEVEIFRALDPFKIEDPVSRIQNLKITNRIKFKVLH 180  
DB 121 MKKVDDIICDSRYSDEPSTEVEIFRALDPFKIEDPVSRIQNLKITNRIKFKVLH 180  
QY 181 TLGNLLDSMEIREKYIYAVYDMVVRGNCFCYGHASCAPVDGVNEVEGHHCHMCR 240  
DB 181 TLGNLLDSMEIREKYIYAVYDMVVRGNCFCYGHASCAPVDGVNEVEGHHCHMCR 240  
QY 241 HNTKGLNCELMDPYHDLPRPAEGNSNACKCNCHNSSCHDFMAVFLATGNVSGV 300  
DB 241 HNTKGLNCELMDPYHDLPRPAEGNSNACKCNCHNSSCHDFMAVFLATGNVSGV 300  
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DB 301 CDNCQHTMGRCQCKPFFQHPERDIRDNLCEPCTCDPAGSENGICDGTDFSVGL 360  
QY 361 IAGQCRKXHVGEBCDVKCEGFFDLSAEDPYGCKSCACNPLGTIPGPNPCDSETCYC 420

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421 KELVTVGRCDCQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQSCCLPHMIGROCN 480  
421 KELVTVGRCDCQCLPQHWGLSNDLDGCRPCDCDLGGALNNSCEDSGQSCCLPHMIGROCN 480  
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661 GDEVTNSAWETFORVRCLENSRVSVKTPMTDVCNRIIFSIISALIHQTGLACECDPQGLS 720  
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1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

## RESULT 3

US-09-562-702A-18  
; Sequence 18, Application US/09562702A  
; Patent No. 6632790

## GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-18

Query Match 100.0%; Score 9429; DB 4; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 62 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 121  
QY 61 TIQLDLAEHFHTLIMTKTFRPAAMLIERSDDFGKTGWYRYFAYDCSSPPGISTGP 120  
DB 122 TIQLDLAEHFHTLIMTKTFRPAAMLIERSDDFGKTGWYRYFAYDCSSPPGISTGP 181  
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DB 182 MKKYVDDIICDSRYSDIEPSTEGEVIFFALDPAPKIEDPSPRIQNLKLTNLRKPKVKLH 241  
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DB 242 TLGNLLDSRMEIREKTYIYAYDMVVRGNCFCYGHASECAPVDCVNEVEGVHGHCMCR 301  
QY 241 HNTKGLNCELCDMFYHDLPMWRPAEGRNSNACKKCNHSSSCHFDMAVFLATGNVSGGV 300  
DB 302 HNTKGLNCELCDMFYHDLPMWRPAEGRNSNACKKCNHSSSCHFDMAVFLATGNVSGGV 361  
QY 301 CDNCQHNMTGNCQCKPFFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 360  
DB 362 CDNCQHNMTGNCQCKPFFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 421  
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Db 482 KELVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGALNNSCEDSGQCSCLPHMIGROCN 541  
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Db 542 EVESGYFTLTHYIYEAEANLPGVGVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEPFI 601  
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QY 1081 PQCDQSTGQCVGVEGPRCDKCTRGYSVDPDCTPCHQCFAWDALIGELTNRTHKFL 1140  
Db 1142 PQCDQSTGQCVGVEGPRCDKCTRGYSVDPDCTPCHQCFAWDALIGELTNRTHKFL 1201  
QY 1141 EKAKALKISGVIPIYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIIGILFEAEKLTMDVT 1200  
Db 1202 EKAKALKISGVIPIYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIIGILFEAEKLTMDVT 1261  
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFINKSDIQGALDSI 1260  
Db 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFINKSDIQGALDSI 1321  
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVQSSALTRDRVEDLMLESPPKEQEQEQAALLDEL 1320  
Db 1322 TKYFQMSLEAEKRVNASTTDPNSTVQSSALTRDRVEDLMLESPPKEQEQEQAALLDEL 1381  
QY 1321 AGKLQSLDLASAAQMTCTGTPPGADCSSECGGPNCTDEGEKCGGPGGLVTVVAHSAW 1380  
Db 1382 AGKLQSLDLASAAQMTCTGTPPGADCSSECGGPNCTDEGEKCGGPGGLVTVVAHSAW 1441  
QY 1381 QKAMDPRDVLALAEVQLSKMWSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLR 1440  
Db 1442 QKAMDPRDVLALAEVQLSKMWSEAKVRADAKQNAQDVLKTNATKEKVDKSNEDLR 1501  
QY 1441 NLIQKIRNFILTEDSADLSIEAVANEVLKSGNASTPQOLQNLTERVERVETLSQVEVIL 1500

Db 1502 NLIQKIRNFILTEDSADLSIEAVANEVLKSGNASTPQOLQNLTERVERVETLSQVEVIL 1561  
QY 1501 QQSAADIARAELLEBEAKSKASATDVKTADVMVKEALBEAKQAQVAEKAIAQOADEIQ 1560  
Db 1562 QQSAADIARAELLEBEAKSKASATDVKTADVMVKEALBEAKQAQVAEKAIAQOADEIQ 1621  
QY 1561 GTONLTSIETSETAASEETLTNASQISKLERNVEELKKAQNSGEAEVIEKVYVSVKQ 1620  
Db 1622 GTONLTSIETSETAASEETLTNASQISKLERNVEELKKAQNSGEAEVIEKVYVSVKQ 1681  
QY 1621 NADDVVKTLDELDEKYEKVESLIAQKTESADARREKALLQNEAKTLAQANSKLQLE 1680  
Db 1682 NADDVVKTLDELDEKYEKVESLIAQKTESADARREKALLQNEAKTLAQANSKLQLE 1741  
QY 1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISKVAVYSTCL 1725  
Db 1742 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISKVAVYSTCL 1786

RESULT 4  
US-09-561-818A-18  
; Sequence 18, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-18

Query Match 100.0%; Score 9429; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPYCVIHLQBDKCKFCIDSRDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 60  
Db 62 EPYCVIHLQBDKCKFCIDSRDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 121  
QY 61 TIQDLLEAEFHTLIMTFTFPAAMLIERSDFGKTGWVYRYFAYDCSSPFGISTGP 120  
Db 122 TIQDLLEAEFHTLIMTFTFPAAMLIERSDFGKTGWVYRYFAYDCSSPFGISTGP 181  
QY 121 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKIITNLRIKFVKLH 180  
Db 182 MKKYDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPRIQNLKIITNLRIKFVKLH 241  
QY 181 TLGDNLLDSRMEIREKYIYAYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240  
Db 242 TLGDNLLDSRMEIREKYIYAYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 301  
QY 241 HNTVGLNCELMDPFDHLPWRPAEGRNSACKKNCNHSCHDFMAVFLATGNVSGGV 300  
Db 302 HNTVGLNCELMDPFDHLPWRPAEGRNSACKKNCNHSCHDFMAVFLATGNVSGGV 361  
QY 301 CDNQHNMTGNCRCQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGI CDGYTDFSVGL 360  
Db 362 CDNQHNMTGNCRCQCKPFYFQHPERDIRDPNLCPECTCDPAGSENGGI CDGYTDFSVGL 421  
QY 361 IAGQCRCKLVGEGRCVCEGFDLSAEDPYGCKSCACNPLGTTIPGNGPCDSETGYCYC 420  
Db 422 IAGQCRCKLVGEGRCVCEGFDLSAEDPYGCKSCACNPLGTTIPGNGPCDSETGYCYC 481  
QY 421 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGALNNSCEDSGQCSCLPHMIGROCN 480  
Db 482 KRLVTGQRCDQCLPOHWGLSNDLDGCRPCDCLGALNNSCEDSGQCSCLPHMIGROCN 541

QY 481 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQRDIQSWTGPFGVVRPEGAYLFFFI 540  
DB 542 EVESGYFTTLDHYIYEAEEANLPGVWVVERQYIQRDIQSWTGPFGVVRPEGAYLFFFI 601  
QY 541 DNIPIYMEYELLIRYEPOLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSGFS 600  
DB 602 DNIPIYMEYELLIRYEPOLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSGFS 661  
QY 601 RYVVLPRPVCPEKGMNVTYRLPELQYTAGSDVSPYTFIDSLVMPYCKSIDIFTVGGS 660  
DB 662 RYVVLPRPVCPEKGMNVTYRLPELQYTAGSDVSPYTFIDSLVMPYCKSIDIFTVGGS 721  
QY 661 GGEVNTSAWETFORYRCLENRSVVKTPTMTDVCNIIIFSISALHQTGLACECDPQSSL 720  
DB 722 GGEVNTSAWETFORYRCLENRSVVKTPTMTDVCNIIIFSISALHQTGLACECDPQSSL 781  
QY 721 SSVCDPNGQCCOCRNNVUGRTNRCAPGTFGPGNGKPCDCHLOGSASAFCDALTGOCH 780  
DB 782 SSVCDPNGQCCOCRNNVUGRTNRCAPGTFGPGNGKPCDCHLOGSASAFCDALTGOCH 841  
QY 781 CFQGIYAROCDCRLPGYMGFFPCQPCQCNHGLDCTVTGECLSQDQYTTGHCNRCIAG 840  
DB 842 CFQGIYAROCDCRLPGYMGFFPCQPCQCNHGLDCTVTGECLSQDQYTTGHCNRCIAG 901  
QY 841 YGDPPIIGSGDHCRPCPCPDGSDGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCASG 900  
DB 902 YGDPPIIGSGDHCRPCPCPDGSDGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCASG 961  
QY 901 FFGNPSDFGSCQPCQCHNIIITDPEACDKTGRCLKLYHTEGDHQLCOYGYGDAL 960  
DB 962 FFGNPSDFGSCQPCQCHNIIITDPEACDKTGRCLKLYHTEGDHQLCOYGYGDAL 1021  
QY 961 RQDRKVCNLYGTVAKEHNGSDCHDKATGQSCSLPNVIGQNCRCAPNTWQLASGTGC 1020  
DB 1022 RQDRKVCNLYGTVAKEHNGSDCHDKATGQSCSLPNVIGQNCRCAPNTWQLASGTGC 1081  
QY 1021 GPCNNAHSGFSPSCNEFTGQCCQMGFGGRTCSQCELFWDGPDVVECRACDDPRGIET 1080  
DB 1082 GPCNNAHSGFSPSCNEFTGQCCQMGFGGRTCSQCELFWDGPDVVECRACDDPRGIET 1141  
QY 1081 PQCDQSTGQCVGVEGPRCDKTRGYSVFPDCTPCHQCPCALMDAIGELTNRTHKPL 1140  
DB 1142 PQCDQSTGQCVGVEGPRCDKTRGYSVFPDCTPCHQCPCALMDAIGELTNRTHKPL 1201  
QY 1141 EKAKALKISGVIQPYRETVDSEKKNETKIDILAQSPAAEPLKNGILFEEAEKLTQDVT 1200  
DB 1202 EKAKALKISGVIQPYRETVDSEKKNETKIDILAQSPAAEPLKNGILFEEAEKLTQDVT 1261  
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDTKVKELAEQLEFIKNSDIQALDSI 1260  
DB 1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEASLDTKVKELAEQLEFIKNSDIQALDSI 1321  
QY 1261 TKYFQMSLEAEKRVNASTTDPNSTVQESALTDRVEDIMLERESPKEQOEQABLLDEL 1320  
DB 1322 TKYFQMSLEAEKRVNASTTDPNSTVQESALTDRVEDIMLERESPKEQOEQABLLDEL 1381  
QY 1321 AGKLQSLDLSAAQMTCTGPPGADCSSECGPNCRDTDEGEKCGGPGCGGLTVVAHSAW 1380  
DB 1382 AGKLQSLDLSAAQMTCTGPPGADCSSECGPNCRDTDEGEKCGGPGCGGLTVVAHSAW 1441  
QY 1381 QKAMDPRDVLALAEVEQLSKMVSFAKVRDEAKQNAQDVLLKTNATKEKVDKSNEDIR 1440  
DB 1442 QKAMDPRDVLALAEVEQLSKMVSFAKVRDEAKQNAQDVLLKTNATKEKVDKSNEDIR 1501  
QY 1441 NLIKQIRNFITEDSADLSITAEVANEVLKSGNASTPQQLQNLITEDIRERVETLSQVEVIL 1500  
DB 1502 NLIKQIRNFITEDSADLSITAEVANEVLKSGNASTPQQLQNLITEDIRERVETLSQVEVIL 1561  
QY 1501 QQSAADIARAELLLEBAKSAKSDATDKVTADMVKEALEBAKQVAEAKAIKQADEDIQ 1560  
DB 1562 QQSAADIARAELLLEBAKSAKSDATDKVTADMVKEALEBAKQVAEAKAIKQADEDIQ 1621

QY 1561 GTQNLTSIETSEETAASEETLTNASQRIKSLERNVELKRAAONSGEABYIEKVYYSVKQ 1620  
DB 1622 GTQNLTSIETSEETAASEETLTNASQRIKSLERNVELKRAAONSGEABYIEKVYYSVKQ 1681  
QY 1621 NADVKKTLDGELDEKXKVESLIAQKTESADARKAELLQNEAKTLLAQANSKLQLE 1680  
DB 1682 NADVKKTLDGELDEKXKVESLIAQKTESADARKAELLQNEAKTLLAQANSKLQLE 1741  
QY 1681 DLRKRYEDNQKYLEDAQELVRLGEVRSLLKDISEKVAIVYSTCL 1725  
DB 1742 DLRKRYEDNQKYLEDAQELVRLGEVRSLLKDISEKVAIVYSTCL 1786

RESULT 5  
US-09-562-702A-16  
; Sequence 16, Application US/09562702A  
; Patent No. 6633790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-16

Query Match 94.1%; Score 8873; DB 4; Length 1765;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLINNVVTFAPNRLKIWQSENGVENV 60  
DB 41 EPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLINNVVTFAPNRLKIWQSENGVENV 100  
QY 61 TIQLDLAEAEHFTHLIMTFKTERPAAMLIERSDFGKTGMYRYEAYDCSSPFGISTGP 120  
DB 101 TIQLDLAEAEHFTHLIMTFKTERPAAMLIERSDFGKTGMYRYEAYDCSSPFGISTGP 160  
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAPKIEDPPSPRIQNLKITNLRKFKVKLH 180  
DB 161 MKKVDDIICDSRYSDIEPSTEGEVIFFRALDPAPKIEDPPSPRIQNLKITNLRKFKVKLH 220  
QY 181 TLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCR 240  
DB 221 TLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCR 280  
QY 241 HNTKGLNCELMDPYHDLPRPAEGRNSACKKCNNEHSSSCHFDMAVYLATGNVSGGV 300  
DB 281 HNTKGLNCELMDPYHDLPRPAEGRNSACKKCNNEHSSSCHFDMAVYLATGNVSGGV 340  
QY 301 CDNCQHNMTGRNCBQCKPFFYQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 341 CDNCQHNMTGRNCBQCKPFFYQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVGL 400  
QY 361 IAGQCRKLVGEGHCDVCKEGFYDLSEDPFGCKSCACNPLGTIPGNCPCDSETGYCYC 420  
DB 401 IAGQCRKLVGEGHCDVCKEGFYDLSEDPFGCKSCACNPLGTIPGNCPCDSETGYCYC 460  
QY 421 KRLVTGRCQCCLPQHWGLSNDLDGCRPCDDCLGGALNNSCSBDSGSCSLPHMIGROCN 480

Db 461 KRLVTGQCHDCOCLPEHWGLSNDLDGCRPCDDDLGGALNNSCFABSGQSCSRPHMIGRCQN 520  
QY 481 EVESGYFTTLDHYLYEAEANLGGVGVVVEROYIQDRIPSWTGPGFVRVPEGAYLEFFI 540  
Db 521 EVESGYFTTLDHYLYEAEANLGGVGVVVEROYIQDRIPSWTGPGFVRVPEGAYLEFFI 580  
QY 541 DNPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSFGS 600  
Db 581 DNPYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSFGS 640  
QY 601 RVVVLPRPVCPEKGMNVTVRLEPQYTAGSDVSPYTFIDSLVMPYCKSLDIFTVGGS 660  
Db 641 RVVVLPRPVCPEKGMNVTVRLEPQYTAGSDVSPYTFIDSLVMPYCKSLDIFTVGGS 700  
QY 661 GGEVNTNSAWETFORRYCLNSRSVVKTPMTDVCNRNIIFSIALLHQTGLACSDPQGS 720  
Db 701 GGEVNTNSAWETFORRYCLNSRSVVKTPMTDVCNRNIIFSIALLHQTGLACSDPQGS 760  
QY 721 SVVCDPNGGQCCRCRNVNVRTNCRCAPGTGFGPNCKPCDCHLQGSASFCDALTGQCH 780  
Db 761 SVVCDPNGGQCCRCRNVNVRTNCRCAPGTGFGPNCKPCDCHLQGSASFCDALTGQCH 820  
QY 781 CFQGIYARQCDRLCPGWFPSQPCQCNHALDCTVTGECISQDVTYTHNCERCLAG 840  
Db 821 CFQGIYARQCDRLCPGWFPSQPCQCNHALDCTVTGECISQDVTYTHNCERCLAG 880  
QY 841 YGDDPIIGSDHCRPCPDGDSGQFARSCYQDPVTLQACVCDPFGYIGSRCDGASG 900  
Db 881 YGDDPIIGSDHCRPCPDGDSGQFARSCYQDPVTLQACVCDPFGYIGSRCDGASG 940  
QY 901 FFGNSDFGSGQPCQCHNITDTPDCAKDGRCLKLYHTGEGHQCQYGYGDAL 960  
Db 941 FFGNSDFGSGQPCQCHNITDTPDCAKDGRCLKLYHTGEGHQCQYGYGDAL 1000  
QY 961 RODCRKVCNLTGTVKHCNSDCHDKATQCSCLPNVIGONCDRCAPNTWOLASGTGC 1020  
Db 1001 RODCRKVCNLTGTVKHCNSDCHDKATQCSCLPNVIGONCDRCAPNTWOLASGTGC 1060  
QY 1021 GFCNNAHSPGSCNFTGQCCMPGPGTSCQELFWGDPDVECRACDQPRGIET 1080  
Db 1061 GFCNNAHSPGSCNFTGQCCMPGPGTSCQELFWGDPDVECRACDQPRGIET 1120  
QY 1081 POCDSGTQCVCEGVEGPRCDKTRGYSGVFPDCTPCHOCFALWDALIGELNTRHKL 1140  
Db 1121 POCDSGTQCVCEGVEGPRCDKTRGYSGVFPDCTPCHOCFALWDALIGELNTRHKL 1180  
QY 1141 EKAKALKISGVIGPVRETVDVSEKKNIEIKDILAQSPAAEPLKNIGLFEAEKLTQV 1200  
Db 1181 EKAKALKISGVIGPVRETVDVSEKKNIEIKDILAQSPAAEPLKNIGLFEAEKLTQV 1240  
QY 1201 EKMAQVEVKLTDTASQSNSTAGELGALQAESEIDKTKELAEOLBEIKNSDIQGLDST 1260  
Db 1241 EKMAQVEVKLTDTASQSNSTAGELGALQAESEIDKTKELAEOLBEIKNSDIQGLDST 1300  
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Db 1301 TKYFQMSLEAEKRVNASTTDPNSTVQSALTRDVEDIMLERSPPKQOEQEARLLDEL 1360  
QY 1321 AKGLQSLDLSAAQMTCTPPGACSESECGNCRTRDEGKCGGPGCGGLTVVAHSAW 1380  
Db 1361 AKGLQSLDLSAAQMTCTPPGACSESECGNCRTRDEGKCGGPGCGGLTVVAHSAW 1420  
QY 1381 QKAMDFDRDVLISALAEVQLSKNYSKAVRADEAKQAOVLLTNATKEKVDKSNEDR 1440  
Db 1421 QKAMDFDRDVLISALAEVQLSKNYSKAVRADEAKQAOVLLTNATKEKVDKSNEDR 1480  
QY 1441 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPOOLQNTLTEREVETLSQVEVIL 1500  
Db 1481 NLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPOOLQNTLTEREVETLSQVEVIL 1540  
QY 1501 QSAADIARAEELLIEEAKRSKATDVKTADMDVKEALEBAEAKQAAEKAHQAQEDTQ 1560  
Db 1541 QSAADIARAEELLIEEAKRSKATDVKTADMDVKEALEBAEAKQAAEKAHQAQEDTQ 1600

QY 1561 GTQNLITSIESETAASBETLTNASORISKLRNVVELKRAAONSGEAEYIEKVYISVKQ 1620  
Db 1601 GTQNLITSIESETAASBETLTNASORISKLRNVVELKRAAONSGEAEYIEKVYISVKQ 1660  
QY 1621 NADDVKTLDGELDEKYKVESLIAQKTESDARRKAELLQNEAKTLLAQANSKLQLLE 1680  
Db 1661 NADDVKTLDGELDEKYKVESLIAQKTESDARRKAELLQNEAKTLLAQANSKLQLLE 1720  
QY 1681 DLERYEDNOKYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1725  
Db 1721 DLERYEDNOKYLEDKQAEVLRLGEVRSLLKDISEKVAVYSTCL 1765

RESULT 6  
US-09-561-818A-16  
; Sequence 16, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1785  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-16

Query Match 94.1%; Score 8873; DB 4; Length 1765;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWNQSENGVENV 60  
Db 41 EPYCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWNQSENGVENV 100  
QY 61 TIQDLDAEFHFTLHMTFPTPAAMLERSDFGKTGWVRYFAYDCESSFPGISGTP 120  
Db 101 TIQDLDAEFHFTLHMTFPTPAAMLERSDFGKTGWVRYFAYDCESSFPGISGTP 160  
QY 121 MKYVDDIICDSRYSYDIEPSTEGEVI FRALDPAPFKIEDPYSRIONLLKITNLRIFVKLH 180  
Db 161 MKYVDDIICDSRYSYDIEPSTEGEVI FRALDPAPFKIEDPYSRIONLLKITNLRIFVKLH 220  
QY 181 TLGNLJLDSRMEIREKYIYAVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 240  
Db 221 TLGNLJLDSRMEIREKYIYAVDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGCMCR 280  
QY 241 HNTKGLNCELNDPFDHDLPRPAEGRNSNACKKCNHSSCHDFDPAVFLATGNVSGGV 300  
Db 281 HNTKGLNCELNDPFDHDLPRPAEGRNSNACKKCNHSSCHDFDPAVFLATGNVSGGV 340  
QY 301 CDNCQHNMTGRNCEOCKPFYFQHPERDIRDPLNCEPCTCDPAGSENGGICDGYTDFSVGL 360  
Db 341 CDDCQHNMTGRNCEOCKPFYFQHPERDIRDPLNCEPCTCDPAGSENGGICDGYTDFSVGL 400  
QY 361 IAGCRCKLHVBERCDVCKEGBFYDLSADDPYCKSCACNPLGTTPGNPCDSSETGYCYC 420  
Db 401 IAGCRCKLHVBERCDVCKEGBFYDLSADDPYCKSCACNPLGTTPGNPCDSSETGYCYC 460  
QY 421 KRLVTGQRCCQLPQHWGLSNDLDGCRPCDDDLGGALNNSCFABSGQSCSRPHMIGRCQN 480  
Db 461 KRLVTGQRCCQLPQHWGLSNDLDGCRPCDDDLGGALNNSCFABSGQSCSRPHMIGRCQN 520  
QY 481 EVESGYFTTLDHYLYEAEANLGGVGVVVEROYIQDRIPSWTGPGFVRVPEGAYLEFFI 540  
Db 521 EVESGYFTTLDHYLYEAEANLGGVGVVVEROYIQDRIPSWTGPGFVRVPEGAYLEFFI 580

QY 541 DNIPIYSMEYELIRYEPOLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 600  
DB 581 DNIPIYSMEYDILLIRYEPOLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 640  
QY 601 RYVVLPRVPCFEKGMNVTYRLELPOYTASGSDVRSPTFIDSLVLMYPYCKSLDIFTVGG 660  
DB 641 RYVVLPRVPCFEKGMNVTYRLELPOYTASGSDVRSPTFIDSLVLMYPYCKSLDIFTVGG 700  
QY 661 GDGEVTNAGWETFORYRCLENSRSVVKTPMTDVCNRIIFSIISALIHOTGLACECDPQGS 720  
DB 701 GDGVVTNAGWETFORYRCLENSRSVVKTPMTDVCNRIIFSIISALLHQTGLACECDPQGS 760  
QY 721 SSVCDPNQGQCCRPVNVGRTNCRCAPGTGFGNGKPCDCHLOGSASAFCDIAITGQCH 780  
DB 761 SSVCDPNQGQCCRPVNVGRTNCRCAPGTGFGNGKPCDCHLOGSASAFCDIAITGQCH 820  
QY 781 CFQGYIARQCDRLCGYWGFPSCQPCQNGHALDCDVTGSCLSQDVTTHGNCERCIALG 840  
DB 821 CFQGYIARQCDRLCGYWGFPSCQPCQNGHALDCDVTGSCLSQDVTTHGNCERCIALG 880  
QY 841 YGDPPIIGSGDHCRPCPCPDGSDGROFARSQYQDPVTILOACVCDPGYIGSRCDDCAG 900  
DB 881 YGDPPIIGSGDHCRPCPCPDGSDGROFARSQYQDPVTILOACVCDPGYIGSRCDDCAG 940  
QY 901 FGNESDFGSGSCOPCQCHNIDTTPBEACDKDTGRCLKLYHTEGDHCOLCOVGYGDAL 960  
DB 941 YFGNDFGSGSCOPCQCHNIDTTPBEACDKDTGRCLKLYHTEGDHCOLCOVGYGDAL 1000  
QY 961 RQDCRKCVCNYLGTVEKHCNGSDCHDKATGQSCCLPNVIGNCDRCAPNTWQASGTGC 1020  
DB 1001 RQDCRKCVCNYLGTVEKHCNGSDCHDKATGQSCCLPNVIGNCDRCAPNTWQASGTGC 1060  
QY 1021 GPCNCAHSGPSNETGQCCWPGFGGRGTCSEQELFWGDDVEGRACDCDPRGLET 1080  
DB 1061 GPCNCAHSGPSNETGQCCWPGFGGRGTCSEQELFWGDDVEGRACDCDPRGLET 1120  
QY 1081 PQCDQSTGQCVVEGVEPRCDKTRGSGVFPDCTPCHQCFALMDAIIGELTNRHFKFL 1140  
DB 1121 PQCDQSTGQCVVEGVEPRCDKTRGSGVFPDCTPCHQCFALMDAIIGELTNRHFKFL 1180  
QY 1141 EKAKALKISGVTGPVRETVDSEKKNELKILQASPAEPLKNTGILFEAEKLIKDV 1200  
DB 1181 EKAKALKISGVTGPVRETVDSEKKNELKILQASPAEPLKNTGILFEAEKLIKDV 1240  
QY 1201 EKMAQVEKVLDTASQNSSTAGELQAEASLDTVKELAEQLEFIKNSDIOGALDSI 1260  
DB 1241 EKMAQVEKVLDTASQNSSTAGELQAEASLDTVKELAEQLEFIKNSDIOGALDSI 1300  
QY 1261 TKYFQMSLEAEKRVNASTPNSVTEQSAITDRVEDLMLRESFKQEQEQAELDEL 1320  
DB 1301 TKYFQMSLEAEKRVNASTPNSVTEQSAITDRVEDLMLRESFKQEQEQAELDEL 1360  
QY 1321 AGKLOSLLSAAAOVTGTPPGADCSGEGGPNCRDTEGKKCGGPGCGGLVTVAHSAW 1380  
DB 1361 AGKLOSLLSAAAOVTGTPPGADCSGEGGPNCRDTEGKKCGGPGCGGLVTVAHSAW 1420  
QY 1381 QKAMPDRDVLASALAEVQSLKXVSEAKVRADEAKQNAQDVLKTNATKVKDKNSDEL 1440  
DB 1421 QKAMPDRDVLASALAEVQSLKXVSEAKVRADEAKQNAQDVLKTNATKVKDKNSDEL 1480  
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DB 1481 NLTKOIRFLTDSADLDSIEAVANEVLKSNASTPQOLQNTEDIRREVLTQVEVIL 1540  
QY 1501 QSAADIAARAELLLBEAKSASATDVKTADMKVEALEEAFKAQVAEAKAQAQADEIDQ 1560  
DB 1541 QSAADIAARAELLLBEAKSASATDVKTADMKVEALEEAFKAQVAEAKAQAQADEIDQ 1600  
QY 1561 GTQNLITSTESTASAEETLTHASORIISKLEBNEVELKRAQNSGEAEYIEKVVYSVKQ 1620  
DB 1601 GTQNLITSTESTASAEETLTHASORIISKLEBNEVELKRAQNSGEAEYIEKVVYSVKQ 1660  
QY 1621 NADDVKKTLDDGELDEKIKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1680

DB 1661 SAEDVKTKTLDDGELDEKIKKVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLE 1720  
QY 1681 DLERKVEDNOKYLEDKAOELVLEGEVRSLLDKISEKVAVYSTCL 1725  
DB 1721 DLERKVEDNOKYLEDKAOELVLEGEVRSLLDKISEKVAVYSTCL 1765  
RESULT 7  
US-09-562-702A-14  
; Sequence 14, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenko, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-14  
Query Match 94.1%; Score 8873; DB 4; Length 1786;  
Best Local Similarity 92.3%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;  
QY 1 EPYCIIVSHLQEDKKFCIDSRDPYHETLNPDSHLIENNVVTFAPNRLKIWQSENGVENV 60  
DB 62 EPYCIIVSHLQEDKKFCIDSRDPYHETLNPDSHLIENNVVTFAPNRLKIWQSENGVENV 121  
QY 61 TIQDLAEAFPHFLHMTFTFPAAMLIERSDCKTGWVYFAYDCESPPGISTGP 120  
DB 122 TIQDLAEAFPHFLHMTFTFPAAMLIERSDCKTGWVYFAYDCESPPGISTGP 181  
QY 121 MKKVDDIIICDSYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNRIKFKVLH 180  
DB 182 MKKVDDIIICDSYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNRIKFKVLH 241  
QY 181 TLGDNLLDSRMEIREKYYAVYDMVYRGNCFCYGHASECAPVDGVNEEVGWHGCMCR 240  
DB 242 TLGDNLLDSRMEIREKYYAVYDMVYRGNCFCYGHASECAPVDGVNEEVGWHGCMCR 301  
QY 241 HNTKGLNCELMDFYHDLPMRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGGV 300  
DB 302 HNTKGLNCELMDFYHDLPMRPAEGRNSNACKKCNNEHSSSCHFDMAVFLATGNVSGGV 361  
QY 301 CDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGTDFSVGL 360  
DB 362 CDNCQHNMTGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGTDFSVGL 421  
QY 361 IAGQCRCKLHVEGERCDVCKEYFDLSAEDPYGCKSCACNPLGTIPGGNCPDSETGYCYC 420  
DB 422 IAGQCRCKLHVEGERCDVCKEYFDLSAEDPYGCKSCACNPLGTIPGGNCPDSETGYCYC 481  
QY 421 KRLVGTQRCQDCLPQHWGLSNDLDGRCPCDCLGGALNNSCSBDSQCSCLPHMIGRQCN 480  
DB 482 KRLVGTQRCQDCLPQHWGLSNDLDGRCPCDCLGGALNNSCSBDSQCSCLPHMIGRQCN 541  
QY 481 EVESGYFTTLDHYIYEAEBANLPGVGVVEROYIQDRIPSWTGPGRVVRPEGAYLEFFI 540  
DB 542 EVESGYFTTLDHYIYEAEBANLPGVGVVEROYIQDRIPSWTGPGRVVRPEGAYLEFFI 601

QY 541 DNPYSMEYELIRYEPOLPDHEWKAIVTVORPGKIPASSRCGNTVPPDDNQVLSLPGS 600  
Db 602 DNPYSMEYELIRYEPOLPDHEWKAIVTVORPGKIPASSRCGNTVPPDDNQVLSLPGS 661  
QY 601 RYVVLPRPVCFKGMNYTVRLBELPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGS 660  
Db 662 RYVVLPRPVCFKGMNYTVRLBELPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGS 721  
QY 661 GDEVTNSAWETFORVRCLENSRSVVKPMTDVCNIIIFSALIHOTGLACEDPOGSL 720  
Db 722 GGVVNTNSAWETFORVRCLENSRSVVKPMTDVCNIIIFSALIHOTGLACEDPOGSL 781  
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QY 841 YTGDPHIGSGDHCRPCPCDPSGQGFARSQYQDPVTQLACVCDPFGYIGSRCDCCASG 900  
Db 902 YTGDPHIGSGDHCRPCPCDPSGQGFARSQYQDPVTQLACVCDPFGYIGSRCDCCASG 961  
QY 901 FFGNPSDFGSCQPCQCHNIDTTPDPAKDKTGRCLKCLYHTEGDCQCLCOYGYGDAL 960  
Db 962 YFGNPSDFGSCQPCQCHNIDTTPDPAKDKTGRCLKCLYHTEGDCQCLCOYGYGDAL 1021  
QY 961 RQCRKVCNYLGTVKEHNGNSDCHDKATQCCSCLPNVIGQNDRCAPNTWOLASGTGC 1020  
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Db 1442 OKAMDIFRDLVLSALAEVQLSKWYSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501  
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Db 1622 QTONLLTSIESETAASBETLNASQRI:SKLERVVEELKRAQAQNSGEAEYIEKVYSVKQ 1681

QY 1621 NADDVKTLDGELDEKVKYVESLIAOAKTESADARBAKAELONEAKTLLACANSKLQLE 1680  
Db 1682 NADDVKTLDGELDEKVKYVESLIAOAKTESADARBAKAELONEAKTLLACANSKLQLE 1741  
QY 1681 DLERKYEDNQYLEDKQAEQVRLGEVRSLLKDISEKAVAVYSTCL 1725  
Db 1742 DLERKYEDNQYLEDKQAEQVRLGEVRSLLKDISEKAVAVYSTCL 1786

RESULT 8  
US-09-561-818A-14  
; Sequence 14, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99, 274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-14

Query Match 94.1%; Score 8873; DB 4; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQEDBKCFICDSRDPVHETLNPDSHLIENVTTPAPNRLKIWQSENGVENV 60  
Db 62 EPYCIIVSHLQEDBKCFICDSRDPVHETLNPDSHLIENVTTPAPNRLKIWQSENGVENV 121  
QY 61 TIQDLAEAFHFTLIMTFTFPAAMLIERSDPFKWTGWYRYFAYDCESFPGISGTP 120  
Db 122 TIQDLAEAFHFTLIMTFTFPAAMLIERSDPFKWTGWYRYFAYDCESFPGISGTP 181  
QY 121 MKYVDDIIICSRYSDEIPESTEGEVIFFALDPAPKIEDPSPRIQNLKITNLRIFVKLH 180  
Db 182 MKYVDDIIICSRYSDEIPESTEGEVIFFALDPAPKIEDPSPRIQNLKITNLRIFVKLH 241  
QY 181 TLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASBCAPVDGVNEVEGWHGCHMC 240  
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QY 421 KRLVTGRCOCCTPOHVGSLNLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRCN 480  
Db 482 KRLVTGRCOCCTPOHVGSLNLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGRCN 541  
QY 481 EVERSGYFTTLDHYIYEABEANLPGVWVVERQYIQDIRIPSWTGFVVRPEGAYLEPFI 540  
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Db 602 DNPYSMEYELIRYEPOLPDHEWKAIVTVORPGKIPASSRCGNTVPPDDNQVLSLPGS 661  
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Db 662 RYVLPVPCVEKGYNYVRLPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGS 721  
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Db 722 GGVVNTNAGWTFYRCLNSRSVVKTPMTDVCNRIIFSIHALIHTGLACEDPOGSL 781  
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Db 902 YGDPILIGSDHCRPCPCPDGSDGRFARSQYQDPVTLQACVCDPGYIGSRDDCASG 961  
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QY 1081 PQCDQSTGQCVGVEGPRCDKTRGVSGVPPDCTPCHQCFALWDIAIIGELTNRHFL 1140  
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QY 1381 QKAMPDRDVLGALAEVEOLSKMWSEAKVRADEAKQNAQDVLTKNATKEKVKDSNEDLR 1440  
Db 1442 QKAMPDRDVLGALAEVEOLSKMWSEAKVRADEAKQNAQDVLTKNATKEKVKDSNEDLR 1501  
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Db 1682 SAEDVKKTLGDELDEKFKKVESLIAQKTEESADARRKAEKLLQNEAKTLLAQNASKLQLE 1741  
QY 1681 DLKRYKEDNQKYLEDKAQBLVLEGEVRSLLKXDISKQVAVYSTCL 1725

Db 1742 DLKRYKEDNQKYLEDKAQBLVLEGEVRSLLKXDISKQVAVYSTCL 1786  
RESULT 9  
US-09-561-709B-9  
; Sequence 9, Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-9  
Query Match 94.1%; Score 8873; DB 4; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIYVSHLOEDKKKICDSDRDPYHETLAPDLSHLINNVTTAPAPLKLKMWQSENGENV 60  
Db 62 EPYCIYVSHLOEDKKKICDSDRDPYHETLAPDLSHLINNVTTAPAPLKLKMWQSENGENV 121  
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Db 122 TIOLDLEAEHPFHLLMTFKTPAPAMLIERSDDFKTGWVYRYFAYDCESSPFGISTGP 181  
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QY 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETCYCYC 420  
Db 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETCYCYC 481  
QY 421 KRLVTGQRCCQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSDSCQCSCLPMIGROCN 480  
Db 482 KRLVTGQRCCQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSDSCQCSCLPMIGROCN 541  
QY 481 EVESGYFTTLDHYIYEABEANLPGVWVVEROYIODRIPSWTGPQFVRVPEGAYLEFFI 540  
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QY 601 RYVLPREVCEKGMNYTVRLEFQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGGS 660  
Db 662 RYVLPREVCEKGMNYTVRLEFQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGGS 721  
QY 661 GGEVTSNAMESFORCLENRSVWVTPMTDVCNIIIFISALIHOTGLACEDPQGL 720  
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QY 781 CFQGYARCCDRCLPGYMGFPSCOPCCNGHALDCTVTCGLSCODYTTHGNCERCLAG 840  
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Db 902 YGDPPIIGSDHCRPCPCPDGPDGSRQPARSCYQDPVTLQACVCPGYIGSRCDCCASG 961  
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Db 1322 TKYFQMSLEAKRVNASTPNSVQSAITRVEDLMLERSPKQEQEBOARLLDEL 1381  
QY 1321 AGKLQSLDLSAAQMTGTPPGADCSSECGPNKRTDEGERKCGGPGCGGLVTVHAWSA 1380  
Db 1382 AGKLQSLDLSAAQMTGTPPGADCSSECGPNKRTDEGERKCGGPGCGGLVTVHAWSA 1441  
QY 1381 QKAMDFFDVLALAEVQISQWVSEAKVRADEAKONADVLKTNATKEKYDKSNEDLR 1440  
Db 1442 QKAMDFFDVLALAEVQISQWVSEAKVRADEAKONADVLKTNATKEKYDKSNEDLR 1501  
QY 1441 NLKIQIRNFLTQDSADLSIEAVANEVYKSGNASTPQOLQNLTPEDIRERVELTSQVEVIL 1500  
Db 1502 NLKIQIRNFLTQDSADLSIEAVANEVYKSGNASTPQOLQNLTPEDIRERVELTSQVEVIL 1561  
QY 1501 QCSAADTARABELLEAKRASKATDVKTADVMKEALEAEKAAVAAEKAKQADEIDQ 1560  
Db 1562 QCSAADTARABELLEAKRASKATDVKTADVMKEALEAEKAAVAAEKAKQADEIDQ 1621  
QY 1561 QTONLLTSISETAASSETLTNASQRIKSLERNVEELKRAAQNQSGEAYIEKVVYVVKQ 1620  
Db 1622 QTONLLTSISETAASSETLTNASQRIKSLERNVEELKRAAQNQSGEAYIEKVVYVVKQ 1681  
QY 1621 NADVKKTLQDELDEKVKYVESLQAKTESADARAKAELLQNEAKTLAQAQNSKLOLLE 1680  
Db 1682 NADVKKTLQDELDEKVKYVESLQAKTESADARAKAELLQNEAKTLAQAQNSKLOLLE 1741  
QY 1681 DLERKYEDNQYLEDKQAELVRUEGEVRSLLDKISQKAVAVYSTCL 1725

Db 1742 DLERKYEDNQYLEDKQAELVRUEGEVRSLLDKISQKAVAVYSTCL 1786  
RESULT 10  
US-08-144-121-4  
; Sequence 4, Application US/08144121  
; Patent No. 5610031  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagnan, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/144,121  
; FILING DATE: 27-Oct-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 1..250  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 251..437  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 438..807  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 808..840  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 841..1196  
US-08-144-121-4

Query Match 58.2%; Score 5489; DB 1; Length 1196;  
Best Local Similarity 82.4%; Pred. No. 3.6e-316;  
Matches 1077; Conservative 46; Mismatches 32; Indels 570; Gaps 1;  
QY 1 EPYCVSHLQEDKKCFICSDRDPYHETLNPDSGLHLENVVTTFAPNRLKIWQSENGVENY 60  
Db 42 EPYCVSHLQEDKKCFICSDRDPYHETLNPDSGLHLENVVTTFAPNRLKIWQSENGVENY 101  
QY 61 TIQDLAEAFHFLHMTKTFPRAMLIERSDGGKTVGVYRYPAYDCESSFPGISGTP 120  
Db 102 TIQDLAEAFHFLHMTKTFPRAMLIERSDGGKTVGVYRYPAYDCESSFPGISGTP 161  
QY 121 MKKVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRTKFKVLH 180

162 MKKYDDIICDSRYSDIPESTGEVIFRALDPAFKIEDPYSPRIQNLKJINLRIKFKVLH 221  
181 TLGNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVDGVNVEEVMGHQCMCR 240  
222 TLGNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVDGVNVEEVMGHQCMCR 281  
241 HNTKGLNCELCHDFYHDLFWPAPAGRSNACKKCNCHSHSSCHFDMAVFLATGNVSGV 300  
282 HNTKGLNCELCHDFYHDLFWPAPAGRSNACKKCNCHSHSSCHFDMAVFLATGNVSGV 341  
301 CDNCOHNTMGNCCECKPFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
342 CDDCOHNTMGNCCECKPFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 401  
361 IAGQCRCKLHVEGRCDCVKCGFYDLSDAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 420  
402 IAGQCRCKLHVEGRCDCVKCGFYDLSDAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 437  
421 KRLVTGQRCDQCLPQHGLSNDLDCRDCDCLGGLNNSCEDSGGSCCLPHMIGRQCN 480  
438 ----- 437  
481 EVESGYFTTLDHYIYEAEBANLGPVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 540  
438 ----- 437  
541 DNIPIYSMEVEILLRIYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDQNVVLSLSPGS 600  
438 ----- 437  
601 RYVWLPFPVCFEKGMYTVRLPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGGS 660  
438 ----- 437  
661 GDGEVTSNWEYFQRYRCLNSRSVVKTPMTDVCNRIIFSALIHQTLGACEDPQGLS 720  
438 ----- 437  
721 SSVCDPBGQCCQCPNVVVRTNCRCAPGTGFGPGRKPCDCHLQGSASAFDAITGOCH 780  
438 ----- 437  
781 CFQGIYARQDRCLPQYWGFPSCQPCQNGHALDCDVTYGECLSCQDYTTGHCNCRCLAG 840  
438 ----- 437  
841 YYGDPITIGSGDHCRPCPCPDGSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG 900  
438 ----- 437  
901 FFGNPSDFGSGCQPCQCHNIDTDPDCAKDTGRCLKLYTEGDHQCQLCOGYGYGDAL 960  
438 ----- 437  
961 RQDRCKVCNLYGTVKEHNGSDCHCDKATGOCCLPNVIGQNCRCAPNTWOLASGTGC 1020  
438 -----CVNLYGTVKEHNGSDCHCDKATGOCCLPNVIGQNCRCAPNTWOLASGTGC 491  
1021 GPCNCAHSGFSCNEFTGQCCQMPFGGRTCSCEQELFWGDPDVECRACDPRGIET 1080  
492 DPCNCAHSGFSCNEFTGQCCQMPFGGRTCSCEQELFWGDPDVECRACDPRGIET 551  
1081 PQCDQSTGQCVGVEGRCDCYKGYSGVFPDCTPCHQCFALMDAIIIGELTNRTHKFL 1140  
552 PQCDQSTGQCVGVEGRCDCYKGYSGVFPDCTPCHQCFALMDAIIIGELTNRTHKFL 611  
1141 EKAKALKISGIVGYRETVDSEKKNYKNDILIAQSPAAPLKNIGILFEEAEKLTQDVT 1200  
612 EKAKALKISGIVGYRETVDSEKKNYKNDILIAQSPAAPLKNIGILFEEAEKLTQDVT 671  
1201 EKAAQVEVKLTDTASQSNSTAGELGALQAEASLDKTYKELAEOLFKNQSDIQALDSI 1260

672 ENMAQVEVKLSDTTSQSNSTAKELDSLQTEASLNTVKELAEOLFKNQSDIQALDSI 731  
1261 TKYFQMSLEAEKRVNASTTDPNSTVEQALTRDRVEDLMLERESPFKEQOEQARLLDEL 1320  
732 TKYFQMSLEAEKRVNASTTDPNSTVEQALTRDRVEDLMLERESPFKEQOEQARLLDEL 791  
1321 AGKLSLDLSAAQMTCTGPPGADCSSECCGPNCRTEGEKXKCGPGCGGLVTVHNSAW 1380  
792 AGKLSLDLSAAQMTCTGPPGADCSSECCGPNCRTEGEKXKCGPGCGGLVTVHNSAW 851  
1381 OKAMPDROVLGALAEVOLSXWVSEAKVRADEAKQADQVLLKTNATKEKVDKSNEDLR 1440  
852 OKAMPDROVLGALAEVOLSXWVSEAKVRADEAKQADQVLLKTNATKEKVDKSNEDLR 911  
1441 NLTKOIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLONTEDIRERVELTSQVEVIL 1500  
912 NLTKOIRNFLTSDSADLDSIEAVANEVLKSGNASTPQOLONTEDIRERVELTSQVEVIL 971  
1501 QOSAAIDIAEAILLEBAKASKATDVKTADWKEALEEAEKAAQVAAEKAIKQADEDIQ 1560  
972 QOSAAIDIAEAILLEBAKASKATDVKTADWKEALEEAEKAAQVAAEKAIKQADEDIQ 1031  
1561 GTQNLITSIETASAEETLTNASQRISEKLERNEVELKEKAAQNSGEAEYIEKVYVSVKQ 1620  
1032 GTQNLITSIETASAEETLTNASQRISEKLERNEVELKEKAAQNSGEAEYIEKVYVSVKQ 1091  
1621 NADVVKTLTGELDEKIKVKSIAQKTESADARKEALLQNEAKTLAQANSKLQLE 1680  
1092 SAEDVVKTLTGELDEKIKVKSIAQKTESADARKEALLQNEAKTLAQANSKLQLE 1151  
1681 DLSEKVEDKQYLEDKAEQELVRLGEVRSLLKQISEKVAIVYSTCL 1725  
1152 DLSEKVEDKQYLEDKAEQELVRLGEVRSLLKQISEKVAIVYSTCL 1196

RESULT 11  
US-08-735-893-4  
; Sequence 4, Application US/08735893  
; Patent No. 5914317  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagon, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/735,893  
; FILING DATE: 18-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/144,121  
; FILING DATE: 27-OCT-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: (MCH-0780.1) MGP-021DV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1196 amino acids	
; TYPE: amino acid	
; TOPOLOGY: linear	
; MOLECULE TYPE: peptide	
; FRAGMENT TYPE: internal	
; FEATURE:	
; NAME/KEY: Domain	
; LOCATION: 1..250	
; FEATURE:	
; NAME/KEY: Domain	
; LOCATION: 251..437	
; FEATURE:	
; NAME/KEY: Domain	
; LOCATION: 438..807	
; FEATURE:	
; NAME/KEY: Domain	
; LOCATION: 808..840	
; FEATURE:	
; NAME/KEY: Domain	
; LOCATION: 841..1196	
; US-08-735-893-4	
Query Match	
Best Local Similarity 58.2%; Score 5489; DB 2; Length 1196;	
Matches 1077; Conservative 46; Mismatches 32; Indels 570; Gaps 1;	
Qy	1 EPYCVSHLQEDKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 60
Db	42 EPYCVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 101
Qy	61 TLQDLEAFHFTLIMFKFPRPAALIERSSDFGTWGVYFYAYDCSSPFGISTGP 120
Db	102 TLQDLEAFHFTLIMFKFPRPAALIERSSDFGTWGVYFYAYDCSSPFGISTGP 161
Qy	121 MKKVDIIICDSYSIEPSTGEVIFRALDPFKIEDPYSPRIQNLKITNLKIFVKLH 180
Db	162 MKKVDIIICDSYSIEPSTGEVIFRALDPFKIEDPYSPRIQNLKITNLKIFVKLH 221
Qy	181 TLGDNLLSRMEIRKYYAYVDMVVRGNCFCYGHASECAPVDGVEEVEGVMVGHCMCR 240
Db	222 TLGDNLLSRMEIRKYYAYVDMVVRGNCFCYGHASECAPVDGVEEVEGVMVGHCMCR 281
Qy	241 HNTKGLNCELMDFYHDLFWRPAEGRNSNAKCKNCNEHSSCHFDMAVFLATGNVSGGV 300
Db	282 HNTKGLNCELMDFYHDLFWRPAEGRNSNAKCKNCNEHSSCHFDMAVFLATGNVSGGV 341
Qy	301 CNCOHNTMGRNCECKEFPYQHPRDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 360
Db	342 CDDCOHNTMGRNCECKEFPYQHPRDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 401
Qy	361 IAGQCRCKLHVEGERCDVCKEFGYDLSABDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420
Db	402 IAGQCRCKLHVEGERCDVCKEFGYDLSABDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 437
Qy	421 KELVTGQRCDQCLPQHWGLSNDLDGCRPCDPCDGLGALNNSCSBDSGQCSCLPHMIGRCQN 480
Db	438 ----- 437
Qy	481 EVESGYFTTLDHYIYEAERANLPGVVVVERQYIQRIPSWTGPQFVRVPEGAYLEPFI 540
Db	438 ----- 437
Qy	541 DNI PYSMEVEIILRYEPQLPDHWEKAVITVQPGKI PASSRCNGTVPDDNQVVSLSPGS 600
Db	438 ----- 437
Qy	601 RYVILPRVCFEKGMMYTRLELPQYTAGSDVESPYTFDLSVLMPYCKSLDIFTVGS 660
Db	438 ----- 437
Qy	661 GDGEVTSNAWETFFQRYRCLENSRVVKTPTMTDVCNIIIPISALIHQTGLACECDPQGS 720
Db	438 ----- 437

RESULT 12  
US-05-845-583A-6  
; Sequence 6, Application US/09845583A

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; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-845-583A-6

Query Match      52.1%; Score 4914; DB 4; Length 1799;
Best Local Similarity 51.0%; Pred. No. 5.7e-282;
Matches 883; Conservative 297; Mismatches 534; Indels 18; Gaps 8;

QY 1 EPCYVSHLQEDKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60
DB 77 QPCYVSHLQDEKKCFICSDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 136
QY 61 TIQLDLEAEFHTLIMTFTKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPDITGP 120
DB 137 TIQLDLEAEFHTLIMTFTKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPDITGP 196
QY 121 MKKYVDIIICDSRYSDIEPTSTGEVIFRALDPFKIEDPVSRIQNLKLTIRIKFKLH 180
DB 197 PRRWDDVCESRYSETEPTEGEVIRVLDPAIPDPYSSRIQNLKLTIRIKFKLH 256
QY 181 TLGDNLDSRMETIREKYYAVDMVVRGNCFCYGHASCAPVDGVNEEVGVMVGHCMCR 240
DB 257 TLGDNLDPREIREKYYALVELVIRGNCFCYGHASCAPAPAPAHAEVGMVGHACICK 316
QY 241 HNTKGLNCLCWDYHDLRPAEAGNSNACKKCNHSSCHFDMAVFLATGNVSGV 300
DB 317 HNTKGLNCEQCCDYQDLRPAEAGNSNACKKCNHSSCHFDMAVFLATGNVSGV 376
QY 301 CNDQNTMGRNCEQCKPFFVQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360
DB 377 CDGQNTAGHCFEFCFPFYRDPFKMDRDPVACRCPDCDPMGSDGGRCDSHDDPVLGL 436
QY 361 IAGQCRKLHVEGERCDVCKGEPYDLSABDPYGCCKSCANPLGTTIPGMPNCDSETGYCYC 420
DB 437 VSGQCRKEHVTRCQCRDGFGLSASDPGRQCQCNSRGTVPGSSPCDSSSGTCFC 496
QY 421 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSCQCSCLPHMIGROCN 480
DB 497 KRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSCQCSCLPHMIGROCN 556
QY 481 EVESGYFTLLDHYIYAEANLPGVWVVRQYIQDRIPSWTGPVVRVPGVYLEPFI 540
DB 557 QVQGPVFRPFLDLTWEAAQ-QGVLEVVVRVLTNRTPSWTGPVVRVPGVYLEPFI 615
QY 541 DNTPYMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCNTVDDDDNQVSLSPGS 600
DB 616 TSLPRAMVDLLLRWEPQPEQWAELELMVQRPVPSAHSPGHVLPKDDRIQGMHFNPT 675
QY 601 RYVVLPRPVCFEKGMNYYRLELPQYTAGSDVESPYT--FIDSLVLMPYCKSLDIFTVG 658
DB 676 RVLVFRPVCLEPGISKYKLLIG-TGGRAPQETSYSGLLIDSLVLQPHVLVLEMF--- 731
QY 659 GSGGGEVTSNWTFRYRCLENSRSVVKPTMTDVCNIIFISALIHQTGLACEDCPG 718
DB 732 -SGGDAALERRTTFERYCHEGLMPSKAPLSETCAPLISVSALYINGALPCQCDPG 790
QY 719 SLSSVCDPNGGQCRPNVVRGTCNRCAPGTGFGPNCCKPCDCHLQGSASFCAITGQ 778

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791 SLSSVCDPNGGQCRPNVVRGTCNRCAPGTGFGPNCCKPCDCHLQGSASFCAITGQ 850
QY 779 CMCFQGIYARQCDRCLPGFWGPPSPQPCQCNHGLDCTVTGECILSCDYTTGHCNCRCL 838
DB 851 CPCRPGAFGLRCDHCQCGQWGFPCPCVNCNRADECDDTHTCACGLCRDRTYTGECERC 910
QY 839 AGYVGDPIIGSDHCRPCPCPDGPDGROFARFSCVQDPVTQLACVCDPGY:GSRCDCCA 898
DB 911 AGPHGDFRLPYGGQCRPCPCPDGPDGROFARFSCVQDPVTQLACVCDPGY:GSRCDCCA 970
QY 899 SGFFGNPDSFGGSCQPCQCHNIDTTPACDKGTGRCLKLYHTGEGHDCQLCQYGYGDD 958
DB 971 PGFFGDPSPKPGRCQCEGSDNIDPMDACDPHTGQCLRLCHNTEGPHGCGYCKPGFHQ 1030
QY 959 ALRQDCEKVCNVLTGVKHEHNGSD--CHCDKATGQSCCLPNVIGONCDRCAPNTWLQSG 1017
DB 1031 AARQSCHRCTCNLLGTDPKRCPSDTLCHCDPSTGQCPCLPHVQGLNCDRCAPNTWLQSG 1090
QY 1018 TGGCPNCNAAHSGPSCNEFTQCCQCMFPGGRTCTSECQELFWGDDPYVECRACDDPRG 1077
DB 1091 RGQPCACHPSRARGTCTNEFTQCHAGFGGRTCTSECQELFWGDDPYVECRACDDPRG 1150
QY 1078 IETPQDQSTGQCVGVEGPRCDKCTRGYSVFPDCTPCHQCFALMDALIGELNTRH 1137
DB 1151 IDKPCQCHRSTGCHGCRPGVSGVRCQCARFGSPFACHPCHACFGDWRVVDLAAATR 1210
QY 1138 KFLKAKALKISGVIGYRETVDSEKVNIEIKDILA--QSPAAEPLKNIIGILFEEAEKL 1195
DB 1211 RLQWAGELQOTGVLGAFSSFLNMQGKLGWQAIMSARNASASTAK---LVEATEGL 1266
QY 1196 TKDV---TERQAQVEVKLTDTASQSNSTAGELCALQAEESLDKTKVELABOEFTKNSD 1252
DB 1267 RHEIGTKTERLTQLEAELTAQDENFNANHALSGLERDGFALNLTLRQLDQHLILKHN 1326
QY 1253 IQGNALDSITKYFQMSLEAEKVNASTTDPNSTVQESALTRDVEDLMLERSEPFKEQOE 1312
DB 1327 FLGAYDSIRHAHQSTEAERANASTAVPSPVNSADTRRTEVLGMQAKENFNQHLA 1386
QY 1313 QARLLDELAKGLSLDLSAAQMTCTGTPGADCSSECCGPNCRDTEGEKKCGGPGCGGL 1372
DB 1387 NQALGRLSAFAHTLSLTGINELVCGAPGAPCATSPCGGAGCRDEDDGQPRCGGLCSGA 1446
QY 1373 VTVHSAWQAMPDFDRDVLASAEVEQLSKWSEAKVRADKQNAQDVLKTNATKEV 1432
DB 1447 AAPADLALGRHSQAELOALVEGGILSRVSETRRQAEAAQQAQALDKANASRGV 1506
QY 1433 DKSNEDELNIKOTRNLFTSDSADLSIEAVANEVLKSGNASTPQQLNLTDIRERVET 1492
DB 1507 EQANQELRELIQNVKDFLSQEGADPDSIENVAIRVLDISIPASPEQIQLASEIAEVRS 1566
QY 1493 LSQVEVILQSAADIAEALLLEAKKASATDKVTADMVKEALEEAEKAAQVAAEKAI 1552
DB 1567 LADVDTILAHMTGDRRAEQLLQDAHRAERAEGERQKAEVQAALEEAQQAQAGAI 1626
QY 1553 KQADEIQGTQNLITSTESETAASEETLTNASORISKLRNVBELKKAQNSGEAEYIE 1612
DB 1627 RGAVVDQNTQETLQVQERMAKESLNSAGEARQLDALLEALKLRAGNSLAASTAE 1686
QY 1613 KVVYSVQKQADDDVKTLQDGLDEKIKVBSLIIAQKTESADARKKALLONEAKTLLAQ 1672
DB 1687 ETAGSAQSRAREAEKQLEQVQGVQTVRALAEKAEGLVLAQARAEQLEARDLQAA 1746
QY 1673 NSKLQLEDLERYKVEDKQLEDAKQLEVLGEGVRSLLDKDISEKVAVYGTG 1724
DB 1747 QCKLQRLQLEEGTYEENRERALEGKAAQDGLGAEARMSVLAQINLOVQIYNTC 1798

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RESULT 13  
 US-09-561-709B-11  
 ; Sequence 11, Application US/09561709B  
 ; Patent No. 6682311  
 ; GENERAL INFORMATION:

APPLICANT: Burgeson, Robert  
APPLICANT: Champlaud, Marie-France  
APPLICANT: Olson, Pamela  
APPLICANT: Koch, Manuel  
APPLICANT: Brunken, William  
TITLE OF INVENTION: LAMININS AND USES THEREOF  
FILE REFERENCE: 10287-060001  
CURRENT APPLICATION NUMBER: US 09/561,709B  
CURRENT FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 09/168,949  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: US 60/061,609  
PRIOR FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 1798  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-561-709B-11

Query Match 50.7%; Score 4783; DB 4; Length 1798;  
Best Local Similarity 49.7%; Pred. No. 3.2e-274;  
Matches 860; Conservative 301; Mismatches 557; Indels 12; Gaps 6;

QY 1 EPYCVSHLQEDKKCFICSDRDPYHETLNPDLPAFKIEDPYSPIQNLKITNIRIKFKVLH 180  
DB 74 QPYCVSHLQEDKKCFICSDRDPYHETLNPDLPAFKIEDPYSPIQNLKITNIRIKFKVLH 133  
QY 61 TIQDLEAEFHFHLLIMTKTRPAAMLIERSDDPGKTGWVRYRAYDCESFPISITGP 120  
DB 134 TIQDLEAEFHFHLLIMTKTRPAAMLIERSDDPGKTGWVRYRAYDCESFPISITGP 193  
QY 121 MKKVDIIICDSRYSDIEPSTEGSVIFRALDPAFKIEDPYSPIQNLKITNIRIKFKVLH 180  
DB 194 PRWDDVVCESRSELEPSTEGSVIFRYVLDPAIPDPYSSRIQNLKITNIRIKFKVLH 253  
QY 181 TLGDNLLDSRMEIRKYYAVYDMVYRGNCFYGHASECAPVDGVNVEEVEGWHGHCWCR 240  
DB 254 TLGDNLLDPRREIRKYYALVELVYRGNCFYGHASECAPAPAGAPAHAGMVGACICK 313  
QY 241 HNTKGLNCLCNDPFDHLPWPAEGNSNACKNCNEHSSCHFDPMVFLATGNVSGV 300  
DB 314 HNTKGLNCEOCQDFYRDLWPAEDDGHSHACRCKDRHGHTHSCHFDPMVFLGSGVSGV 373  
QY 301 CDNCQHTMGRNCEQCKPFYQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 374 CDGQCHNTAVHCELCPFFYRDPDKLDPACVCRSCDCDPMQSDGGRCDSDHDDPALGL 433  
QY 361 IACQCKLHVEGRCDCVCKEYDLSAEDPYGCKSCACNPLGTIPGPNPCDSEYCYC 420  
DB 434 VSGQCKRKHVGTQCCQCRDGFGLSISDPSCRCQCQCNARGTVPGSTPCDPNPGSCYC 493  
QY 421 KRLVTGRCQCLPQHWGLSNDLDGRCPCDCDILGALNNSCSDSCQCSCLPHMIGRCN 480  
DB 494 KRLVTGRCQCLPQHWGLSNDLDGRCPCDCDVGGLDPCQDEGTQCHCRQHWGRRCE 553  
QY 481 EVSSGYFTLLDHYIYEAEENLPGVWVVERGYIQDRIPSTWGTGPFVVPAGVLEPPI 540  
DB 554 QVQPGYFRPFLDLHWEAENR-GQVLDVVERLVTPGETPSTWGTGPFVVPAGVLEPPI 612  
QY 541 DNIYPNVEYILIRYBPQDPHEKAVITVORPGKIPASSRCQNTVPDDNQVVSLSPGS 600  
DB 613 ASVFNAMVDLLRLRLEPQVQWAELELIVORPGVPAHSLGHLVPRDDRIGQTLQPHA 672  
QY 601 RYVLPFVCFEKGMYNTVALELPQVYTAGSDVESPYT----FIDSLVMPYCKSLDIPT 656  
DB 673 RYLIFPNVCLPGLISYKHLKLV-TGSAQAPETPYSGPGLLIDSLVLLPRVLEMP- 730  
QY 657 VGSQGDGEVNTSANEWQRYRCLNSRSVVKPTMTDVCNIIIFSISALIHOTGLACECDP 716  
DB 731 ---SGDAAALERQATERYCCEGLVPSKTSFSEACAPLLISLTLYNGALPCQCP 787

RESULT 14

US-09-583A-8

; Sequence 8, Application US/09845583A

; Patent No. 6635616

QY 717 QGSLSSVCDPNGGQCCOCRRNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFDAIT 776  
DB 788 QGSLSSCNPHGQCCCKCKPGVVRRCCTCAPGYIGFGPTGQCCQCSQPRGALSSLCERTS 847  
QY 777 GQCHCFQGIYARQCDRLPGYMGFPSCQPCQCCNGHALDCDVTGECLSQDYTTGNCR 836  
DB 848 GQCLCRGTGAFGLRCDACQCGWGFPCRCPCVNCNGHADCNTHTGACLCGRDHTGGSHCR 907  
QY 837 CLAGYVDDPIIGSDHCRPCPCPDGSDGQRFARSQVDPVTLQALACVCDPGYIGSRCD 896  
DB 908 CIAGFHGDPRLPYGAQCRPCPCPEGPGSRHFATSCHQDEYSQOIYVCHCRAGTGLRCEA 967  
QY 897 CASGFFGNPSDFGSCQPCQCHHNIITDPEACDKDTGRCLKCLYHTEGDHCOLCYGY 956  
DB 968 CAPQFGDPSRPGRCQLCECSGNIDPMDPADCPHFGQCLRCLHTEGPHCAHSPGPH 1027  
QY 957 GDALRQDCKRCVNYLGTVEHNGSD-CHCDXATGQCSCLPNVIGQCDRCAPNTWQLA 1015  
DB 1028 GQAAQSCHECTCNLLGTNPQCPSPDQCHDPSGQCCPLPNVQALAVDRCAPNFWLT 1087  
QY 1016 SGTGCGPCNCAHSPGSCNEFTGQCCQMPGFGGRTCSQELFWGDPDVECRACDCDP 1075  
DB 1088 SHGQCFACLPSPESGPTCNFTGQCHCLCGFGGRTCSQELHMGDPGLQCHACDCDS 1147  
QY 1076 RGIETPCDOSTGQCVVEGVEGPRCDKTRGVSGVFPDCTPCHQCFALWDALIGILTNR 1135  
DB 1148 RGIETPCHEFTGCTCRPGVSGVRCDQARGSGIFPACHPCFACGMDWRVVDLAAR 1207  
QY 1136 THKFLKAKALKTSVIGPYRETVDSEKKNVBIKDIL-AQSPAABFLKNIGILFBEAEK 1194  
DB 1208 TORLEQRAQLQOTGVLAGFESSFWHQEKLGIQVIGARNTSAASTAQLVEATEELRR 1267  
QY 1195 LTKDVTKMAQVEVKLTDTASQNSNAGELGALQAEBSLDTVKELALQLEFIKNSDIQ 1254  
DB 1268 EIGATEHLTQLEADLTVDQDENFNANHALSGLERDLALNLTQLDQHLDLKHSNFL 1327  
QY 1255 GALSITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLERSPPKEQBEQA 1314  
DB 1328 GAYDSIRHANSQAEABERRANTSALAVSPVSNASARHRTALMDAQKEDFNSKMANQ 1387  
QY 1315 RLDELAKGLQSLDSAAAQMTCTPPGADCSBECGGPNCRITDEGKCKGCGGCGGLVT 1374  
DB 1388 RALGKLSAHTHTLSLTDINELVCGAQLHHDRTSPCGGAGCRDEGQPCGGSLSCNGAA 1447  
QY 1375 VAHSANQKAMDPRDVLALAEVQLSKMYSEAKVADEAKONAQDVLLKTNATKEKVKD 1434  
DB 1448 TADLALGRARHTQAEIQRALAEGLSILSRVAETRRQASEAQQAALDKANASRGVEQ 1507  
QY 1435 SNEDRLRIKQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEIDIRVETLS 1494  
DB 1508 ANQELQELIQSVKDFLNQEGADPDSIEMVATRVLELSIPASAEQIOHLAIAERVSLA 1567  
QY 1495 QVEVILQGSAAADTARABELLIEAEKASKSATDVKTADVMYKEALEAEKAAQVAAEKIKQ 1554  
DB 1568 DVDAILARTVGDVRRARQLQDARRARSWAEDSKQAEVQAALEAEQRAQQAQOAGIRG 1627  
QY 1555 ADEDIQGTQNLITSESETAASBETLTNASQRISKLEENVEELKRAAQNSEAEYIEKY 1614  
DB 1628 AVATRTTEQTLVQVQEMAGAEALSSAGERARQLDALLEALKLKAGNSLAASAEET 1687  
QY 1615 VYSVKQADDVKTLTDELDEKVKVBSLIAQKTESADARRKELLONEAKTLLQAANS 1674  
DB 1688 AGSAQGAQAEQALRGLPGDQVTVKALAEKAAQGVLAQAARABLPDDEARDLQAQD 1747  
QY 1675 KLOLLEDLERVEDNOKYLEDKAEQELVLEGEVRSLKDKISEKAVYSTC 1724  
DB 1748 KLOLLELEGTIYENEARLSKAAQLDGLAEWRSLVQAINLQVINYTC 1797

GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert  
APPLICANT: Brunken, William Joseph  
APPLICANT: Champlaud, Marie-France  
APPLICANT: Hunter, Dale  
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
FILE REFERENCE: 10287-056001  
CURRENT APPLICATION NUMBER: US/09/845,583A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/200,863  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 1798  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-845-583A-8

Query Match 50.7%; Score 4778; DB 4; Length 1798;  
Best Local Similarity 49.7%; Pred. No. 6.2e-274;  
Matches 859; Conservative 301; Mismatches 558; Indels 12; Gaps 6;

QY 1 EYCVTVSHLODKKFCICDRDPYHETLNPDSHLLIENVVTFAPNRLKIWQSENGVENV 60  
DB 74 QPYCIVSHLODKKFCICDRDPYHETLNPDSHLLIENVVTFAPNRLKIWQSENGVENV 133  
QY 61 TIQLDLAEAFHETHLIMTEKTPPAAMLIERSDFGKTGWVYRYPAYDCESFPGISGTP 120  
DB 134 TIQLDLAEAFHETHLIMTEKTPPAAMLIERSDFGKTGWVYRYPAYDCESFPGISGTP 193  
QY 121 MKKVDIIDCYSYDIETPSTEGEVIFRALDPAFKIEDPYSPRIQNLKILNIRKFKVLH 180  
DB 194 PRHWDVVCESYSEIETPSTEGEVIFRALDPAFKIEDPYSPRIQNLKILNIRKFKVLH 253  
QY 181 TLGDNLDSREIREKYVAVYVDMVVRGNCFCYGHASECAPVDGVNEEVGVHGHCMCR 240  
DB 254 TLGDNLDSREIREKYVAVYVDMVVRGNCFCYGHASECAPVDGVNEEVGVHGHCMCR 313  
QY 241 HNTKGLNCLCMDFYHDLRPAEGRNSNACKKCNNEHSSCHPDMVAVLATNVSGGV 300  
DB 314 HNTKGLNCLCMDFYHDLRPAEGRNSNACKKCNNEHSSCHPDMVAVLATNVSGGV 373  
QY 301 CNQCQNTWGRNCEQCKPYFOHPPERDIDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
DB 374 CNQCQNTWGRNCEQCKPYFOHPPERDIDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 433  
QY 361 IAGQCRCKLHVEGERCDVCEGFDYLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 420  
DB 434 VSGQCRCKLHVEGERCDVCEGFDYLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCYC 493  
QY 421 KRLVTGQRCDQCLPQHWGLSNLDGCRPCDDCGALNNSCEDSGQSCULPHMITGRCN 480  
DB 494 KRLVTGQRCDQCLPQHWGLSNLDGCRPCDDCGALNNSCEDSGQSCULPHMITGRCN 553  
QY 481 EYESGYFTTLDHYIEAEANLPGVWVVERQYIQRIPSWTGPFGVVRPEGALIEFFI 540  
DB 554 QVQPGYFRFLOHLIWEAENR-GQVLDVVERLVTGPTSPWTSQGFVRLQEGQTLFVLV 612  
QY 541 DNIPIYMEYELLIRVEPQPDHWEKAVITVQRPKIPASSRCNVTVPDDNQVLSLSPGS 600  
DB 613 ASVPNAMYDILLRLLEPQVPEQWAELELIVRPGVPAHSLGCHLVPDRDRIRQGTLPQHA 672  
QY 601 RYVVLPRPVCFEKGMNVTYRLELPOYTAGSDVVEGSPYT---FIDSLVMPYCKSLDIFT 656  
DB 673 RYVVLPRPVCFEKGMNVTYRLELPOYTAGSDVVEGSPYT---FIDSLVMPYCKSLDIFT 730  
QY 657 VGGSGDGEVNTSAWETPQRYRCLNRSRVVTPMTDVCNRIIFSALIHOTGLACEDCP 716  
DB 731 ---SGGDAALERQATFERYQCHEEGLVPSKTSPEACAPLLISLSTLYNGALPCQNP 787  
QY 717 QGSLSVCDPNGCOCRCRNVVTRCNRCAPGTFFGPNCKPCDCHLQGSASAFCDAIT 776

DB 788 QGSLSVCDPNGCOCRCRNVVTRCNRCAPGTFFGPNCKPCDCHLQGSASAFCDAIT 847  
QY 777 GOCHCFQGIYAROCDFCLPGYWGFPSCPCQCNHGLDCDVTGECSCQDVVTGHCNCR 836  
DB 848 GOCHCFQGIYAROCDFCLPGYWGFPSCPCQCNHGLDCDVTGECSCQDVVTGHCNCR 907  
QY 837 CLAGYVYGDPIIGSDHRCRCPDPCDPSGRQRFARSQYQDPVTLQLACVCDPGVIGRCD 896  
DB 908 CLAGYVYGDPIIGSDHRCRCPDPCDPSGRQRFARSQYQDPVTLQLACVCDPGVIGRCD 967  
QY 897 CASGFTGNPSDFGSCPCQPCQCHNNTTTPPEACDXTGRCLKCLVHTEGHDHCLQCYGVY 956  
DB 968 CASGFTGNPSDFGSCPCQPCQCHNNTTTPPEACDXTGRCLKCLVHTEGHDHCLQCYGVY 1027  
QY 957 GDALRQDCRKCVCNLTGTVKEHCNGSD-CHCKATQCCSCPLNVIQNCDCRCAPTWOLA 1015  
DB 1028 GDALRQDCRKCVCNLTGTVKEHCNGSD-CHCKATQCCSCPLNVIQNCDCRCAPTWOLA 1087  
QY 1016 SGTGCGPCNCAHSPGSCNFTGOCQWPGFGGRTCECQELFWGDDPVECAACDCP 1075  
DB 1088 SGTGCGPCNCAHSPGSCNFTGOCQWPGFGGRTCECQELFWGDDPVECAACDCP 1147  
QY 1076 RGITETPOCQDQSTQCVCVEGVEGPRCDKTRGVSGVFPDCTPCHQCFALWDAIIGLTNR 1135  
DB 1148 RGITETPOCQDQSTQCVCVEGVEGPRCDKTRGVSGVFPDCTPCHQCFALWDAIIGLTNR 1207  
QY 1136 THKPLEKAKALKITSGVIGPYRETVDVSEKKNVIEKIL-AQSPAAEPKNIIGILFEAEK 1194  
DB 1208 THKPLEKAKALKITSGVIGPYRETVDVSEKKNVIEKIL-AQSPAAEPKNIIGILFEAEK 1267  
QY 1195 LTKDVTKEAQAQVVKLTDTASQSNSTAGELGAQAEISLDKTVKLAQLEFIKNSDIQ 1254  
DB 1268 LTKDVTKEAQAQVVKLTDTASQSNSTAGELGAQAEISLDKTVKLAQLEFIKNSDIQ 1327  
QY 1255 GALDSITKTFQMSLEAKRVNASTTDPNSTVQSALTDRVEDLMLESPPFKQEEQEA 1314  
DB 1328 GALDSITKTFQMSLEAKRVNASTTDPNSTVQSALTDRVEDLMLESPPFKQEEQEA 1387  
QY 1315 RLDELAKGLQSLDLSAAQMTGTPGADCSSECGGPNCRDDEKXCGGPGCGGLVT 1374  
DB 1388 RLDELAKGLQSLDLSAAQMTGTPGADCSSECGGPNCRDDEKXCGGPGCGGLVT 1447  
QY 1375 VAHSAMQKAMDPRDVLALAEVQSLKMSVSEAKVRADEAKQNAQDVLLKTNATKSKVDK 1434  
DB 1448 VAHSAMQKAMDPRDVLALAEVQSLKMSVSEAKVRADEAKQNAQDVLLKTNATKSKVDK 1507  
QY 1435 SNEDLNLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOLNLTEDIRREVETLS 1494  
DB 1508 SNEDLNLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOLNLTEDIRREVETLS 1567  
QY 1495 QVEVILQOQSAADIAEALILEAKRASKATDVKVTADMVKEALEBAEAKVAEAKIKQ 1554  
DB 1568 QVEVILQOQSAADIAEALILEAKRASKATDVKVTADMVKEALEBAEAKVAEAKIKQ 1627  
QY 1555 ADSDIQOTNLLTSISSETAASEETUNASQIRISKLERVVEELKRAQNSGEAEVIEKV 1614  
DB 1628 ADSDIQOTNLLTSISSETAASEETUNASQIRISKLERVVEELKRAQNSGEAEVIEKV 1687  
QY 1615 VYSVKQNAQDVLLKTNATKSKVDKMSVSEAKVRADEAKQNAQDVLLKTNATKSKVDK 1674  
DB 1688 VYSVKQNAQDVLLKTNATKSKVDKMSVSEAKVRADEAKQNAQDVLLKTNATKSKVDK 1747  
QY 1675 KLQLEDLERKEDNQKYLEDKAQELVRLGEVRSLLKDKISEKAVYSTC 1724  
DB 1748 KLQLEDLERKEDNQKYLEDKAQELVRLGEVRSLLKDKISEKAVYSTC 1797

RESULT 15  
US-09-561-709B-1  
Sequence 1, Application US/09561709B  
Patent No. 6882911  
GENERAL INFORMATION:  
APPLICANT: Burgeson, Robert



```

/ APPLICANT: Champliand, Marie-France
/ APPLICANT: Olson, Pamela
/ APPLICANT: Koch, Manuel
/ APPLICANT: Brunken, William
/ TITLE OF INVENTION: LAMININS AND USBS THEREOF
/ FILE REFERENCE: 10287-060001
/ CURRENT APPLICATION NUMBER: US/03/561,709B
/ CURRENT FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 09/168,949
/ PRIOR FILING DATE: 1998-10-09
/ PRIOR APPLICATION NUMBER: US 60/061,609
/ PRIOR FILING DATE: 1997-10-10
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1761
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-561-709B-1

Query Match      39.4%; Score 3712.5; DB 4; Length 1761;
Best Local Similarity 40.9%; Pred. No. 5.6e-211;
Matches 726; Conservative 299; Mismatches 627; Indels 125; Gaps 30;

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DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 TLODLEAEFFHLLIMFKTPRAAMLIRESSDFGKTMGYRYFAVDCSSPGISTGP 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 SIRLDEALFPFHLITFKTPRAAMLEVERSTDIYGNWVKFYAKDCATSPNITSQ 174
QY 121 MKKVDIIICDSRYSDIEPSTEGEIVFRALDPAFKIEDPYSPRIQNLKIITNLRIKVKLH 180
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 AQGVGDIVCDKSYSDIEPSTEGEVKLVLPDSFEIENPYFYIQLDVLTLNLRIKFKLH 234
QY 181 TLGDNLDSRM-EIREKYVYAYDMVMVGRNCFYGHASECAPVDGYNEEV---EGMVHGH 236
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 235 TLGDALLGRQNSLDKYYALYEMIVRGSCFNGHASECRPMKMGVDVFPSPGMVHQ 294
QY 237 CMCNHTKGLNCELCMPDHYDLWPRPABGRNSNACKKCNHSSCHDFMAYFLATGV 296
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 295 CVQCNTDGNPCERCKDFQAPWRPAADLQDNACRSCNSHSHRCHDFMTTYLASGGL 354
QY 297 SGVCNDCQNTMGRNCEQKPFYFOHPERDIRPNICEPTCDPAGSENGGICDGYTF 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 355 SGVCNDCQNTMGRNCEQKPFYFOHPERDIRPNICEPTCDPAGSENGGICDGYTF 414
QY 357 SVGLIAGQCRCKLHVEGERCDVCKEYPYLSAEDPYGCKSCACNPLGTIPGPNPCDSE 416
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 415 ALGSVAGQCLCKENVEGAKDQCPNHYGLSATDPLGCPQPCDNCNPLGSLP-FLTC 473
QY 417 YCYKRLVTGQRCQCLPQHWGLNLDGCRPCDDLGALNNSCEDSDSCQSCLPHTMG 476
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 474 QCLCLSYVTGAHCECTVYGLNHLHGSPCDDCIGGAYSNVCFKNGQCECRPHVTG 533
QY 477 RQCNVEGEGYFTLIDHYIYAEAN-----LG-----PGVVVERQYIQDRIPSW 522
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 534 RSCSEPAEPYFPAFLNPLYIAEAEATTLOGLAPLGSETFGQSPAVHVLGEPVPGNPVTW 593
QY 523 TPGGVRVPEGALEFFDNIPIYSMEYELIRYEPOLPDHWEKAVITVORPGKIPASSRC 582
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 594 TPGGFARVLPAGLRFPAVNNIPFPVDTHIAHETQSAADWTQIV-VNPPG---GSEHC 649
QY 593 GNTVPDDNDQVVSLSPGSRVYVLPFRVCFEKGMYTVRLPELPOYTASGSDVSPYTFIDS 642
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 650 IPKTLQSKPQSFALPAATRLMLPTICLPEFDYQSIDVYFSPQLQGESHAHS-HVLVDS 708
QY 643 LVLMYPKSLDIFTVGGSGDGEVNTSAWETFQRYCLNLSRSVVKTPMTDVCNRIIFSIS 702
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 709 LGLIPQINSLENF-----CSKQDLDEYQHLNCFVETASANGPQVLPACERLIISWS 759
QY 703 ALIHQTGLACBDCPQGSLSVCDPNGGQCRNPVNVGRTNCRCAPGTFGFGNGCKPCDC 762

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Search completed: May 19, 2004, 15:02:19

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DB 760 AKLHDGAVACKHPQGSVSGSCSELGGQCCOCKLVLVGRCCDRCTSGSYDLGHHGCHPCHC 819
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DB 820 HPQSKQDVTCDQVGTGQCPCHGEVSGRCDRLAGYGFPSCHPCPNRFAELCDPPTGSC 879
QY 823 LSCQDYTTGHNCRCLAGYGDPIIGSGDRCPCCPDGPDGSRQRFARSQCYQDPVTLQLA 882
DB 880 FNCGGFTTGRNCERCIDGYGNP--SSQGPCRCLCPDDPSSNQYFAHSCYQNLWSSDVI 937
QY 883 CVCPGYIGSRCDDCASGFFGNPSDFGSCOPQCHNIDTTTPRACDXTGBCCLXVH 942
DB 938 CNLCQYGTGTCGECSTGFGNPRISGAPCQACANNIDVTPESCSRVTGCLRCLHN 997
QY 943 TEGDHQCLQYGYGDALRQDCRCKVCNYLGTVKEHC--NGSDCHCDKATGQCSCLPNVI 1000
DB 998 TQGANCOLCKPFGHYGSALNQTCCRRCSCHASGVSPMECPGGGACLCDPVTGACPCLPNVT 1057
QY 1001 GQNCDCRCPNTWQLASCTGCGPCNCAAHFSGSCNEFTGOCOCMPGFGGRTCECEOLF 1060
DB 1058 GLACDRCADGVNVLVPRGQCQCDPRTSQSSHCDLTGQCPCKLGYGGRGCEQENY 1117
QY 1061 WGPDPVECRACDCCDPRIETPQCDOSTGCVQVEGVEGPRCDKCTRGYSVFPDCTFCHQ 1120
DB 1118 YGDPGPRCIPCDNCRAGTQKPICDPDTGMCRCREGVSGQRCDCRARGHSEFPCLQCHL 1177
QY 1121 CFALWDALIGELNTRHTKFLKAKALKISGVIGPYEETVDSVEK-----KVNETKDL 1173
DB 1178 CFQDWDHTISLSKAVOGLMRLAANME-----DKRETLPVCEADFKDLRGVSELERL 1231
QY 1174 AQS--PAAEPLKNIGILFEAEKLTXTDVTKMAQVE--VKLTDTASQSNSTAGELGALQA 1229
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QY 1230 EAESLDTKVELAEOLEF---IKNSDIQALDLSITKYFOWSLEAEKVNASTTDPNSTVE 1286
DB 1283 -----DLLESDLOEBEIDLQSSVUNASIASSENKIKYTHISSAEKKIN-----EISSIN 1333
QY 1287 QSALTRDRVEDMLERESPFEKQEEQCARLLDELACK---LQSL-----DLSAAQMT 1336
DB 1334 TSANTRN---DLJ-----TILDTLTSKGLSLERLKOIKIPDIQILNEKV 1375
QY 1337 CGTPPGADCSSESOGGPNCRKTDEKCKGCGGGLVTVVAHSAWOKAMDFDRDVLALAE 1396
DB 1376 CGDPENVPVCPVPCGAGLCTGRKGRKCRGPGCHGSLTSTNALQAQAKSIIRNLQK 1435
QY 1397 VEOLSKMWSEAKVRADEAKONAQDVLTKTNATKVKDSNEDLRLNIKOIRNFLTEDSAD 1456
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QY 1457 LDSTEAVANVLKSGNASTPQQLONLTED--IRREVETLSQVEVILQOSAADIARAELL 1513
DB 1496 PEDIEKVANGL---DIHLPIPSQNTDELVKIQKMQLCEDYRTDENRSNEADGAQKL 1552
QY 1514 LEEAKRASKATDVKTADVMEALAEAEAKAQAQAEKAIKQADEDIQGTQNLILLTSEIET 1573
DB 1553 LVKAKAAEKAA-NILLNLDKTLNQLQAQITQGRANSTITQLTANITIKKNVLAENQT 1611
QY 1574 AASEETLTNASQIRISKERNVEBELKEKAQNSGEAEYIEKVVYVSKQNAADDVKKTLDEL 1633
DB 1612 REMKSELELAKOR-SGLEDGLSILQTKLQKHODHNAVNAKVAQESAQHAQ-----GSL 1662
QY 1634 DEKY---KKVESLIAQKTESA---DARKABELLONEAKTLIAQANSKULLEDLERKYE 1687
DB 1663 EKEFVELKKQYALQKRTSTGLTKETLGVKQLKDAAEKLAGDTEAKIRITDLERKIQ 1722
QY 1688 DNQKYLEDKAELVRLEGEVRSLLKDISKVAIVSTC 1724
DB 1723 DLNLSRQAKADQLRIELEDQVWAIKNEIVEQEKYARC 1759

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 43.8855 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-12  
Perfect score: 9429  
Sequence: 1 EPYCIVSHLQEDKKCFICDS.....EVRSLKDISKAVAVSTCL 1725

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues 1145568

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*
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- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pcp.\*
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- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*
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- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
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- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9429	100.0	1725	14	US-10-037-182-12
2	9429	100.0	1786	9	US-09-938-275-7
3	9429	100.0	1786	14	US-10-037-182-10
4	8873	94.1	1765	14	US-10-037-182-8
5	8873	94.1	1786	9	US-09-873-676-113
6	8873	94.1	1786	9	US-09-938-275-6
7	8873	94.1	1786	14	US-10-037-182-6
8	5482	58.1	1196	16	US-10-443-349-4
9	4936	52.3	1801	9	US-09-938-275-8
10	4914	52.1	1799	9	US-09-845-583-6
11	4890	51.9	1798	9	US-09-938-275-9
12	4778	50.7	1798	9	US-09-845-583-8
13	3646	38.7	1808	15	US-10-369-493-5986
14	2967	31.5	1101	12	US-10-287-971-18
15	2154	22.8	527	12	US-09-925-298-703

16	2154	22.8	527	14	US-10-102-806-703	Sequence 703, Appl
17	1730	18.3	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1649	17.5	3712	12	US-10-037-417-48	Sequence 48, Appl
19	1649	17.5	3712	13	US-10-108-605-103	Sequence 103, Appl
20	1645	17.4	3712	12	US-10-037-417-51	Sequence 51, Appl
21	1637.5	17.4	1572	14	US-10-037-182-20	Sequence 20, Appl
22	1637.5	17.4	1605	14	US-10-037-182-18	Sequence 18, Appl
23	1622.5	17.2	1576	14	US-10-037-182-16	Sequence 16, Appl
24	1622.5	17.2	1609	14	US-10-037-182-14	Sequence 14, Appl
25	1622.5	17.2	1609	14	US-10-299-058-12	Sequence 12, Appl
26	1618.5	17.2	1609	9	US-09-938-275-11	Sequence 11, Appl
27	1618.5	17.2	1609	15	US-10-372-683-36	Sequence 36, Appl
28	1610.5	17.1	1607	9	US-09-938-275-10	Sequence 10, Appl
29	1608	17.1	1557	15	US-10-369-493-6816	Sequence 6816, Ap
30	1584	16.8	3635	9	US-09-845-583-2	Sequence 2, Appl
31	1584	16.8	3635	12	US-10-037-417-47	Sequence 47, Appl
32	1584	16.8	3635	14	US-10-037-182-4	Sequence 4, Appl
33	1562.5	16.6	3696	15	US-10-312-088-31	Sequence 31, Appl
34	1558	16.5	2743	14	US-10-037-182-36	Sequence 36, Appl
35	1558	16.5	3695	12	US-10-312-352-22	Sequence 22, Appl
36	1558	16.5	3695	14	US-10-037-182-2	Sequence 2, Appl
37	1553	16.5	3690	12	US-10-112-944-347	Sequence 347, App
38	1538	16.3	3705	15	US-10-312-088-30	Sequence 30, Appl
39	1535	16.3	3075	9	US-09-938-275-5	Sequence 5, Appl
40	1527.5	16.2	3070	10	US-09-961-403-7	Sequence 7, Appl
41	1493	15.8	1575	12	US-10-262-839-212	Sequence 212, App
42	1484	15.7	1587	9	US-09-845-583-10	Sequence 10, Appl
43	1484	15.7	1587	12	US-10-262-839-210	Sequence 210, App
44	1482	15.7	3084	9	US-09-938-275-4	Sequence 4, Appl
45	1482	15.7	3084	14	US-10-262-670-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-037-182-12  
; Sequence 12, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-12

Query Match	100.0%	Score	9429	DB	14	Length	1725
Best Local Similarity	100.0%	Pred. No.	0				
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Gaps	0						
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Qy	61	TIQDLAEAFHFTLIMTFTFPAAMLIERSD	FGKTGWGVYFAYDCSSPPGISTGP	120			
Db	61	TIQDLAEAFHFTLIMTFTFPAAMLIERSD	FGKTGWGVYFAYDCSSPPGISTGP	120			
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## RESULT 2

US-09-938-275-7  
; Sequence 7, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P02469  
; DATABASE ENTRY DATE: 1989-07-01  
US-09-938-275-7

Query Match 100.0%; Score 9429; DB 9; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1681 DLERYEDNOKYLEDKAQELVRLEGEVRSLLKQISEKAVYSTCL 1725  
1742 DLERYEDNOKYLEDKAQELVRLEGEVRSLLKQISEKAVYSTCL 1786

## RESULT 3

US-10-037-182-10  
; Sequence 10, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: DO, Masayuki  
; APPLICANT: Thyoll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-10

Query Match 100.0%; Score 9429; DB 14; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TIQDLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWYRYFAYDCESSFFGISTGP 120  
DB 122 TIQDLEAEFHTLIMTFTFRPAAMLIERSDDFGKTGWYRYFAYDCESSFFGISTGP 181  
QY 131 MKKVDDIICDSRYSDISBPSTEGEVIFFALDPAPKIEPYPRIQNLKLTNLRKFKVLH 180  
DB 182 MKKVDDIICDSRYSDISBPSTEGEVIFFALDPAPKIEPYPRIQNLKLTNLRKFKVLH 241  
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Db 242 TLGNDLLSRMEIRKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVGMVHGCMCR 301  
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Db 302 HNTKGLNCELCHMDFYHDLPRPABGRNSNACKKCNENHSSCHDFMAVFLATGNVSGV 361  
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Db 542 EVESGYFTTLDHYIYEAEANLPGVWVVEROYIQDRIPSWTGPVVRVPEGAYLEFFI 601  
QY 541 DNIPIYSMEYELLRYBPQLPDHWEKAVITVORPKIPASSRCQNTVPDDNNOVSLSPGS 600  
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QY 661 GDEVTNSANETQRYRCLNENSVVKTMTDVCNRIIFSIHALHOTGLACEDPOQSL 720  
Db 722 GDEVTNSANETQRYRCLNENSVVKTMTDVCNRIIFSIHALHOTGLACEDPOQSL 781  
QY 721 SSVCDPNGGQCQRPNVVGRTCNRCAPGTGFGNGCKPCDCHLOGSASAFCDAITGQCH 780  
Db 782 SSVCDPNGGQCQRPNVVGRTCNRCAPGTGFGNGCKPCDCHLOGSASAFCDAITGQCH 841  
QY 781 CFQGIYARQCDRLPGVWGPSPQPCQCNCHALDCTVTGECCLSCODYTTHNCERCLAG 840  
Db 842 CFQGIYARQCDRLPGVWGPSPQPCQCNCHALDCTVTGECCLSCODYTTHNCERCLAG 901  
QY 841 YGDPPIIGSDHCRPCPCPGDPSGRQFARSCYQDPVTQLQACVCPGPGVIGSRCDCCASG 900  
Db 902 YGDPPIIGSDHCRPCPCPGDPSGRQFARSCYQDPVTQLQACVCPGPGVIGSRCDCCASG 961  
QY 901 FFGNPSDFGSGCQPCQCHNIDTDPACDKDTRCLKCLYHTEGHDHCLQYGYGDAL 960  
Db 962 FFGNPSDFGSGCQPCQCHNIDTDPACDKDTRCLKCLYHTEGHDHCLQYGYGDAL 1021  
QY 961 RQDCRKCVCNVLGVTRKCHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTGC 1020  
Db 1022 RQDCRKCVCNVLGVTRKCHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPNWQLASGTGC 1081  
QY 1021 GPCNCAAHGFGPSCNEFTGQCQCPMPGFGGRTCSQCLFWGDPDVECRACDCDPRGIET 1080  
Db 1082 GPCNCAAHGFGPSCNEFTGQCQCPMPGFGGRTCSQCLFWGDPDVECRACDCDPRGIET 1141  
QY 1081 PQCDQSTGQCVCEVGEVGRPCDKTRCYSGVFPDCTPCHOCFALWDAIIGELNTRTHKFL 1140  
Db 1142 PQCDQSTGQCVCEVGEVGRPCDKTRCYSGVFPDCTPCHOCFALWDAIIGELNTRTHKFL 1201  
QY 1141 EKAKALITSGVIGPYRETVDSEVKKVNEIKDILAQSPAAPFLKNIGILPEEAELTKDVT 1200  
Db 1202 EKAKALITSGVIGPYRETVDSEVKKVNEIKDILAQSPAAPFLKNIGILPEEAELTKDVT 1261  
QY 1201 EKMAQVEVKLTDTTASQNSSTAGELGALQAEASLDKTVKELAQLEFIKNSDTCGALDSI 1260  
Db 1262 EKMAQVEVKLTDTTASQNSSTAGELGALQAEASLDKTVKELAQLEFIKNSDTCGALDSI 1321  
QY 1261 TKYFQMSLEAKRVNASTTDPNSTVQESALTRDRVEDLMLERESPKEQOEQARLLDEL 1320

Db 1322 TKYFQMSLEAKRVNASTTDPNSTVQESALTRDRVEDLMLERESPKEQOEQARLLDEL 1381  
QY 1321 AGKLOSLDLGAAQMTCTPPGADCSBSECGGPNCRTRDEGEKCGGPGCGGLVTVHASAW 1380  
Db 1382 AGKLOSLDLGAAQMTCTPPGADCSBSECGGPNCRTRDEGEKCGGPGCGGLVTVHASAW 1441  
QY 1381 QKAMDFDRDVLASAEVEQLSKMVSEAKVTRADAKQVADVLKTNATKEKVDKSNEDLR 1440  
Db 1442 QKAMDFDRDVLASAEVEQLSKMVSEAKVTRADAKQVADVLKTNATKEKVDKSNEDLR 1501  
QY 1441 NLIKQIRNFITDESADLDSIEAVANEVLKSGNASTTPOQLQNLTEDIRERVETLSQVEVIL 1500  
Db 1502 NLIKQIRNFITDESADLDSIEAVANEVLKSGNASTTPOQLQNLTEDIRERVETLSQVEVIL 1561  
QY 1501 QQSAAIDARAEILLLEAKRASKGATDVKTADVMVKEALBEAEKAQVAAEKAKOADEDIQ 1560  
Db 1562 QQSAAIDARAEILLLEAKRASKGATDVKTADVMVKEALBEAEKAQVAAEKAKOADEDIQ 1621  
QY 1561 GTQNLLTSISSETAASBETLTNASQISKLERNVEELKRKAQNSGEAEYIEKVYYSVKQ 1620  
Db 1622 GTQNLLTSISSETAASBETLTNASQISKLERNVEELKRKAQNSGEAEYIEKVYYSVKQ 1681  
QY 1621 NADVVKTKTLDGELDEKYKVESLIAQKTESADARRKAEILLONEAKTLLAQANSKLQLE 1680  
Db 1682 NADVVKTKTLDGELDEKYKVESLIAQKTESADARRKAEILLONEAKTLLAQANSKLQLE 1741  
QY 1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKAVVYSTCL 1725  
Db 1742 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKAVVYSTCL 1786

RESULT 4

US-10-037-182-8  
; Sequence 8. Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-8

Query Match 94.1%; Score 8873; DB 14; Length 1765;  
Best Local Similarity 92.1%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLQDQKCKFCICSDRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVENV 60  
Db 41 EPYCIIVSHLQDQKCKFCICSDRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVENV 100  
QY 61 TIQLDLEAEFFTHLIMTFKTRFAAMLIERSSDPGKWTGVYRFAVYDCESSFFGISTGP 120  
Db 101 TIQLDLEAEFFTHLIMTFKTRFAAMLIERSSDPGKWTGVYRFAVYDCEASFFGISTGP 160  
QY 121 MKKVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPSPRIQNLLKITNLRKFKVLH 180  
Db 161 MKKVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPSPRIQNLLKITNLRKFKVLH 220  
QY 181 TLGMDLLSRMEIRKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVGMVHGCMCR 240

Db 221 TLGNLLDSRMEIREKYYAVVDMVVRGNCFCYGHASECAPVDGFMNEVEGMVHGCMCR 280  
Qy 241 HNTKGLNCELCHDFDHPWPAEGRNSNACKKNCNEHSSCHDFDPAVPLATGNVSGV 300  
Db 281 HNTKGLNCELCHDFDHPWPAEGRNSNACKKNCNEHSSCHDFDPAVPLATGNVSGV 340  
Qy 301 CDNCHNTMGRNCECKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
Db 341 CDDCHNTMGRNCECKPFYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 400  
Qy 361 IAGQCRCKLHVEGRCDCVCKEFGYDLSAEDPYGCKSCACNPLGTPGNCPCDSEGTGYC 420  
Db 401 IAGQCRCKLHVEGRCDCVCKEFGYDLSAEDPYGCKSCACNPLGTPGNCPCDSEGTGYC 460  
Qy 421 KLVLTGQRCDQCLPQHWGLSNDLDCRCDLGGALNNSCSEDSGQSCCLPHMIGRCN 480  
Db 461 KLVLTGQRCDQCLPQHWGLSNDLDCRCDLGGALNNSCSEDSGQSCCLPHMIGRCN 520  
Qy 481 EVESGYFTLLDHYIYEAENLGRGVVVERQYIQRIPSWTGPFGVRVPEGAYLEFFI 540  
Db 521 EVESGYFTLLDHYIYEAENLGRGVVVERQYIQRIPSWTGPFGVRVPEGAYLEFFI 580  
Qy 541 DNIPIYMEVEILLIRYEPQLPDHWEKAVITVQSPGKI PASSRCGNTVPDDNQVVSLSPGS 600  
Db 581 DNIPIYMEVEILLIRYEPQLPDHWEKAVITVQSPGKI PASSRCGNTVPDDNQVVSLSPGS 640  
Qy 601 RYVVLPRPVCFFKGMNYTVRLSELQVTSDSVSPYTLIDSLVLMYPYCKSLDIPFTVGS 660  
Db 641 RYVVLPRPVCFFKGMNYTVRLSELQVTSDSVSPYTLIDSLVLMYPYCKSLDIPFTVGS 700  
Qy 661 GGEVNTSNWETFORVRCLENRSVVKTPMTDVCNIIIPFISALIHQTGLACECDPQSL 720  
Db 701 GGEVNTSNWETFORVRCLENRSVVKTPMTDVCNIIIPFISALIHQTGLACECDPQSL 760  
Qy 721 SSVCDPNGGQCRCRPNVVRGRTCNRCAPGTGFGPNCKPCDCHLQGSASFCDALITGQH 780  
Db 761 SSVCDPNGGQCRCRPNVVRGRTCNRCAPGTGFGPNCKPCDCHLQGSASFCDALITGQH 820  
Qy 781 CQGIYARQCDCLPGYNGFPSCPCQNGHALDCDVTGECCLSCODYTHGNCERCLAG 840  
Db 821 CQGIYARQCDCLPGYNGFPSCPCQNGHALDCDVTGECCLSCODYTHGNCERCLAG 880  
Qy 841 YGDPITIGSGDHCRPCPCPDGSPDRQFARSQYQDPVTILQLACVCDPGYIGSRCDCCASG 900  
Db 881 YGDPITIGSGDHCRPCPCPDGSPDRQFARSQYQDPVTILQLACVCDPGYIGSRCDCCASG 940  
Qy 901 FFGNPSDFGSGCQPCQCHNIDITDPEACDKTGRCLKLYHTEGDHCOLGOYVYGDAL 960  
Db 941 FFGNPSDFGSGCQPCQCHNIDITDPEACDKTGRCLKLYHTEGDHCOLGOYVYGDAL 1000  
Qy 961 RQDRCVCNLYLTVEHCNCSCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1020  
Db 1001 RQDRCVCNLYLTVEHCNCSCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGC 1060  
Qy 1021 GPCNNAHSGFSPCNFTGQCCMPGFGRTCSCEQLFWGDDPVECHACDCDPRGIET 1080  
Db 1061 GPCNNAHSGFSPCNFTGQCCMPGFGRTCSCEQLFWGDDPVECHACDCDPRGIET 1120  
Qy 1081 PQCDQSTGQCVGVEGPRCDKTRGYSQVFPDCTPCHQCFCALMDAIIIGELTNRTHKFL 1140  
Db 1121 PQCDQSTGQCVGVEGPRCDKTRGYSQVFPDCTPCHQCFCALMDAIIIGELTNRTHKFL 1180  
Qy 1141 EKAKALKISGVIQYFRETVDVSEKKNYKIDILAQSPAAPPLKNIGILFEEAEKTKOVT 1200  
Db 1181 EKAKALKISGVIQYFRETVDVSEKKNYKIDILAQSPAAPPLKNIGILFEEAEKTKOVT 1240  
Qy 1201 EKMAQVEKLTDTASQSNSTAGELGALQABESLDTKVELAEOLEFIKNSDIOGALDSI 1260  
Db 1241 EKMAQVEKLTDTASQSNSTAGELGALQABESLDTKVELAEOLEFIKNSDIOGALDSI 1300  
Qy 1261 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESFPKQEQEQAARLLDEL 1320  
Db 1301 TKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLESFPKQEQEQAARLLDEL 1360

Qy 1321 AGKQLSLDLSAAAOQMTCTGTPGADCSSESCEGPNCRTEGEKKCGGPGCGGLVTVHAHSAW 1380  
Db 1361 AGKQLSLDLSAAAOQMTCTGTPGADCSSESCEGPNCRTEGEKKCGGPGCGGLVTVHAHSAW 1420  
Qy 1381 OKAMDPRDVLNLAARVEQLSKWVSEAKYRADAENQADVLLKTNATKEKVDKSNEDLR 1440  
Db 1421 OKAMDPRDVLNLAARVEQLSKWVSEAKYRADAENQADVLLKTNATKEKVDKSNEDLR 1480  
Qy 1441 NLTKQIRNFELTDSADLSIEAVANEVLKSGNASTPQOLQNLITEDIRERVELTSQVEVIL 1500  
Db 1481 NLTKQIRNFELTDSADLSIEAVANEVLKSGNASTPQOLQNLITEDIRERVELTSQVEVIL 1540  
Qy 1501 QOSAAIDIAARELLLEAKKASKSATDVKTADWKEALEAEAKAOVAEAKAIKQADEDIQ 1560  
Db 1541 QOSAAIDIAARELLLEAKKASKSATDVKTADWKEALEAEAKAOVAEAKAIKQADEDIQ 1600  
Qy 1561 GTQNLTSIESETAASEETLTFNASQRISELRNVEELKKAQNSGEAEYIEKVYVSVKQ 1620  
Db 1601 GTQNLTSIESETAASEETLTFNASQRISELRNVEELKKAQNSGEAEYIEKVYVSVKQ 1660  
Qy 1621 NADVVKTLDELDEKVKVESLIQKTESADARKEALLONEAKTLAQANSKLQILLE 1680  
Db 1661 NADVVKTLDELDEKVKVESLIQKTESADARKEALLONEAKTLAQANSKLQILLE 1720  
Qy 1681 DLKRYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
Db 1721 DLKRYEDNOKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1765

RESULT 5  
US-09-873-676-113  
; Sequence 113, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: Macdonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 052113-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873, 676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209, 065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289, 387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 113  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-873-676-113

Query Match 94.1%; Score 8873; DB 9; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy 1 EPYCIVSHLOEDKCKFCICSDRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV 60  
Db 62 EPYCIVSHLOEDKCKFCICSDRDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENV 121  
Qy 61 TIQLDLAEAFHFTLHMTKTRPAAMLIERSSDFGTWGVYRFAVYDCSSPFGISTGP 120  
Db 122 TIQLDLAEAFHFTLHMTKTRPAAMLIERSSDFGTWGVYRFAVYDCSSPFGISTGP 181  
Qy 121 MKKVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPSPRIQNLKIITNRIKFKVLH 180  
Db 182 MKKVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPSPRIQNLKIITNRIKFKVLH 241  
Qy 181 TLGNLLDSRMEIREKYYAVVDMVVRGNCFCYGHASECAPVDGFMNEVEGMVHGCMCR 240  
Db 242 TLGNLLDSRMEIREKYYAVVDMVVRGNCFCYGHASECAPVDGFMNEVEGMVHGCMCR 301



QY 241 HNTKGLNCLMDYFHDLPWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGV 300  
DB 302 HNTKGLNCLMDYFHDLPWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGV 361  
QY 301 CDMCOHNTWGRNCEQCKPFFOHBERDARDNLCBPCTCDPAGSENGICDGVYDFRSVL 360  
DB 362 CDMCOHNTWGRNCEQCKPFFOHBERDARDNLCBPCTCDPAGSENGICDGVYDFRSVL 421  
QY 361 IAGQCKLHVGERCDVCKGFDYLSAEDPYGCKSCACNPLGTIPGNCPCDSTGYCYC 420  
DB 422 IAGQCKLHVGERCDVCKGFDYLSAEDPYGCKSCACNPLGTIPGNCPCDSTGYCYC 481  
QY 421 KRLVTQORCDQLPQHWGLSNDLDCRCPDCCDLGALNNSCEDSGCSCPLPHMIGRCN 480  
DB 482 KRLVTQORCDQLPQHWGLSNDLDCRCPDCCDLGALNNSCEDSGCSCPLPHMIGRCN 541  
QY 481 EYSGYFTTLHYIYEAENLGGVGVVERQYIQDRIPSWTGGFVRVPEGAYLEFFI 540  
DB 542 EYSGYFTTLHYIYEAENLGGVGVVERQYIQDRIPSWTGGFVRVPEGAYLEFFI 601  
QY 541 DNIPIYMEYIILRYEPOLPDHWEKAVITVORPGKI PASSRCGNTVDDNNQVVSLSFGS 600  
DB 602 DNIPIYMEYIILRYEPOLPDHWEKAVITVORPGKI PASSRCGNTVDDNNQVVSLSFGS 661  
QY 601 RYVLPBPCFKGMNYTVRLBELPQYTAGSDVSPTFFIDSLVMPYCKSLDIFTVGS 660  
DB 662 RYVLPBPCFKGMNYTVRLBELPQYTAGSDVSPTFFIDSLVMPYCKSLDIFTVGS 721  
QY 661 GDEVTNSAWEFORVRCLENRSVVKTPMTDVCNIIFFSALIHOTGLACEDPOGSL 720  
DB 722 GDEVTNSAWEFORVRCLENRSVVKTPMTDVCNIIFFSALIHOTGLACEDPOGSL 781  
QY 721 SSVCDPNGGQCCRPNNVGRNCRNAPGTFFGPNCKPCDCHLQGSASAFCDAITQCH 780  
DB 782 SSVCDPNGGQCCRPNNVGRNCRNAPGTFFGPNCKPCDCHLQGSASAFCDAITQCH 841  
QY 781 CFQGIYAROCRLPGYMGFPSCQCNHGDCTVTGECSCQDYTTGHCNCRCLAG 840  
DB 842 CFQGIYAROCRLPGYMGFPSCQCNHGDCTVTGECSCQDYTTGHCNCRCLAG 901  
QY 841 YGDPPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVDCPGYIGSRCDCCASG 900  
DB 902 YGDPPIIGSDHCRPCPCPDGSDGRQFARSCYQDPVTLQACVDCPGYIGSRCDCCASG 961  
QY 901 FFGNPSDFGSGQPCQCHNIDITDPEACDXTGRCLKCLVHTGEGHCLQCGYIGDAL 960  
DB 962 YFGNPSDFGSGQPCQCHNIDITDPEACDXTGRCLKCLVHTGEGHCLQCGYIGDAL 1021  
QY 961 RQCRKVCNLYGTQVHCHGNSDCHDKATGQCSCLPNVIGQNCDCRCPNTWQASGTGC 1020  
DB 1022 RQCRKVCNLYGTQVHCHGNSDCHDKATGQCSCLPNVIGQNCDCRCPNTWQASGTGC 1081  
QY 1021 GPCNCAHSGFPGSCNFTGQCCQMPFGGRTCECQELFWDGDPDVECRACDCCDPRGIET 1080  
DB 1082 DPCNCAHSGFPGSCNFTGQCCQMPFGGRTCECQELFWDGDPDVECRACDCCDPRGIET 1141  
QY 1081 PQCDQSTGQCVGVEGPRCDKTRGYSVPFDPCTPCHQCFALWDALIGELNTRHFL 1140  
DB 1142 PQCDQSTGQCVGVEGPRCDKTRGYSVPFDPCTPCHQCFALWDALIGELNTRHFL 1201  
QY 1141 EKAKALKISGVIGPRTVDSVEKKNBIKQILQSPAAEPKNIIGLFEAEKLIKDV 1200  
DB 1202 EKAKALKISGVIGPRTVDSVEKKNBIKQILQSPAAEPKNIIGLFEAEKLIKDV 1261  
QY 1201 EKMAQVEVLKLTDTASQNSSTAGELGALQABESLDKTVKELABQLEFKNSDTCGLDLSI 1260  
DB 1262 EKMAQVEVLKLTDTASQNSSTAGELGALQABESLDKTVKELABQLEFKNSDTCGLDLSI 1321  
QY 1261 TKYFQMSLEAEKRVNASITDPSNSTVEQSALTRDRVEDIMLIERESPFFKEQEEQARLDEL 1320  
DB 1322 TKYFQMSLEAEKRVNASITDPSNSTVEQSALTRDRVEDIMLIERESPFFKEQEEQARLDEL 1381  
QY 1321 AGKQLSLDLASAAQMTCTGPPGACDSESECGGPNCRDTEGEKCKGCGGLVTVAHSAW 1380

DB 1382 AGKQLSLDLASAAQMTCTGPPGACDSESECGGPNCRDTEGEKCKGCGGLVTVAHSAW 1441  
QY 1381 OKAMDPRDVLASAEVQSLSKWSEAKVRADAKQNAQDVLTKTNATKEKVDKSNEDLR 1440  
DB 1442 OKAMDPRDVLASAEVQSLSKWSEAKVRADAKQNAQDVLTKTNATKEKVDKSNEDLR 1501  
QY 1441 NLIKQIRNFLTSDSADLSIEAVANEVLYKSGNASTPQOLQNLFTEDIRERVETLSQVEVIL 1500  
DB 1502 NLIKQIRNFLTSDSADLSIEAVANEVLYKSGNASTPQOLQNLFTEDIRERVETLSQVEVIL 1561  
QY 1501 QOSAADTARABLLLEAKRASKSATDVKTADVMVKEALBEAEKAAKQADDEDIQ 1560  
DB 1562 QOSAADTARABLLLEAKRASKSATDVKTADVMVKEALBEAEKAAKQADDEDIQ 1621  
QY 1561 GTONLLTSIESETAASBETLTNASQISKLERNVEBELKRAAONSGEAEYIEKVYYSVKQ 1620  
DB 1622 GTONLLTSIESETAASBETLTNASQISKLERNVEBELKRAAONSGEAEYIEKVYYSVKQ 1681  
QY 1621 NADVVKTKLDELDEKVKYKESLIAQKTESDARRKAELOEAKTLLAQANSKLQLE 1680  
DB 1682 NADVVKTKLDELDEKVKYKESLIAQKTESDARRKAELOEAKTLLAQANSKLQLE 1741  
QY 1681 DLERYEDNQYLEDKAEQELVRLEGEVRSLLKQISEKVAVYSTCL 1725  
DB 1742 DLERYEDNQYLEDKAEQELVRLEGEVRSLLKQISEKVAVYSTCL 1786

RESULT 6  
US-09-938-275-6  
; Sequence 6, Application US/09938275  
; Patent No. US2002011309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P07942  
; DATABASE ENTRY DATE: 1988-08-01  
US-09-938-275-6

Query Match: 94.1%; Score 8873; DB 9; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIVSHLOEDKCKFTCDSDPDVHETLAPDPSHLIENNVTTTAPNRLKIWQSENGENV 60  
DB 62 EPYCIVSHLOEDKCKFTCDSDPDVHETLAPDPSHLIENNVTTTAPNRLKIWQSENGENV 121  
QY 61 TIQDLAEAFHFTLIMTFTFRPAAMLIERSDFGKTGWVRYPAYDCESSPGISTGP 120  
DB 122 TIQDLAEAFHFTLIMTFTFRPAAMLIERSDFGKTGWVRYPAYDCESSPGISTGP 181  
QY 121 MKYVDDIICDSYSDIEPSTEGEVIERALDPAEKIEDPSPRIQNLKLTNLRKFKVLH 180  
DB 182 MKYVDDIICDSYSDIEPSTEGEVIERALDPAEKIEDPSPRIQNLKLTNLRKFKVLH 241  
QY 181 TLGNLLDSRMEIREKYIYAVDMVGRNCFCYGHASECAPVDGVNVEGVHGHCMCR 240  
DB 242 TLGNLLDSRMEIREKYIYAVDMVGRNCFCYGHASECAPVDGVNVEGVHGHCMCR 301  
QY 241 HNTKGLNCLMDYFHDLPWRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGV 300

302 HNTKGLNCELQMDPYHDLPRWPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGV 361  
301 CDNCOHNTMGNCBCKPFYQHPRDIRDNLCEPTCTCDPAGSENGGICDGYTDFSVGL 360  
362 CDDCOHNTMGNCBCKPFYQHPRDIRDNLCEPTCTCDPAGSENGGICDGYTDFSVGL 421  
361 IAGQCRCKLHVEGERCDVCKEGFDLSAEDPVGCKSCACNPLGTIPGNPCDSETGYCYC 420  
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421 KELVTGQRCDQCLPQHWGLSNDLDCRCPDCLGGALNNSCSBDSGQSCCLPHMIGRQCN 480  
482 KELVTGQRCDQCLPQHWGLSNDLDCRCPDCLGGALNNSCFABSGQSCSRPHMIGRQCN 541  
481 EVESGYTFTLIDHYLYEAEANLGRGVVVERQYIQRIPSWTGPVVRVPEGAYLEFFI 540  
542 EVESGYTFTLIDHYLYEAEANLGRGVVVERQYIQRIPSWTGPVVRVPEGAYLEFFI 601  
541 DNIPIYSMEVEILIRYEPQLPDHWEKAVITVQPGKIPASSRCNGTVPDDDNQVLSLSPGS 600  
602 DNIPIYSMEVEILIRYEPQLPDHWEKAVITVQPGKIPASSRCNGTVPDDDNQVLSLSPGS 661  
601 RYVVLPRVCFKGMNYTVRLPELOYTASGVESPYTFIDSLVAMPYCKSIDIPTVVGGS 660  
662 RYVVLPRVCFKGMNYTVRLPELOYTASGVESPYTFIDSLVAMPYCKSIDIPTVVGGS 721  
661 GDGEVNTSAWETFORVCRLENRSVVKTPTMTDVCNIIIPSISALIHOTGLACECDPQSSL 720  
722 GUGVNTSAWETFORVCRLENRSVVKTPTMTDVCNIIIPSISALIHOTGLACECDPQSSL 781  
721 SSVCDPNGQCCQCRPNVVRTNCRAPGTFGPGNGKPCDCHLOGSASACDAITGOCH 780  
782 SSVCDPNGQCCQCRPNVVRTNCRAPGTFGPGNGKPCDCHLOGSASACDAITGOCH 841  
781 CFQGIVAROCRLPGYMGFPSCQPCQCNHGLDCTVTGECLSQDQYTTGHCERCILAG 840  
842 CFQGIVAROCRLPGYMGFPSCQPCQCNHGLDCTVTGECLSQDQYTTGHCERCILAG 901  
841 YGDPPIIGSDHCRPCPCDGPDSGRQFARSQYQPVTLQACVCDPGYISRCDDCAG 900  
902 YGDPPIIGSDHCRPCPCDGPDSGRQFARSQYQPVTLQACVCDPGYISRCDDCAG 961  
901 FEGNPSDFGSCQPCQCHNIDTDEACDKOTGRCLKLYHTEGDHCOQCYGYGDAL 960  
962 YFNPBPVSGSCQPCQCHNIDTDEACDKOTGRCLKLYHTEGDHCOQCYGYGDAL 1021  
961 RQDCRCVCNYLGTVXHECHNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGC 1020  
1022 RQDCRCVCNYLGTVXHECHNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGC 1081  
1021 GPCNCAHNSFGSCNEFTGQCCMPGFRGTSCQELFWGDDPVECRACDPRGIET 1080  
1082 DPCNCAHNSFGSCNEFTGQCCMPGFRGTSCQELFWGDDPVECRACDPRGIET 1141  
1081 PQCDQSTGQCVGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALMDAIIIGELTNRTHKPL 1140  
1142 PQCDQSTGQCVGVEGPRCDKCTRGYSVGFDPCTPCHQCQFALMDAIIIGELTNRTHKPL 1201  
1141 EKAKALKISGIVGYRETVDVSVEKKVNEIKDILAQSPAAPLEPLKNIGILPEEAEKLTQVVT 1200  
1202 EKAKALKISGIVGYRETVDVSVEKKVNEIKDILAQSPAAPLEPLKNIGILPEEAEKLTQVVT 1261  
1201 EKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDTKVELAQLEFFIKNSDIOGALDSI 1260  
1262 EKMAQVEVKLTDTASQSNSTAGELGALQAEBSLDTKVELAQLEFFIKNSDIOGALDSI 1321  
1261 TKYFQMSLEABKRVNASTTDPNSTVQSQALTRDRVEDLMLERESPKEQOEQARLLDEL 1320  
1322 TKYFQMSLEABKRVNASTTDPNSTVQSQALTRDRVEDLMLERESPKEQOEQARLLDEL 1381  
1321 AGKLQSLDLSAAAMTCGTPPGACDSESECGGPNCTDGEKCKGCGGGLVTVVAHSAW 1380  
1382 AGKLQSLDLSAAAMTCGTPPGACDSESECGGPNCTDGEKCKGCGGGLVTVVAHSAW 1441

1381 QKAMDPRDVLASALAEVQLSRWSEAKVRADAEKQNAQDVLTKTNATKEKVDKGNEDLR 1440  
1442 QKAMDLDQDVLASALAEVQLSRWSEAKVRADAEKQNAQDVLTKTNATKEKVDKGNEDLR 1501  
1441 NLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASPTQQLQNLTEDIRERVELTSQVEVIL 1500  
1502 NLIKQIRNFILTEDSADLDSIEAVANEVLKSGNASPTQQLQNLTEDIRERVELTSQVEVIL 1561  
1501 QQSAADIARAELLLLEAKKASKSATDVKTADVMVKEALEEAEKAAQVAEKAQKQADEDIQ 1560  
1562 QHSAADIARAELLLLEAKKASKSATDVKTADVMVKEALEEAEKAAQVAEKAQKQADEDIQ 1621  
1561 GTQNLTSIETSEETAASEETLTNASSQISIKLERNVELKKAQNSGEAEVIEKVYVSVKQ 1620  
1622 GTQNLTSIETSEETAASEETLTNASSQISIKLERNVELKKAQNSGEAEVIEKVYVSVKQ 1681  
1621 NADDVKTLDELDKVKVYESLIAQKTESADARRKAEKLLQNEAKTLLAQANSKLQLE 1680  
1682 SAEDVKTLDELDKVKVYESLIAQKTESADARRKAEKLLQNEAKTLLAQANSKLQLE 1741  
1681 DLKRYEDNQYLEDKAQELVRLEGEVRSLLKDISSKVAVYSTCL 1725  
1742 DLKRYEDNQYLEDKAQELVRLEGEVRSLLKDISSKVAVYSTCL 1786

RESULT 7  
US-10-037-182-6  
; Sequence 6, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thybøll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-037-182-6

Query Match 94.1%; Score 8873; DB 14; Length 1786;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 EPYCIIVSHLOEDKKCFCTCSRDPPHETLNPDSHLIENNVTTAPNRLKIWMQSENGVENV 60  
DB 62 EPYCIIVSHLOEDKKCFCTCSRDPPHETLNPDSHLIENNVTTAPNRLKIWMQSENGVENV 121  
QY 61 TIQDLDAEHPFTHLIMTKTFRPAAMLIERSSDFGTGWTGVYFYAYDCSSPPGISTGP 120  
DB 122 TIQDLDAEHPFTHLIMTKTFRPAAMLIERSSDFGTGWTGVYFYAYDCSSPPGISTGP 181  
QY 121 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAPKIEPYPSPRIQNLKIKTLNRIKFKVLH 180  
DB 182 MKKVDDIICDSRYSDIEPSTEGEVI FRALDPAPKIEPYPSPRIQNLKIKTLNRIKFKVLH 241  
QY 181 TLGNLSDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEVEGVMVGHGCMCR 240  
DB 242 TLGNLSDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGVNEVEGVMVGHGCMCR 301  
QY 241 HNTKGLNCELQMDPYHDLPRWPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGV 300  
DB 302 HNTKGLNCELQMDPYHDLPRWPAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSGV 361

301 CNCOHNTMGRNCEQCKPFFYFOHPRDRIRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
362 CDDCCCHNTMGRNCEQCKPFFYCHPRDRIRDNPNFCERCTCDPAGSQNGEGICDSTYDFSTGL 421  
361 IAGQCRCKLHVEGERCDVCKEFGYDLSAEDPVGCKSCACNPLGTIPGNPCDSESTGYCYC 420  
422 IAGQCRCKLHVEGERCDVCKEFGYDLSAEDPVGCKSCACNPLGTIPGNPCDSESTGYCYC 481  
421 KELVTGQRCDQCLPHQWGLSNDLDCRCPDCLDGLGALNNSCEDSGCSCCLPMMGRQCN 480  
482 KELVTGQRCDQCLPHQWGLSNDLDCRCPDCLDGLGALNNSCFABSGQSCSRPHMGRQCN 541  
481 EYESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTCGPFVRYPEGAYLEFFI 540  
542 EYEGYFATLDHYIYEAEANLPGVWVVERQYIQDRIPSWTCGPFVRYPEGAYLEFFI 601  
541 DNPFSMEYELIRYEPOLPHWEKAVITVORPKIPASSRCGNVTDPDDNQVVSISPGS 600  
602 DNPFSMEYELIRYEPOLPHWEKAVITVORPKIPTSSRCGNVTDPDDNQVVSISPGS 661  
601 RYVVLPRPVCFEKGMNYTVRLLEPQYTAGSDVESPVTFFDLSVLMPCYCKSLDIFTVGGG 660  
662 RYVVLPRPVCFEKGMNYTVRLLEPQYTAGSDVESPVTFFDLSVLMPCYCKSLDIFTVGGG 721  
661 GGEVTNSAWETFORIRCLNSRSVVTPTMTDVCNRIIFSISALIHOTGLACSDPQGS 720  
722 GGEVTNSAWETFORIRCLNSRSVVTPTMTDVCNRIIFSISALIHOTGLACSDPQGS 781  
721 SSVCDPNGQCCOCPNVVGRICNRCAPGTGFGNGCKPCDCHLQGSASAFCDATGQCH 780  
782 SSVCDPNGQCCOCPNVVGRICNRCAPGTGFGNGCKPCDCHLQGSASAFCDATGQCH 841  
781 CFQGYARQCDCLRGYNGFSPQCCQNGHALDCDVTGECISQDQYTHGNCERCLAG 840  
842 CFQGYARQCDCLRGYNGFSPQCCQNGHALDCDVTGECISQDQYTHGNCERCLAG 901  
841 YGDDPIIGSDHCRPCDGPDSGRQFARSQYDQVTLQACVCDPGYIGSRCDCCASG 900  
902 YGDDPIIGSDHCRPCDGPDSGRQFARSQYDQVTLQACVCDPGYIGSRCDCCASG 961  
901 PFNPSDFGGSCQPCQCHNITDTPDPCADKQTCRCLKLYHTEGHCQCLQYGYGDAL 960  
962 YFNGSEYGGSCQPCQCHNITDTPDPCADKQTCRCLKLYHTEGHCQCLQYGYGDAL 1021  
961 RQDCKVCNVLGTVKEHCHGSDCHDKATQCCSCLPNVIGONCDRCAPNTWOLASGTGC 1020  
1022 RQDCKVCNVLGTVKEHCHGSDCHDKATQCCSCLPNVIGONCDRCAPNTWOLASGTGC 1081  
1021 GPCNNAHSGPSCNBTGQCCQMPFGGRTSCQELFWGDPDVECRACDCDPRGIET 1080  
1082 DFCNNAHSGPSCNBTGQCCQMPFGGRTSCQELFWGDPDVECRACDCDPRGIET 1141  
1081 POCQOSTQCCVCEGVEGPRCDKTRGYSVGFVFPDCTPCHOCFALWDALIGELTNRTHKFL 1140  
1142 POCQOSTQCCVCEGVEGPRCDKTRGYSVGFVFPDCTPCHOCFALWDALIGELTNRTHKFL 1201  
1141 EKAKALKISGIVGPVRETVDVSEKQVNEIKDILAQSPAAPLKNIGILLPEAEKLIKDYT 1200  
1202 EKAKALKISGIVGPVRETVDVSEKQVNEIKDILAQSPAAPLKNIGILLPEAEKLIKDYT 1261  
1201 EKQAOVEVKLTDITASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1260  
1262 EMNAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIOGALDSI 1321  
1261 TKYFQMSLEAEKRVNASTTDPNSVTQSGALTRVEDLMLERESPYPKEQOEQOARLLDEL 1320  
1322 TKYFQMSLEAEKRVNASTTDPNSVTQSGALTRVEDLMLERESPYPKEQOEQOARLLDEL 1381  
1321 AGKLOSLDLASAAQMTCTGTPGACSSSECGPNCRDEGEKCGGPGCGGLVTVAHSAW 1380  
1382 AGKLOSLDLASAAQMTCTGTPGACSSSECGPNCRDEGEKCGGPGCGGLVTVAHSAW 1441

1381 QKAMDPRDVLASAEVEQLSKMVSSEAKVTRADBEAKQNAQDVLTKTNATKEKVDKSNEDLR 1440  
1442 QKAMDQDVLASAEVEQLSKMVSSEAKVTRADBEAKQNAQDVLTKTNATKEKVDKSNEDLR 1501  
1441 NLIQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1500  
1502 NLIQIRNFILTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1561  
1501 QCSAADTARABELLLEBEAKGASKATDVVKVTADVMVKALBEAEKAAQVAEKAHKOADEDIQ 1560  
1562 QHSAADTARAEMLLEBEAKGASKATDVVKVTADVMVKALBEAEKAAQVAEKAHKOADEDIQ 1621  
1561 GTQNLTSIESETAASSETLTNASORISKLENNVBEELKKAQNSGEAEYIEKVVSQVK 1620  
1622 GTQNLTSIESETAASSETLTNASORISKLENNVBEELKKAQNSGEAEYIEKVVSQVK 1681  
1621 NADDVKTLDELDEKVKYKVESLIAQKTESADARKAEKLLQNEAKTLLAQANSKLQLE 1680  
1682 SAEVDKTLDELDEKVKYKVESLIAQKTESADARKAEKLLQNEAKTLLAQANSKLQLE 1741  
1681 DLERYEDNQYLEDKQAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725  
1742 DLERYEDNQYLEDKQAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 8  
US-10-443-349-4  
; Sequence 4, Application US/10443349  
; Publication No. US20040023856A1  
; GENERAL INFORMATION:  
; APPLICANT: Buigeson, Robert E.  
; APPLICANT: Wagon, David W.  
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE  
; FILE REFERENCE: 10287/021003  
; CURRENT APPLICATION NUMBER: US/10/443,349  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/161,872  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 08/735,893  
; PRIOR FILING DATE: 1996-10-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(250)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (251)...(437)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (438)...(807)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (808)...(840)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (841)...(1196)  
; OTHER INFORMATION: Human B1 chain  
US-10-443-349-4

Query Match 58.1%; Score 5482; DB 16; Length 1196;  
Best Local Similarity 62.4%; Pred. NO. 1.4e-300;  
Matches 1076; Conservative 46; Mismatches 33; Indels 570; Gaps 1;  
1 EPYCIIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTTAPNRLKIWWQSENGVENV 60

Db 42 EYCVSHLQEDKCFIENSQDPYHETLNPSHLIENVTTPAPNRLKIWQSENGVNV 101  
Qy 61 TIQLDEAEFFTHLIMFKTPRPAAMLIERSSDFGKTGWVRYPAYDCESFFPGISTGP 120  
Db 102 TIQLDEAEFFTHLIMFKTPRPAAMLIERSSDFGKTGWVRYPAYDCESFFPGISTGP 161  
Qy 121 MKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSRIQNLKIKITLRIKFKVLH 180  
Db 162 MKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSRIQNLKIKITLRIKFKVLH 221  
Qy 181 TLGDNLLSRMEIRKYYAVYVDMVVRGNCFCYGHASECAPVDGVNNEEVGVHGHCMCR 240  
Db 222 TLGDNLLSRMEIRKYYAVYVDMVVRGNCFCYGHASECAPVDGVNNEEVGVHGHCMCR 281  
Qy 241 HNTKGLNCELQMDFTDHPWRPAEGRNSVACKKNCNEHSSCHFDMAVFLATGNVSGV 300  
Db 282 HNTKGLNCELQMDFTDHPWRPAEGRNSVACKKNCNEHSSCHFDMAVFLATGNVSGV 341  
Qy 301 CNDCHNTMGRNCECKPFPYQHPERDIRDPNLCBPCTCDPAGSENGICGDIYDFSVGL 360  
Db 342 CDDCCQNTMGRNCECKPFPYQHPERDIRDPNLCBPCTCDPAGSENGICGDIYDFSVGL 401  
Qy 361 TAGQCRCKLHVEGERCDVCKEFGYDLSAEDPYGCKSCACNPLGTTIPGNCPCDSEYCYC 420  
Db 402 TAGQCRCKLHVEGERCDVCKEFGYDLSAEDPYGCKSCACNPLGTTIPGNCPCDSEYCYC 437  
Qy 421 KSLVGTQRCDQLPQHWGLSNDLDCRCDLGLGALNNSCEDSGQSCCLPHMIGRCN 480  
Db 438 ----- 437  
Qy 481 EVESGYFTTLDHYIYEAEANLGPVVVVERQYIQDRIPSWTGPFGFVRVPEGAYLEFFI 540  
Db 438 ----- 437  
Qy 541 DNIPIYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVLSLSPGS 600  
Db 438 ----- 437  
Qy 601 RYVLPFRVCFEKGMYTVRLPELPOVTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGGS 660  
Db 438 ----- 437  
Qy 661 GDGEVNTSAWETFORVCLSENSVVKTPMTDVCERNLIFSALIHQTLGACECDPQSL 720  
Db 438 ----- 437  
Qy 721 SSVCDPNGGQCQCPNVVGRTCNRCAPGTFGFGPNGCKPCDCHLQGSASFDAITGQCH 780  
Db 438 ----- 437  
Qy 781 CFQGIYAROCRLCPGYWGFSPCQPCQNGHALDCDVTGECLSQDVTGHCNRCERCLAG 840  
Db 438 ----- 437  
Qy 841 YYGDPITIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTILQACVCDPGYIGSRCDDCASG 900  
Db 438 ----- 437  
Qy 901 FFGNPSDFGSGCQPCQCHNIDTDPDCAKDTGRCLKLYTEGDHQCQLCOYGYGDAL 960  
Db 438 ----- 437  
Qy 961 RQDCRCVCNLYLTVEKHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCPNTWQLASGTGC 1020  
Db 438 -----CVNLYLTVEKHCNGSDCHCDKATGQCSCLPNVIGQNCDCRCPNTWQLASGTGC 491  
Qy 1021 GPCNCAHSGFSGSCNEFTGQCCQMPFGGRGTCSCQELFWGDDPVECRACDCDPRGIET 1080  
Db 492 DPCNCAHSGFSGSCNEFTGQCCQMPFGGRGTCSCQELFWGDDPVECRACDCDPRGIET 551  
Qy 1081 PQCDOSTGQCVGVEGPRCKTRGYSVFPDCTPCHQCFALDAIIGELTNRTHKFL 1140

Db 552 PQCDOSTGQCVGVEGPRCKTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHREL 611  
Qy 1141 EKAKALKISGVIGPYRETVDSEKKNWEIKDILASPAEPKLNIGILFEEAEKLIKQVT 1200  
Db 612 EKAKALKISGVIGPYRETVDSEKKNWEIKDILASPAEPKLNIGILFEEAEKLIKQVT 671  
Qy 1201 EKMAQVEVKLTDTASQSNSTAGELQALQAEBSLDTKVKELAEQLEFFIKNSDIQGALDSI 1260  
Db 672 EKMAQVEVKLTDTASQSNSTAGELQALQAEBSLDTKVKELAEQLEFFIKNSDIQGALDSI 731  
Qy 1261 TKYFQMSLEAEKVNASTTDPNSTVQSALTRDRVEDLMLERESPKEQOEQOEARLLDEL 1320  
Db 732 TKYFQMSLEAEKVNASTTDPNSTVQSALTRDRVEDLMLERESPKEQOEQOEARLLDEL 791  
Qy 1321 AGKLSLDLSAAQMTCTGPPGADCSSECGGPNCTDEGEKKCGGPGCGGLVTVAFSAW 1380  
Db 792 AGKLSLDLSAAQMTCTGPPGADCSSECGGPNCTDEGEKKCGGPGCGGLVTVAFSAW 851  
Qy 1381 QKAMDPRDVLSEAEVQESLKMVSEAKVADBAKQADQVLLKTNATKEKVDKSNEDLR 1440  
Db 852 QKAMDPRDVLSEAEVQESLKMVSEAKVADBAKQADQVLLKTNATKEKVDKSNEDLR 911  
Qy 1441 NLIKOIRNFUTSDADLDSIEAVANVLKSGNASTPQOLQNTLTERIRVETLSQVEVIL 1500  
Db 912 NLIKOIRNFUTSDADLDSIEAVANVLKSGNASTPQOLQNTLTERIRVETLSQVEVIL 971  
Qy 1501 QOSADITARELLEBAKASKATDKVTADVVKALBEAEAKAQAIAKQADEDIQ 1560  
Db 972 QOSADITARELLEBAKASKATDKVTADVVKALBEAEAKAQAIAKQADEDIQ 1031  
Qy 1561 GTQNLTSISEETAASEETLTNASQISKLERNVEELKKAQNSGEAEYIEKVYVSVKQ 1620  
Db 1032 GTQNLTSISEETAASEETLTNASQISKLERNVEELKKAQNSGEAEYIEKVYVSVKQ 1091  
Qy 1621 NADDVKTKLDGELDEKYEKVESLIAQTESADARKAELLQNEAKTLQAQNSKLQLE 1680  
Db 1092 SAEDVKTKLDGELDEKYEKVENLIAKTESADARKAELLQNEAKTLQAQNSKLQLE 1151  
Qy 1681 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISKVAVYSTCL 1725  
Db 1152 DLERKYEDNOKYLEDKAQELVRLEGEVRSLLKDISKVAVYSTCL 1196

RESULT 9  
US-09-938-275-8  
; Sequence 8, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 1801  
; TYPE: PRT  
; ORGANISM: Rattus No. US20020111309A1vegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P15800  
; DATABASE ENTRY DATE: 1990-04-01  
US-09-938-275-8

Query Match 52.38; Score 4936; DB 9; Length 1801;  
Best Local Similarity 51.28; Pred. No. 1.5e-269;  
Matches 887; Conservative 297; Mismatches 530; Indels 20; Gaps 8;  
Qy 1 EYCVSHLQEDKCFIENSQDPYHETLNPSHLIENVTTPAPNRLKIWQSENGVNV 60  
Db 77 QPYCIVSHLQDEKKCFIENSQDPYHETLNPSHLIENVTTPAPNRLKIWQSENGVNV 136

QY 61 TTQLDLAEFFHTHLIMFKTFRPAAMLIERSDFGKTGWVYRFPAYDCESSFFGISTGP 120  
DB 137 TTQLDLAEFFHTHLIMFKTFRPAAMLIERSDFGKTGWVYRFPAYDCESSFFGISTGP 196  
QY 121 MKKVDIICDSYSOIEPSTEGEVIFRALDPKFIKEDPSRIQNLKIKTIRIKFKVLH 180  
DB 197 PRWDVVCESYSIEPSTEGEVIFRALDPKFIKEDPSRIQNLKIKTIRIKFKVLH 256  
QY 181 TLGDNLDRMIREKYYAVYVDMVRGNCFCYGHASECAPVDGVEEVEGVHGHCMCR 240  
DB 257 TLGDNLDRMIREKYYAVYVDMVRGNCFCYGHASECAPVDGVEEVEGVHGHCMCR 316  
QY 241 HNTKGLNCLCNDMFYHDLRWRPABGRNSNAKCKNCNEHSSCHFDMAVFLATGNVSGV 300  
DB 317 HNTKGLNCLCNDMFYHDLRWRPABGRNSNAKCKNCNEHSSCHFDMAVFLATGNVSGV 376  
QY 301 CNCONHTWGRCEQCPYFQHPERDIRDPNLCEPCTCDPAGSNGGICDGYTDFSVGL 360  
DB 377 CDGQCHNTAGRHCLCRPFYFDRDPKMDRDPACRCPDCCDPGSGDGGCDSDHDPVGL 436  
QY 361 IAGQCRKLFVEGERCDVCKEGPYDLSABDPYCKSCANPLGTPPGNCPDSETGYCYC 420  
DB 437 VSGQCRKEHVWTRCQCRDGFGLSAGNPRGQCRQCNSRGTPGCTCDSSSGTCFC 496  
QY 421 KRLVTGRCDOCLPQHWGLSNDLDCRCPDCCDLGGALNNSCSEDSQCSCLPHMIGROCN 480  
DB 497 KRLVTGRCDOCLPQHWGLSNDLDCRCPDCCDLGGALNNSCSEDSQCSCLPHMIGROCN 556  
QY 481 EVESGYFTLTHYIYEAEANLPGVWVYEROYIQRIPSWTGPFGVVRPAGVLEPFI 540  
DB 557 QVQPGYRPLDLHTWAEAGH-GQVLEVVRLVTRNRETPSTMGVGVRLREGQVEFV 615  
QY 541 DNPYSMEYILLRYEPOLPDHWEKAVITVORPKTPASSRGNTVPDDNQVUSISPGS 600  
DB 616 TSLFRAMDYOLLRWEPQVQWAELELVVQRPVPSAHSPCHVLFUDRDRQGMHLHPT 675  
QY 601 RYVLPREPVECFEGMNYVLELPPQVYTAGSDVESPYT---FIDSLVLMYPCKSIDIFT 656  
DB 676 RVLVFRPVLCLPGLSKLXLKLTG-TGGRAPHTPTPGSGGILDSLVLQPHVLMLEP- 733  
QY 657 VGSGBGEVNTSAWETQVRVRCLENSRSVVKTMPTDVCNRIIPSIHALHQTGLACECDP 716  
DB 734 ---SGDAAALERTTTPERYRCHEEGLMPSKTPLEACVPLISASLVYNGALPQCCDP 790  
QY 717 QGSLSSVCDNGGQCRCPVWVGRTCNRCAPTGFGPGNCKPCDCHLQGSASAFCDALT 776  
DB 791 QGSLSSVCDNGGQCRCPVWVGRTCNRCAPTGFGPGNCKPCDCHLQGSASAFCDALT 850  
QY 777 GQCHFCQGIYARQCDRLPGYWGPPSCQPCCNHGLDDBTVTGECLSCODYTTGNCHER 836  
DB 851 GQCLCRTGAFGLRCHDQCRGOWGFPNCRPCVGNRADECDADHTGACGLGCRDYGGEHCHER 910  
QY 837 CLAGYGDPIIGSDHCRPCPCDGPDSGRQFARSQVDPVTLQLACVCDPVGYSRCD 896  
DB 911 CIAGFHGDPLPYGGQCRPCPEGPGSQRHATSCHRDYSQIVCHCRAGTGLRCEA 970  
QY 897 CASGFFGNPSDFGSCQPCQCHNIDTTPDCAKDTGRCLCLYHTEGHQCLQCYGY 956  
DB 971 CAPGHGDPKXPGRCQLCECSGNIIDTDFGACDPHTGQCLRLHTEGPHGCHCKPGFH 1030  
QY 957 GDALRQCRKVCNLYLTVHEHNGSD-CHCDKATGQCSCLPNVIGONCDRCAPNTWOLA 1015  
DB 1031 GQAAARQCHRTCNLLGTDPOCRFSTDLCHDSTGQCPCLPHVQGLSCDRCAPNTWFT 1090  
QY 1016 SGTGCGPCNNAHSFPGSCNEFTGQCCMPFGFRGTCSCEQLFWGDDPVECRACD 1075  
DB 1091 SGRGQCPACHPSPARGPTCNEFTGQCHCHAGFGRTCSCEQLHWDGDPGLQCRACD 1150  
QY 1076 RGIETPOCDQSTGQCVVEGVEGRPCNKTGYSGVFPDCTPCHQCFALWDALIGELTNR 1135  
DB 1151 RGIDKPOCHRTGHCSCRPGVSGVRCQCGARGFSGFVFPACHPCACFDWDRVVDLAAR 1210

QY 1136 THXLEKAKALKISVIGPYRETVDSEKVKNEIKDILA--OSPAAEPLKNIGILPEEAE 1193  
DB 1211 TRLEQWAOELOQTGVLGAFESSFLNLQKLGHWQAIVARNTISAATAK----LVEATE 1266  
QY 1194 KLTKDV---TEKMAQVEVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIN 1250  
DB 1267 GLAHEIGKITERITOLEAELTDQDENFNANHALSGLERDGLALNLTQLDQHLDLKH 1326  
QY 1251 SDTQGLSDITKYPQMSLAERKVNASTTDPNSTVEQSALTDRDVEDLMLERESPKEQ 1310  
DB 1327 SNFIGNYDSIRHAHSOSTEABRSANASTFAIPSPVNSADTTRRAEVLMAQARENROH 1386  
QY 1311 EQQARLDLDELAKQLSLDLSAAQMTCTGTPPGADCSSESCGPGNCRTEBGEKCGGPGCG 1370  
DB 1387 LANQOALGRLSHTHTLSLTGNNELVCGAPDAPCATSPCGGACRDEQDQPRCGGLGCS 1446  
QY 1371 GLVTVAHSAQKMDRDRVLSALAEVEQLSKVSEAKVRADEAKQNAQDVLKTNATKE 1430  
DB 1447 GAAATADALAGRARHTQAEQALVEGGGILSVSETRRQAEEAQQRAQALDKANASRG 1506  
QY 1431 KVDKSNEDLENLIKQIRNFLETSDSLDSTEAVANEVLKSGNASTPQQQLNLTEDIRERV 1490  
DB 1507 QVEGANQELRELQNVKDFLSQSGADPDSIEMVATRVLDISIIPASPEQIQRLASEIAERV 1566  
QY 1491 ETLSQVEVILQOQSAADTARAELLLEERAKASKATDVKVTADVMVKEALEBAEAQVAAEK 1550  
DB 1567 RSLADVDTILAHMTGMDVRAEQQLQDAQRARSRAEGERQKAETVQAALEEAQAAQAG 1626  
QY 1551 AIKQADDEDIQTQNLTSIESETAASEETLUNASQISKLERNVEELKRAAQNSEAEY 1610  
DB 1627 AIRGAVVDTKNTQTLQOQVEMAGTEQSLNSASERARQLHALLEALKKRAAGNSLAAS 1686  
QY 1611 IEKVYVSVQNADDVKTLDGELDEKYEKVKYVESLIAKTEESADARRKAEQLONEAKTLLA 1670  
DB 1687 AEETAGSAQSRAREAEKQLEQVGDQYQTVRAAERKAEGVLAQAARAEQLEARDERGLQ 1746  
QY 1671 QANSKLQLEDLEKYEKEDNQYLEDKAEQELVLEGEVRSLLKDISSEKVAVYSTC 1724  
DB 1747 AAQDKLQRLQLEGTYBENERELEVKAAQJGLAEKRSVLQAINQVQIYNIC 1800

## RESULT 10

US-09-845-583-6  
; Sequence 6, Application US/09845583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champiaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1799  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-6

Query Match 52.1%; Score 4914; DB 9; Length 1799;

Best Local Similarity 51.0%; Pred No. 2,5e-268;

Matches 883; Conservative 297; Mismatches 534; Indels 18; Gaps 8;

QY 1 EPHYCVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKHWQSENGENV 60

DB 77 QPYCIVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKHWQSENGENV 136

QY 61 TTQLDLAEFFHTHLIMFKTFRPAAMLIERSDFGKTGWVYRFPAYDCESSFFGISTGP 120

Db 137 TIQDLEAEFHFTLHMTKTFRAAMLVERSDFGRTWVYRFSYDCGADFFGIPLAP 196  
Qy 121 MKYVDDIICDSRYSDIEPSTGEVIFRALDPFAKIEDPYSPRIQNLKIKTNLRKFKVLH 180  
Db 197 PRWDVVCESSRYSEIEPSTGEVIVRLDPAIPDPYSRIQNLKIKTNLRVNLRLH 256  
Qy 181 TLGNLDSRMEIREKYYAVYVDMVRNCFYGHASECAPDVGNEEVEGMVHGQWCR 240  
Db 257 TLGNLDDPREIREKYYAYELVIRGNCFYGHASQCAPAPAHAEWVHGACICK 316  
Qy 241 HNTKGLNCELQWDFYHDLPMRPAEGRNSNACKCNHESSCSHFDMVFLATGNVSGV 300  
Db 317 HNTKGLNCEQODFYDLPWHPAEADGHTHACKCECNHGHSHCFDMVFLATGNVSGV 376  
Qy 301 CDNCOHNTMGNCEOCKEYFQHPERDIPNLCPECTCDPAGSENGICDGYVDFSVGL 360  
Db 377 CDGQHNTHAGHCECRFFFYDPTKMRDFAVRCPCDDPMGQDGRCDHDDPVLGL 436  
Qy 361 IAGQCRKLVHEGERCDYCKEGFYDLSAEDPYGKSCACNPLGTIPGNPCDSTGYCYC 420  
Db 437 VSGQCRCKEHVVGTRCQCRDGFGLSASDPRGQRCQCNRGTVPGSSPCDSSSGTCFC 496  
Qy 421 KELVTGQRCDQLPOHWGLSNDLDCRCPCDCLGALNNSCESDSGQSCLPNMGIRQCN 480  
Db 497 KELVTGHCGRCLPGHWSLHDLGRCPCDCLGALDPPQDEATGQCPCRQHEMIGRCE 556  
Qy 481 EVESGYVFTLDHYIYEAEEANLPGVVVVRQVYQIDRIPSWTGPFGFVRPEGAYLEFFI 540  
Db 557 QVQPGYFRFLDLHTWEAAQ-GQVLEVVRELVNRETPTSWTGGFVRLREGQVEFLV 615  
Qy 541 DNIPTSMYEILIRVEPOLPDHWEKAVITVORPGKIPASSRCNVTVPDDNQVSVLSFGS 600  
Db 616 TSLPRAMDYLLRWEPPQVEQWAELELMVORPGFVSASHSCGHVLPKDDRIQMLHPNT 675  
Qy 601 RVVLPVRVCFKGMNVTYRLPEQYTAGSDVESPT--FIDSILVMPYCKSDIDFTVG 658  
Db 676 RVLVFRPVPCLPEPGYSYKLLKLG-TGRQAQPEYSYGLLIDSLVLQPHVLEMP--- 731  
Qy 659 GSGDGEVNTSAWETFORXRCLENSRSVVKTPMTDYCRNIIFISALIHQTGLACDPPQ 718  
Db 732 -SGGDAALERRTFTERYRCHBEGLMPSKAPLSETCAPLLISVSALIVNGALPCQDPPQ 790  
Qy 719 SLSSVCDPNGGQCRPNVVGRTNRCAPGTGFGPNCKPCDCHLQGSASFCDALTGQ 778  
Db 791 SLSSCSPHGGQCRKPGVVGRRDVCATGYVGGPGACQACQSPDGLSALCEGTSGQ 850  
Qy 779 CHCFQIIVARQCDCLPGVWGPSPQPCQCNHALDCDVTGECILSCODYTTHNCERCL 838  
Db 851 CFCRGAFLGRCDHCRQGWGFNCRPCVNGRADECDTHTGACLGCRDYTGGEHCRCI 910  
Qy 839 AGYGDPIIGSDHCRPCPCPDGDSGRQPARSCVQDPVTQLACVCDPGVIGSRCDDCA 898  
Db 911 AGFHGDPLPYGGQCRPCPCPEGPGSQRHFAFCHRDYSGQIVCHCRAGYTLRCEACA 970  
Qy 899 SGFFGNPSPFGSCOPCOCHNIDTTPDPAKDKTGRLKCLYHTEGDCOLCOVGYGYD 958  
Db 971 PGPFGSPSPGRCQLCECSGNIDPMDPADCPHTGQCLRLCHNTEGPHCGYCKPGFHGQ 1030  
Qy 959 ALRQDCKRCVNYLGTVEKHGNSD-CHCDKATGQSCCLPNVIGONCDRCAPNTWQLASG 1017  
Db 1031 AARQSCHRCTNLLGTPRRCFSTDLCHCDPSTGQCPCLPHVQGLNCDHCAFNFMFTSG 1090  
Qy 1018 TSCGPNCAHNSFGPCNNEFTGQCCMPFGGRTCSCEQLFMWDPPVECRACDPCRG 1077  
Db 1091 RCQPCACHPSRAGPTCNEFTGQCHAGFGGRTCSCEQLYWGDPGLQCRACDPCRG 1150  
Qy 1078 IFTPCDQSTGQCVCEVGEGRBCDKTRGYSGVFPDCTPCHQCPCALWDALIGELTNRTH 1137  
Db 1151 IDKPOCHRSTGCSRCRPGSVGRVQCCARGFSGFPFACHPCFACFGDWDVVDLAATR 1210  
Qy 1138 KELEKALKISGVITGPIRETVDSEKKNYETKDLA--QSPAEPPLKNIGLPEAEKL 1195

Db 1211 RLEQWAQELQQTGVLGAFESFPLNQGKLGVMYQAIMSARNASAASTAK---LVBATBGL 1266  
Qy 1196 TKDV--TEKMAQVVKLTDTASQSNSTAGELGALQAEASLDKTKVLAELQLEIKNSD 1252  
Db 1267 RHEIGKTTBRLTQLEABLTAVODENPNANHALSGLERDGFALNLTLRQLDQHLLEIKHSN 1326  
Qy 1253 IQGALDSITKYFQMSLEAKRVNASTTDPNSTVQSALTRORVEDMLERESPFFKEQEE 1312  
Db 1327 FLGAVDSIRHAHSQSTEARERANASTFAVPSVNSADTTRRTEVLMGAQKENFNROHLA 1386  
Qy 1313 QARLLDELAKGLQSLDLSAAQMTCTGTPPGADCSSECGGNCRDTEBEKKCGPGCGGL 1372  
Db 1387 NQALGRLSAHAHTLSLTGINELVGAPODAPCATSPCGGACGRDEGPGCGGLGCSA 1446  
Qy 1373 VTVASAWOKAMDFDRDVLASALAEVQLSKMVSEAKVRADAEAKQNAQDVLLKTNATKEV 1432  
Db 1447 AAPADLALGRARHSQAELQALVEGGILSRVSETRRQAEAAQRAQAALDKANASRGV 1506  
Qy 1433 DKSNEIDLNLIIQIRNFLTEDSADLDSIEAVANVLKSGNASTPQOLQNLITEDIRERET 1492  
Db 1507 EQANQELRELIQNVDFUSQEGADPDSIEMVATRVLDISIPASPEQIQLASEIARVRS 1566  
Qy 1493 LSOVEVILQOSAADIARAEELLEAEKASKSATDVKVTADMVKEALEEAEKQVAABKAI 1552  
Db 1567 LADVTLIHTMCDVRAEQQLQDAHRAERSRAEGERQKAETVQAALEEAQRAQGAAGAI 1626  
Qy 1553 KQADEIQOTONLLTSIESETTASBETLVNASQRIKERNVEELKRXAAQNSGEAEYIE 1612  
Db 1627 RGAVPTQNTQETLQVQERMAEKSLNSAGERARQDLALLEALKLKRAAGNSLAATAE 1686  
Qy 1613 KVYVSKQVQADVKKTLDCGLDEKVKYKVESLTAQKTESADARRKAEILLQNEAKTLLQA 1672  
Db 1687 ETAGSQSARAEAKQKQREVGQDQVTVZALAEKAEGLVLAQAQARAEQLRDEARDLQAA 1746  
Qy 1673 NSKLQLEDLERKYEDNQYKEDKAQELVRLGEVRSLLKDKISEKVAVYSTC 1724  
Db 1747 QDKLQLELEGTYEENERALEGKAAQLDGLAEARMSVLQAINLQVQIYNTC 1798  
RESULT 11  
US-09-938-275-9  
; Sequence 9, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1798  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P55268  
; DATABASE ENTRY DATE: 1996-10-01  
; US-09-938-275-9  
Query Match 51.9%; Score 4890; DB 9; Length 1798;  
Best Local Similarity 50.3%; Pred. No. 5.7e-267;  
Matches 871; Conservative 305; Mismatches 542; Indels 12; Gaps 6;  
Qy 1 EPYCIVSHLCEDKKCFICSDRDPVHETPLNPSHLIENVVTTFAPNKLKIWQSENGENV 60  
Db 74 QPVCIVSHLQDEKKCFICSDRDPVHETPLNPSHLIENVVTTFAPNKLKIWQSENGENV 133  
Qy 61 TIQDLEAEFHFTLHMTKTFRAAMLVERSDFGRTWVYRFSYDCGADFFGIPLAP 120  
Db 134 TIQDLEAEFHFTLHMTKTFRAAMLVERSDFGRTWVYRFSYDCGADFFGIPLAP 193





Db 194 PRHWDVVCESYSEIEPSTEVEIYRVLDAIPDPYSSRIQNLKLTNRVNLRLH 253  
Qy 181 TLGDNLDSRMBEIRKYYAVDVNRGNCFCYGHASCAPVDGVNVEEVMGHCHCMR 240  
Db 254 TLGDNLDSRMBEIRKYYAVDVNRGNCFCYGHASCAPVDGVNVEEVMGHCHCMR 313  
Qy 241 HNTKGLNCELMDFYHDLFWPRAEAGNRSNACKKNCNEHSSCHFDMAVFLATGNVSGV 300  
Db 314 HNTKGLNCELMDFYHDLFWPRAEAGNRSNACKKNCNEHSSCHFDMAVFLATGNVSGV 373  
Qy 301 CNCOHNTMGRNCEOCKEPPYFPHREDIRDNLCPECTCDPAGSENGICGDTDFVGL 360  
Db 374 CDGCOHNTMGRNCEOCKEPPYFPHREDIRDNLCPECTCDPAGSENGICGDTDFVGL 433  
Qy 361 IAGQCRCKLHVEGERDVCCEGYDLSAEDPDYGCCKSCACNPLGTPPGNCPDSETGYCYC 420  
Db 434 VSGQCRCKEHVGTTCQCRDGFGLSISDPGCRRCQCNARGTVPGTPCDPNSGSCYC 493  
Qy 421 KGLVGTQRCDCQCLPOHWGLSNDLDCRCPDCLDGGALNNSCSEDSGCSCUPLMIGROCN 480  
Db 494 KGLVGTQRCDCQCLPOHWGLSNDLDCRCPDCLDGGALNNSCSEDSGCSCUPLMIGROCN 553  
Qy 481 EYESGYFTLTHYIYEAEANLPGVNVVERQYIQRIPSTGTFVVRPEGAYLEFFI 540  
Db 554 QVQPGYFRPFLDELLEAENR-GQVLDVVERLVTGPTSPWTGSGFVRLQEGQTEFLV 612  
Qy 541 DNPVSMVEIILIRVEPQLPDHWEKAVITVQPGKIPASSRCGNVTPDDQVQVLSPGS 600  
Db 613 ASVPNAMDYLLRLLEPQVPEQWAELELIVRPGVPVPAHSLGCHLVPRDRIRQGTLPQHA 672  
Qy 601 RVVLPVPRVCFEKGMYTVRLPELPOVTASGVDSVSPYT----FIDSLVIMPYCKSLDIFT 656  
Db 673 RVLIFPNVCLPFGISYKHLKLV-RGSAQAPETPYSGPGLLIDSLVLPVLENF- 730  
Qy 657 VGSQDGEVNTSAWETPQRYRCLNRSRVKTPMTDVCNRIIFPSALIHQTLACBCDP 716  
Db 731 ---SGDAALERQATFERYQCHEEGLVPSKTSPEACAPLLISLTLYNGALPCQNP 787  
Qy 717 QGSLSVCDPNGCQOCQRCVNRVGTNRNRCAPGTGFGNGKPCPCDCHLQGSASFCDAIT 776  
Db 788 QGSLSVCDPNGCQOCQRCVNRVGTNRNRCAPGTGFGNGKPCPCDCHLQGSASFCDAIT 847  
Qy 777 GQCHFCQGIYARQCDRLCPGYGFPSCQPCQNGHALDCDVTGBCSLCQDVTYTHGNER 836  
Db 848 GQCLRTGAFGLRCDACQCGQWGFSCPCVNGHADECNTHTGACGLGRDITGGEHCR 907  
Qy 837 CLAGYVGDPIIGSDHCRCPDGDGQRCQFARSCYQDPVTLQACVDCPYIGSCDD 896  
Db 908 CIAGFPGDPRLPYGAQRCPCPCPEGSGQRHFSCHQDEYSQQIVCHCRAGTGLRCEA 967  
Qy 897 CASGFFGNPSDFGSGCQPCQCHNIDITDPEACDKDTRCLKLYHTEGDHQCQCYGY 956  
Db 968 CAPGQFGDPSRPGRCQCLCECSGNDPMDPDACDPHGGQLRCLHTEGPHCAHSGKPGFH 1027  
Qy 957 GDAIROCDKRCVNYLGTVEHNGSD-CHCDKATGQCSCLPNVIGQNCDCRCAPIWQLA 1015  
Db 1028 GQAARQSCRCCTCNLLGTNPQPCSPDQCHCPSSGQPCLENVQALAVDRCAPIWQLA 1087  
Qy 1016 SFTGCGPCPCNAHSPGSCNFTGQOCQWPGFGRTCECCBLFWGDPDVECRACDDP 1075  
Db 1088 SHGQCPACLPSPGEGPCNFTGQCHCLCGFGRTCECCBLFWGDPDVECRACDDP 1147  
Qy 1076 RGIETPQDQSTGQCVVCVGVGBCPKCTKTRGYSGVFPDCTPCHQCFALWDAILGELTNR 1135  
Db 1148 RGIETPQDQSTGQCVVCVGVGBCPKCTKTRGYSGVFPDCTPCHQCFALWDAILGELTNR 1207  
Qy 1136 THKFLKAKALITSGVIGVRETVDSVEKKVNEIKDIL-AQSPAEPKNIIGLFEAEK 1194  
Db 1208 TORLEORAGELQGTGVLGAFEGSFWIMQKGLIVQGIIVGARNTSAASTAQLVEATEELRR 1267  
Qy 1195 LTKDVTETKMAQVEVKLTDTASQNSSTAGBELQALQAEASLDTKTVKELABQLBFKNSDIQ 1254

Db 1268 EIGEATEHLTQLEADLTDVQDENFNANHALSGLERDLALNLTLRQLDQHLDLLKHSNFL 1327  
Qy 1255 GALSITSITKYFQMSLEAEKRVNASTTDPNSTVQSALTDRVRVEDLMLERSPPKEQEEBOA 1314  
Db 1328 GAYDSIRHAHSQSAEARRANTSALAVSPVPSNSASARHRTIEMDAQKEDFNSKEMANO 1387  
Qy 1315 RLDELAKGLQSLDLSAAQMTCTGTPPGADCSSECGGPNCRTEDEKCKGPGCGGLVT 1374  
Db 1388 RALGKUSANTHTLUSLTDINELVCGAGLHHDRTSPCGGACRDEDDGPRCGGLSCNGAAA 1447  
Qy 1375 VAHSAMQKAMDFDRDVLASAEVQLSKMVSEAKVRADEAKQNAQDVLLKTNAKVKVDK 1434  
Db 1448 TADLALGRAHTQAEQLRALAEGSILSRVAETRRQASEAQQAALDANASRGQVEQ 1507  
Qy 1435 SNEDLNLIKQIRNFUTEDSADLDSIEAVANVILKSGNASTPOOLQNLITEDIRVETLS 1494  
Db 1508 ANQELQISQVDFLNQEGADPDS-EMVATRVLELSIPASAEQIOHLAGATIERVSLA 1567  
Qy 1495 QVEVILQOASADTARAELEELIEAKRASKGATDVKTADVMVKEALEEAEAKQAQAAEKIKQ 1554  
Db 1568 DVAILARTVGDVRAEQQLQDARRARSWAEDKQKAEVQAAALEEAQRAQGAIRG 1627  
Qy 1555 ABEDIQGTQNLTSISSETAASEETITNASQRIKSLERNVEELKRKAQNSGEAEVIEKV 1614  
Db 1628 AVADTRDTEQTLVQVQERWAGAEALSSAGERARQDLALLEALKRAGNSLAASAEET 1687  
Qy 1615 VYSVKQADDDVKTLDGELDEKVKYKYESLIAQKTESADARRKAELEIQAETLLAQANS 1674  
Db 1688 AGSAQGAQAEQQLRGPLGDOYQTVKALAEKKAQGVLAQAQAEQLPDEARDLLQAAQD 1747  
Qy 1675 KLQLEDEKRYEDNOKYLEDKAEQVRLGEVRSLLKQISEKAVVYSTC 1724  
Db 1748 KLQRLQLEGTYENBERALESKAAQLDGLAEARMRSVLQAINLQVQYNTC 1797

## RESULT 13

US-10-369-493-5986  
; Sequence 5986, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 5986  
; LENGTH: 1808  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-5986

Query Match 38.7%; Score 3646; DB 15; Length 1808;  
Best Local Similarity 39.5%; Pred. No. 8.5e-197;  
Matches 720; Conservative 307; Mismatches 613; Indels 184; Gaps 37;

Qy 3 YCIVSHLEQDKKFCICDRDPYHETLNP--SHLIENVVTTFAPNRLKIWMQSENGVNV 60  
Db 66 FCIVSHLEQDKKFCICDRDPYHETLNP--SHLIENVVTTFAPNRLKIWMQSENGVNV 125  
Qy 61 TIQDLAEAFHFLHMTFTFRPAAMLIERSDFGKTGWVYRYFAYDCSSFPFGISTGP 120  
Db 126 SISFDLEAFHFLHMTFTFRPAAMLIERSDFGKTGWVYRYFAYDCSSFPFGISTGP 185  
Qy 121 MKVDDIICRSRSDIEPSTGEVIFALDPKAFKIDTVPRIQNLKLTNAIKFKVLH 180

186 PKKHTDVICTSOSVAPSTGGEIYVYKVISPHIVTENPYADEISTLLKITTNLRFNFTKLH 245  
181 TLGDMNLSRMEIRKYYIYAVDMVRGNCFCYGHASCAPVD---GVNEEVE--GMVHG 235  
246 TLGDDLLDVRPRIDEKYYIYAYEIVVRGSCSYGHASRCIPIDPHVSPNTVMERADIVHG 305  
236 HMCWRHNTKGLNCELCEMDPYHDLPRPAEGRNSNACKCNHSSCHSDFMAYFLATGN 295  
306 RCEMNTTEGLNCEKCAFYNLPRPALGDKEKRCQCNHARLCHDFRAVYESSGT 365  
296 -----VSGVCNQCNTMGRNCECKPYPFOHPERDTRDPLNLCPC 337  
366 NSFSKSPFSKFSYFSGVGVGVCDDMHTQCKNCEQCKPFFYRDPRTTDDHVCCLPC 425  
338 TCDPAGSENGGICDGYTDFSVGLIAGCRCKLHVEGERCDVCKEGFYDLSEAEDPYGCKSC 397  
426 ECKAGSQKNGICEBEDAERGLVAGCYCKTVNVDGRCDCRCNGYWNLTETNVDGVCAC 485  
398 ACNPLGTIPGPNPCDBETCYCKLVTCORCDQLPOHWGLSNLDGCRPCDDCLGAL 457  
486 TCNLLGTY--NNEGCDKYTGCTCKRLVTGENDCQCLPEHYGLSEHVDGCKACDCCDIGGY 544  
458 NNSCSDSGCSCLPHWICRQNEVESGYFTLDDHYIYEAEEANLPGVWVVERQYIQD 517  
545 DNTCEITTCCKRBFSGRRRETADSSPYCADIHYVYEAAYNLTRGEVKTREWPSQP 604  
518 RIPSWTGPGFVRVPEGAYLEFFIDN--IPYSMEYELIRYE--POLPDHWEKAVITVQRP 574  
605 HEQTF--GEGFAQAVEGTITV--NPIVEVSQKYNVIIRHGDARDPVGWENIQTWVRP- 660  
575 KIPASRCNGTVPDDNOVLSLSPGSRVYVLRPVCFEKGMNVTVRLEL-----POY 626  
661 EAEGDCSDAPSDDFLARIYFGSRYTEVQPAICLEAGVYELRIQFNEKXGNHQHPE 720  
627 TASGSVDESPTFIDSLVMPYCKSDIFTVGSGDGEVTSAMETQRYRC--LENSRS 684  
721 RAAAN-----ILIDSILLAPPTSELHIPOGSAEAOHLTE-----YNYRQCHLALSLS 769  
685 VIKPTMTDVCNRIIFISALIHOTGLACBDCDQGSLSVSCDNGGCGCQCRPNVVCRTNR 744  
770 LFPDQORNEVCERYVCPFAAALLNKTSECNDCATGVSVCNVOGGQCECKPNVVRRCDDQ 829  
745 CAPGTGFGNGCKPCDCHLQGSASAFCDAITQCHCFQ--GIYARQCDRLCPGYWGFPC 803  
830 CALGTTGFGSGCKKCDCAVSLGNDCKQSCQVCYREKGIYGRQCNCQCGFWGFPEC 889  
804 QPCQCNHALDCDVTGECLSQDYTTGNHCRCLAGYGDPIIGSGDHCRPCPCDGD 863  
890 RTCCQNDHANICQSSGACIECRDLATGHYCDRCQDGYGDFRGLGVGIPCKPCPCGGPT 949  
864 SGQFARSQV---QDPVTLOLACVDPGYIGSRCDDCASGFFGNPDSFGSCQPCQCHN 920  
950 SGYQHADTCYLRNSGNTQDIVCNCKSGYQGERCGCAQNHWSPREVGTGTCERDCN 1009  
921 IDTTDPEACDKDTCRLKCLYHTEGHDHCCQYGYGDALRQDCKVCNVLGTGTVKECN 980  
1010 IDNAMESSCAATGECLKCLHHTEGAQCEHCVGDYGDALKTQCRVCVNELGST-----N 1064  
981 GSDCHDKATGQSCSLPNVIGQNCDCAPNTWOLASGTGCPNCNA-----AHSFGP-- 1033  
1065 STKGADRVSGQPCPDHNIIGMQDQCAENHFWLASGAGEACGCCDSNGVVLNHEGVPHL 1124  
1034 SCNEFTQCCQMPFGGRTCEQELFWGDPDVE--CRACDCCPRGIEPTQCDQDSTGQCV 1091  
1125 QCNIFDQCCQKFGGRKCDQCEDLYWGDPTTDPGCHRCENCPNTPGSKSLQCHRNNGTCE 1184  
1092 QVEGVGPRCKDTRGVSGVFPDCTPCHQCFAWDALIGELTNHTRHFKLEKAKALISGV 1151  
1185 CQAGSGALCNECARGYTGWPYCNPCGECFHOWDNIOMKLOKQVHALIDTANNIEDTV 1244  
1152 IGPVRETVDSEKKNVNEIKDILAQSPAEPKNIIGILFEEAKLTKDVT-----E 1201  
1245 ASAYDADFEMKEETLKETK-----KALSDANISKEDIEEMSKLALLKKQVIAGRE 1295

1202 KMAQVEKVLTDTSQSNSTAGELGALQABAEISLDTKVKELARQLEFIKNSDIQGLDST 1261  
1296 KLGAIETRISNITQAVDPAQKLEH--QKEVDKVTKATIELEDKASKIKEADVLAGNITR 1355  
1262 KYFQMSLEAKRVNATTTDPNSTVQESALTRVEDMLERSPPFKPEQOEQOARLLDE-- 1319  
1356 ESASKSLDAQRRTDAA--IGKLAANQAL---RASELLEKKNKDFEQVYENEEALNEAE 1411  
1320 -LAGLQSLDLSAAQWTCGTPPGADCSSECGGPNCRITDEGEKCGGPG---CGGLVT 1374  
1412 TLILGLLESV--LPKLNQVCG-----ASSAPC-----DALCGGSGCGFCG--- 1451  
1375 VAHSAQKAMDFDRDVLALAEVQESKMYSEAKVRADAKQNAQ-----DVLKTNVA 1427  
1452 -----QSCME-----GAVSKANQAKSPATEADTDLDEKQKEAEVLSIVRDLVLTETTK 1499  
1428 TKEKVDKSN-----DRLNIKIQIRNFLTSDSADLDSIEAVANEVLKSGNA 1473  
1500 AKAEKAYEVAKNTAQANSSRAEDDKTAEELGEFLTAKSSPEQIRNLAEVLGKEIS 1559  
1474 STPQQLNLTEDIRERVETLSQVEVILQOQSAADIAEAEILLEAKRASKSATDVKTADM 1533  
1560 LTPDQITDLTGKIKESLAKINNIDEILNETRGNKSIANLESRAVKANKEAEILLQKAMEE 1619  
1534 VKEALEBAEAKQVAEAKAIKQADEDIQGTQNLILTSIETETAASEETLNTASQRIKSLERN 1593  
1620 IREALQADQAYNNVTSLVEIDTMOVQARELIDKARNSTEAVEGKAQAANTTLAELEGV 1679  
1594 VEELKRAAQNSGEAEYIEKVYVSVKQNAADDVKTLDGEL-----DEKVKVYES----- 1642  
1680 MSGVK-----VEYLQ-----ISEAKNALTTVDAALAAATNAEQNKQIQTDLERA 1725  
1643 --LIAQKTESADARRKAEILLQNEAKTLLAQANSKLQLEDLERKVEDNQKYLEDKAQEL 1700  
1726 TELEKMEGVPAPQQAERAKLRERAKLLYQAORHNDIDNLSK--DSTEMRLDDYETIL 1783  
1701 VRLEGEVRSLLKDISEKVVAVYSTC 1724  
1784 ADLNSRLRVRTREDIHEKTDPHATC 1807

## RESULT 14

US-10-287-971-18  
; Sequence 18, Application US/10287971  
; Publication No. US20040067882A1  
; GENERAL INFORMATION:  
; APPLICANT: Alebrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO 18  
; LENGTH: 1101  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-10-287-971-18

Query Match 31.5%; Score 2967.5; DB 12; Length 1101;  
Best Local Similarity 47.6%; Pred No. 8.4e-159;  
Matches 526; Conservative 168; Mismatches 327; Indels 85; Gaps 12;

QY 1 BPYCVSHLQBDKCFICDSRDPYHETLNPSHLIENVVTFAPNRLKIWQSENGVENV 60  
DB 55 QKYLILSLEGEKQKICDSRDPYHETLNPSHLIENVVTFAPNRLKIWQSENGVENV 114

QY 61 TLOLDEAEFFHLLIMPKTERPAMLIERSDFGKTGWVRYFAYDCSSSFPGLSTGP 120  
DB 115 SRLDEALFRESHILILFKTERPAMLIERSDFGKTGWVRYFAYDCSSSFPGLSTGP 174

QY 121 MKVDIIICDSYSDIEPTEGEVIFRALDPFKTIEDPYSPIQNLKILNIRKFKVLH 180  
DB 175 AQGVGDIVCDYSYSDIEPTEGEVIFRALDPFKTIEDPYSPIQNLKILNIRKFKVLH 234

QY 181 TLGDNLDSRM-EIREKYYAVYDMVRGNCFCYGHASECAPVDGVNEV---EGMVHGH 236  
DB 235 TLGDNLDSRM-EIREKYYAVYDMVRGNCFCYGHASECAPVDGVNEV---EGMVHGH 294

QY 237 CMCRHNTKGLNCELCWDFYHD-LPWRPAEGRNSNACKNCNEHSSCHFDMAVFIATGV 296  
DB 295 CVQHTNDGPNCEKCKDFQDAPWRPAADLQDNACRSCSCNHSRCHFDMTTYLASGGL 354

QY 297 SGVCDNCCHNTWGRNCECKDFYHCHERDIRDNLCEPCTCDPAGSENGGICDGYTDF 356  
DB 355 SGVCDNCCHNTWGRNCECKDFYHCHERDIRDNLCEPCTCDPAGSENGGICDGYTDF 414

QY 357 SVGLIAGQCRKLIHVEGERCDYKGEFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETG 416  
DB 415 ALGSAVAGQCLKENVEGAKCDCKPNHYGLSATDPLGCPQCDNPLGLSLP-PLTCDVDTG 473

QY 417 YCYKRLVTGQRCDQLPQHWGLSNDLDCRCDCDGLGALNNSCEDSGCSCPLHMIG 476  
DB 474 QCLCLSYVTGAHCEBECTVGYWGLHGLHAGCSPDCDDIGGAYSNVCSKPNQCCERPHVTG 533

QY 477 RCNVESEGYFTTLDHYIYEAEAN-----LG-----PGVVVVERQVIQDIRPSW 522  
DB 534 RQSEPAQYFPAPLNFVLYEAEATTLQGLAPLGEITFGQSPAVHVLGEVPVGNVTV 593

QY 523 TQGFVRVPEGAYLEFIDNIPYSMEYELIYEPQLPDHWEKAVITVORPKIPASRRC 582  
DB 594 TQGFVRVPEGAYLEFIDNIPYSMEYELIYEPQLPDHWEKAVITVORPKIPASRRC 649

QY 583 GNTVPDDNOVSLSPGSRVYVLPVPCPEKGMVTVLELPQYTAGSDVESPVTFIDS 642  
DB 650 IPTKQSKQSFALPAATKIMLLPTICLEPDVQYISIDVYFQPLQGESHAHS-HVLVDS 708

QY 643 LVLMPCSKSLDFTVGGSGDGEVTSANETFORCLNRSVVKTPMTDVCNRIIFIS 702  
DB 709 LGLIPQINSLENF-----CSKQDLDEYQHLNVCVEIASAMGPOVLPGACERLIISMS 759

QY 703 ALIHQTLACEDCPQGLSSVCDPNGGOCOCQPNVVGTRCNRCAPTFGFGNGCKPCDC 762  
DB 760 AKLHDGAVACKHPQGSVSGSSRLGGQCCQKPLVWGRCCDRCSGVSVDLGHGHCPC 819

QY 763 HLQGSASAFCDALTGCHCFQGYAQCDRLCPGYWGPSPCCQCNHGLDCTDVTGEC 822  
DB 820 HPQSKDVTCDQVTCQPCHEVSGRCDRLAGYFGFSPCHPCNPAELCDPETGSC 879

QY 823 LSCQDVTGHNRCERLAGYGDPIITGSGDHCPCCPCPDGPDGROFARSCYQDPVTLQIA 882  
DB 880 FNGCGFTTGRNCERCITDGYGNP--SSGQPCRCPLCPDDPSSNQYFAHSCYQNLWSSDVI 937

QY 883 CVCDPGYIGSRCDGASGFGNPSDFGGSCQPCQCHNIDITDDBACKDTCGRCLKLYH 942  
DB 938 CNLQGYTGTQGCSTGYGNPRISGAPCQACANNIDVTDPSRCSVTEGCLRLN 997

QY 943 TEGDHQCLQCYGYGDALQDCKKVCNVLGTVKEHC--NGSDCHCDKATGQCSCLPNVI 1000

998 TQGANCOLCKPHYGSALNQTCTCRCSHASGVSPMECPGGACLCDPVTGACPCLPNVT 1057

QY 1001 GQNCDCRCAVNTWOLASGTGCGPCNCMAHSPGSCNEFTGQCCQCMFPGGRTCECQELF 1060

DB 1058 GLACDRCADGYMNLVPERG----- 1076

QY 1061 WGPDPVECRACDCDPRGIETPQCDQS 1086

DB 1077 -----CQSCDCDPRTSQSHCDQA 1095

RESULT 15  
US-09-925-298-703  
; Sequence 703, Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103  
; CURRENT APPLICATION NUMBER: US/09/925,298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 703  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (243)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (257)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (259)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (471)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (477)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (480)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (484)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (511)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (519)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-298-703

Query Match 22.8%; Score 2154; DB 12; Length 527;  
Best Local Similarity 79.7%; Pred. No. 2.5e-113;  
Matches 437; Conservative 33; Mismatches 42; Indels 36; Gaps 3;

QY 1090 CVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCQFALWDALIGELTNRTHKLEKAKALKIS 1149

DB 1 CVCVEGVEGPRCDKCTRGYSVFPDCTPCHQCQFALWDALIGELTNRTHKLEKAKALKIS 60

QY 1150 GVIGPYRETVDSEKKNWEIKDILASPAEPLKNTGILFEEAEKLTQDTEKMAQVEVK 1209

DB 61 GVIGPYRETVDSEKKNWEIKDILASPAEPLKNTGILFEEAEKLTQDTEKMAQVEVK 1209

QY	1210	LTTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSITIKYFQMSLE	1269
Db	121	LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITIKYFQMSLE	180
QY	1270	AEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEQEQEQAARLLDELAKLQSLDL	1329
Db	181	AEERVNASTTEPNSTVEQSALWDRVEDVMMERESQFEKQEQEQAARLLDELAKLQSLDL	240
QY	1330	SAAQWTCGTPPGADCSSECGGPNCRTEGEEKCGGCGGLVTVVAHSAMOKAMDFDRD	1389
Db	241	SAXAEMTCGTPPGASCXEXECGGPNCRTEGERKCGGCGGLVTVVAHNAMOKAMDLPOD	300
QY	1390	VLSALAEVQLSKVSEAKVRADKQNAODVLLKTNATKEKVDKSNEDLRNLKQIRNF	1449
Db	301	VLSALAEVQLSKVSEAKLRDADEAKQSAEDILLKTNATKEKMDKSNELRNLKQIRNF	360
QY	1450	LTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVILQSSAADIR	1509
Db	361	LTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQSSAADIR	420
QY	1510	AELLLEAKKASATDVKTADMYKEALEEAKQVAAKAIKQADEDIQGTQNLTSI	1569
Db	421	AEMLLLEAKKASATDVKTADMYKEALEEAKQVAAKAIKQADEDI-----	470
QY	1570	ESETAASEETLTNASORISKLEARNVE-----ELKRAAQNNGEAEYIEKVYVYKQNAADV	1625
Db	471	-----XENPEXNFXLEFXKQLSG-GNLVQVRVPRASSEFREDV	508
QY	1626	KKTLDQEL	1633
Db	509	GRXLSGKL	516

Search completed: May 18, 2004, 15:42:45  
Job time : 50.8855 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 ; Search time 10.0352 seconds  
(without alignments)

9158.169 Million cell updates/sec

Title: US-10-037-182-8

Perfect score: 9654

Sequence: 1 QEPFSGYCAEGSCYPATG.....EVRSLLKDISQKVAVYSTCL 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9654	100.0	1786	1 LMB1_HUMAN	P07942 homo sapien
2	9032	94.2	1786	1 LMB1_MOUSE	P02469 mus musculus
3	5084	52.7	1801	1 LMB2_RAT	P15800 rattus norv
4	5048	52.3	1798	1 LMB2_HUMAN	P55268 homo sapien
5	5046	52.3	1799	1 LMB2_MOUSE	P61292 mus musculus
6	3844.5	39.8	1790	1 LMB1_DROME	P11046 drosophila
7	1759	18.2	1639	1 LMB1_DROME	P21313 caenorhabdi
8	1729.5	17.9	3672	1 LMB2_CAEEL	P18823 caenorhabdi
9	1696.5	17.6	1535	1 LMB1_CAEEL	P11047 homo sapien
10	1676.5	17.4	1809	1 LMB1_HUMAN	P02468 mus musculus
11	1653	17.1	1807	1 LMB1_MOUSE	P00174 drosophila
12	1637	17.0	3712	1 LMB1_DROME	P61001 mus musculus
13	1617	16.7	3718	1 LMB1_CHICK	P01635 gallus gall
14	1583	16.4	303	1 LMB1_HUMAN	P15230 homo sapien
15	1560.5	16.2	3695	1 LMB2_HUMAN	P24043 homo sapien
16	1559.5	16.2	3110	1 LMB3_MOUSE	P09086 mus musculus
17	1558.5	16.1	1581	1 LMB3_HUMAN	P13751 homo sapien
18	1552.5	16.1	1172	1 LMB2_MOUSE	P60675 mus musculus
19	1535.5	15.9	3106	1 LMB1_HUMAN	P25391 homo sapien
20	1525	15.8	3075	1 LMB2_HUMAN	P09566 mus musculus
21	1515.5	15.7	1587	1 LMB3_HUMAN	P19137 mus musculus
22	1507.5	15.6	3084	1 LMB1_MOUSE	P61087 mus musculus
23	1483.5	15.4	1168	1 LMB3_MOUSE	P61789 mus musculus
24	1372	14.2	3333	1 LMB2_MOUSE	P61092 mus musculus
25	891	9.2	1191	1 LMB2_MOUSE	P13753 homo sapien
26	873	9.0	1193	1 LMB2_HUMAN	P95631 homo sapien
27	695.5	7.2	604	1 NET1_HUMAN	P09118 mus musculus
28	695.5	7.2	604	1 NET1_MOUSE	P09092 gallus gall
29	690.5	7.2	606	1 NET1_CHICK	P05793 mus musculus
30	666	6.9	3707	1 PGBM_MOUSE	P98160 homo sapien
31	657	6.8	4391	1 PGBM_HUMAN	P09323 gallus gall
32	600	6.2	581	1 NET2_CHICK	
33	582.5	6.0	1816	1 LMB4_HUMAN	P16363 homo sapien

#### RESULT 1

LMB1\_HUMAN STANDARD; PRT; 1786 AA.

AC P07942; 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Laminin beta-1 chain precursor (Laminin B1 chain).  
 GN LAMB1.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;

RP MEDLINE=90368768; PubMed=1975589;  
 RA Vuolteenaho R., Chow L.T., Tryggvason K.;  
 RT "Structure of the human laminin B1 chain gene.";  
 RL J. Biol. Chem. 265:15611-15616(1990).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=87280097; PubMed=3611077;  
 RA Pikkariainen T., Eddy R., Fukushima Y., Evers M., Shows T.,  
 RA Philejanemi T., Saraste M., Tryggvason K.;  
 RT "Human laminin B1 chain. A multidomain protein with gene (LAMB1)  
 locus in the q22 region of chromosome 7.";  
 RL J. Biol. Chem. 262:10454-10462(1987).  
 RN [3]

RP SEQUENCE OF 1276-1709 FROM N.A.  
 RX MEDLINE=88021029; PubMed=3661559;  
 RA Jays M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,  
 RA Drohan W.N.;  
 RT "Isolation of a cDNA clone for the human laminin-B1 chain and its  
 gene localization.";  
 RL Am. J. Hum. Genet. 41:605-615(1987).

CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
 is thought to mediate the attachment, migration and organization  
 of cells into tissues during embryonic development by interacting  
 with other extracellular matrix components.

CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
 different polypeptide chains (alpha, beta, gamma), which are bound  
 to each other by disulfide bonds into a cross-shaped molecule  
 comprising one long and three short arms with globules at each  
 end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),  
 laminin-2 (merosin), and laminin-6 (K-laminin).

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major  
 component).

CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact  
 with other laminin chains to form a coiled coil structure.

CC -!- DOMAIN: Domains VI and IV are globular.

CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.

CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.

CC -!- SIMILARITY: Contains 1 laminin IV domain.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC EMBL; M61951; AAA59486.1; JOINED.  
 CC EMBL; M58147; AAA59486.1; JOINED.  
 CC EMBL; M61317; AAA59486.1; JOINED.  
 CC EMBL; M61318; AAA59486.1; JOINED.  
 CC EMBL; M61321; AAA59486.1; JOINED.  
 CC EMBL; M61322; AAA59486.1; JOINED.  
 CC EMBL; M61323; AAA59486.1; JOINED.  
 CC EMBL; M61324; AAA59486.1; JOINED.  
 CC EMBL; M61325; AAA59486.1; JOINED.  
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 CC EMBL; M61328; AAA59486.1; JOINED.  
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 CC EMBL; M55370; AAA59485.1; JOINED.  
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 CC EMBL; M55352; AAA59485.1; JOINED.  
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 CC EMBL; M55364; AAA59485.1; JOINED.  
 CC EMBL; M55366; AAA59485.1; JOINED.  
 CC EMBL; M55367; AAA59485.1; JOINED.  
 CC EMBL; M55368; AAA59485.1; JOINED.  
 CC EMBL; M55369; AAA59485.1; JOINED.  
 DR EMBL; M61916; AAA59482.1; --.  
 DR EMBL; M20206; AAA59487.1; --.  
 DR FIR; S13547; MMRUB1.  
 DR HSSP; P02468; IKLO.  
 DR Genew; HGNC:6486; LAMB1.  
 DR MIN; I50240; --.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR008211; LamNT.  
 DR Pfam; PF00053; laminin\_EGF; 13.  
 DR PRINTS; PR00011; EGFLAMININ.  
 DR SMART; SMO0180; EGF Lam; 12.  
 DR SMART; SMO0136; LamNT; 1.  
 DR PROSITE; PS00022; EGF 1; 9.  
 DR PROSITE; PS01186; EGF 2; 2.  
 DR PROSITE; PS01248; LAMININ TYPE EGF; 11.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.  
 FT SIGNAL 1 21  
 FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.  
 FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).  
 FT DOMAIN 271 334 LAMININ EGF-LIKE 1.  
 FT DOMAIN 335 397 LAMININ EGF-LIKE 2.  
 FT DOMAIN 398 457 LAMININ EGF-LIKE 3.  
 FT DOMAIN 458 509 LAMININ EGF-LIKE 4.  
 FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 FT DOMAIN 541 771 LAMININ DOMAIN IV.  
 FT DOMAIN 772 820 LAMININ EGF-LIKE 6.  
 FT DOMAIN 821 866 LAMININ EGF-LIKE 7.  
 FT DOMAIN 867 916 LAMININ EGF-LIKE 8.  
 FT DOMAIN 917 975 LAMININ EGF-LIKE 9.  
 FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.  
 FT DOMAIN 1028 1083 LAMININ EGF-LIKE 11.  
 FT DOMAIN 1084 1131 LAMININ EGF-LIKE 12.  
 FT DOMAIN 1132 1178 LAMININ EGF-LIKE 13.  
 FT DOMAIN 1179 1397 DOMAIN II.  
 FT DOMAIN 1398 1430 DOMAIN ALPHA.  
 FT DOMAIN 1431 1786 DOMAIN I.  
 FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).  
 FT DOMAIN 1353 1388 COILED COIL (POTENTIAL).  
 FT DOMAIN 1442 1781 COILED COIL (POTENTIAL).  
 FT DISULFID 271 280 BY SIMILARITY.  
 FT DISULFID 273 298 BY SIMILARITY.  
 FT DISULFID 300 309 BY SIMILARITY.  
 FT DISULFID 312 332 BY SIMILARITY.  
 FT DISULFID 335 344 BY SIMILARITY.  
 FT DISULFID 337 362 BY SIMILARITY.  
 FT DISULFID 365 374 BY SIMILARITY.  
 FT DISULFID 377 395 BY SIMILARITY.  
 FT DISULFID 398 411 BY SIMILARITY.  
 FT DISULFID 400 426 BY SIMILARITY.  
 FT DISULFID 428 437 BY SIMILARITY.  
 FT DISULFID 440 455 BY SIMILARITY.  
 FT DISULFID 458 472 BY SIMILARITY.  
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 FT DISULFID 481 490 BY SIMILARITY.  
 FT DISULFID 493 507 BY SIMILARITY.  
 FT DISULFID 507 527 BY SIMILARITY.  
 FT DISULFID 527 540 BY SIMILARITY.  
 FT DISULFID 540 557 BY SIMILARITY.  
 FT DISULFID 557 574 BY SIMILARITY.  
 FT DISULFID 574 583 BY SIMILARITY.  
 FT DISULFID 583 600 BY SIMILARITY.  
 FT DISULFID 600 617 BY SIMILARITY.  
 FT DISULFID 617 634 BY SIMILARITY.  
 FT DISULFID 634 651 BY SIMILARITY.  
 FT DISULFID 651 668 BY SIMILARITY.  
 FT DISULFID 668 685 BY SIMILARITY.  
 FT DISULFID 685 702 BY SIMILARITY.  
 FT DISULFID 702 719 BY SIMILARITY.  
 FT DISULFID 719 736 BY SIMILARITY.  
 FT DISULFID 736 753 BY SIMILARITY.  
 FT DISULFID 753 770 BY SIMILARITY.  
 FT DISULFID 770 787 BY SIMILARITY.  
 FT DISULFID 787 804 BY SIMILARITY.  
 FT DISULFID 804 821 BY SIMILARITY.  
 FT DISULFID 821 838 BY SIMILARITY.  
 FT DISULFID 838 855 BY SIMILARITY.  
 FT DISULFID 855 872 BY SIMILARITY.  
 FT DISULFID 872 889 BY SIMILARITY.  
 FT DISULFID 889 906 BY SIMILARITY.  
 FT DISULFID 906 923 BY SIMILARITY.  
 FT DISULFID 923 940 BY SIMILARITY.  
 FT DISULFID 940 957 BY SIMILARITY.

Query Match				100.0%; Score 9654; DB 1; Length 1786;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	QEPFSGCAEGSCYPATGDLII	GRAOKLSVSTCGLHKPEPYCI	VSHLQEDKCKFCINS	60		
DB	22	QEPFSGCAEGSCYPATGDLII	GRAOKLSVSTCGLHKPEPYCI	VSHLQEDKCKFCINS	81		
QY	61	QDPVHETLNDPSHLIENNV	TFAPNRLKI	WQSENGVNTIQLDL	EAFFHFLHWTXK	120	
DB	82	QDPVHETLNDPSHLIENNV	TFAPNRLKI	WQSENGVNTIQLDL	EAFFHFLHWTXK	141	
QY	121	TFPAAALIERSSDFGKTGW	YRIFAYDCEASPGI	STGPMKKVDII	ICDSRYSDIEPST	180	
DB	142	TFPAAALIERSSDFGKTGW	YRIFAYDCEASPGI	STGPMKKVDII	ICDSRYSDIEPST	201	
QY	181	EGEVIFRALDPAFKIEDPY	SPRIQNLKI	TNLRKFKV	LHTLGNLLDSRMEIREKYVA	240	
DB	202	EGEVIFRALDPAFKIEDPY	SPRIQNLKI	TNLRKFKV	LHTLGNLLDSRMEIREKYVA	261	
QY	241	YDMVVRGNCFCYGHASE	CAPVDGFNEEVEG	VMVHGCVRHNTK	GLNCELMDFYHDLPW	300	
DB	262	YDMVVRGNCFCYGHASE	CAPVDGFNEEVEG	VMVHGCVRHNTK	GLNCELMDFYHDLPW	321	
QY	301	RPAEGRNSNACKNCNEHSI	SCHFDMAVILATGN	VSVCDDOHNMTGRNCEQCKPFY	360		
DB	322	RPAEGRNSNACKNCNEHSI	SCHFDMAVILATGN	VSVCDDOHNMTGRNCEQCKPFY	381		
QY	361	YQHPERDIRDNFCERCT	CDPAGSQNEGICDSY	TFSTGLIAGCRCKLAVGEHCDVCK	420		
DB	382	YQHPERDIRDNFCERCT	CDPAGSQNEGICDSY	TFSTGLIAGCRCKLAVGEHCDVCK	441		
QY	421	EGFYDLSSDFGKSCACN	PLGTIPGNCPCDSTGCHYCKRLVTGQHCDOCL	PEHWGLS	480		
DB	442	EGFYDLSSDFGKSCACN	PLGTIPGNCPCDSTGCHYCKRLVTGQHCDOCL	PEHWGLS	501		
QY	481	NLDGCRPCDCLGALNNS	CFASGQSCRP	HIMGRQCNVEPGYFATLDHYLYEAE	540		
DB	502	NLDGCRPCDCLGALNNS	CFASGQSCRP	HIMGRQCNVEPGYFATLDHYLYEAE	561		
QY	541	ANLPGFVSIVEROYIQ	DRIPSWTGA	FVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600		
DB	562	ANLPGFVSIVEROYIQ	DRIPSWTGA	FVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621		
QY	601	DHWEKAVITVORPGR	IPTSSRCGNTIPDDNQVLSLSPGSR	YVLPVPVCFEKGNTYVR	660		
DB	622	DHWEKAVITVORPGR	IPTSSRCGNTIPDDNQVLSLSPGSR	YVLPVPVCFEKGNTYVR	681		
QY	661	LELPQYTSDDVS	PYTLIDSLVLMPCYKSLDIFT	VGGSGDVVTNSAWETFORYRCLE	720		
DB	682	LELPQYTSDDVS	PYTLIDSLVLMPCYKSLDIFT	VGGSGDVVTNSAWETFORYRCLE	741		
QY	721	NSRSVVKTPMTDVC	RNIIFISALLHQTGLACE	CDPQGSLSVCDPNQGGCQCRPNVVR	780		
DB	742	NSRSVVKTPMTDVC	RNIIFISALLHQTGLACE	CDPQGSLSVCDPNQGGCQCRPNVVR	801		
QY	781	TCNRCAPGTGFGSGCK	PCHECHLQGSVNAFCNPVTGQCHCFQGVYARQDCRCLPGHWGF	840			
DB	802	TCNRCAPGTGFGSGCK	PCHECHLQGSVNAFCNPVTGQCHCFQGVYARQDCRCLPGHWGF	861			
QY	841	PSQPCQCNHADD	CDPVTG	BECLNCQDYTMGHNCERCLAGYIGDPIITGSDHCRPCPCPD	900		
DB	862	PSQPCQCNHADD	CDPVTG	BECLNCQDYTMGHNCERCLAGYIGDPIITGSDHCRPCPCPD	921		
QY	901	GPDSGRQFARS	CYQDPVT	LQACVCDPGYISGRDCCASGYFGNPSVGGSCQPCQCHN	960		
DB	922	GPDSGRQFARS	CYQDPVT	LQACVCDPGYISGRDCCASGYFGNPSVGGSCQPCQCHN	981		
QY	961	IDTTFEACDKETGR	CKLXYHTEGEHCQFRCFYIGDALRQD	CRKVCNVLGTVQVHCN	1020		
DB	982	IDTTFEACDKETGR	CKLXYHTEGEHCQFRCFYIGDALRQD	CRKVCNVLGTVQVHCN	1041		

RESULT 2	
LMBI_MOUSE	
ID	LMBI_MOUSE
AC	P02469;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Laminin beta-1 chain precursor (Laminin B1 chain).
GN	LAMB1-1 OR LAMB-1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=87147212; PubMed=3493487;
RA	Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT	"Sequence of the cDNA encoding the laminin B1 chain reveals a
RT	multidomain protein containing cysteine-rich repeats.";
RL	Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).

QY	1021	GSDQCQDKATQCC	CLPNVIGQNC	DRCAPNTW	OLASGTG	CDPCNCAHSP	CGPCNEFTG	1080
DB	1042	GSDQCQDKATQCC	CLPNVIGQNC	DRCAPNTW	OLASGTG	CDPCNCAHSP	CGPCNEFTG	1101
QY	1081	QCQCPFGGRT	CSCEQEL	FWGDPD	VECRACD	CDPRGIET	PQCDSQ	1140
DB	1102	QCQCPFGGRT	CSCEQEL	FWGDPD	VECRACD	CDPRGIET	PQCDSQ	1161
QY	1141	CDKCTRG	SGVFPD	CTPCHQ	CFALWD	VIIEALN	TRHTRFLEKAKAL	1200
DB	1162	CDKCTRG	SGVFPD	CTPCHQ	CFALWD	VIIEALN	TRHTRFLEKAKAL	1221
QY	1201	SVERKVS	IKDILAQ	SPAAEP	KLKIGNL	FEEAEK	LKDVTENMAQ	1260
DB	1222	SVERKVS	IKDILAQ	SPAAEP	KLKIGNL	FEEAEK	LKDVTENMAQ	1281
QY	1261	AKELDSLQ	TEAESL	DNTVKEL	AEQLEF	TKNSDIR	GALDSITKYFOM	1320
DB	1282	AKELDSLQ	TEAESL	DNTVKEL	AEQLEF	TKNSDIR	GALDSITKYFOM	1341
QY	1321	PNSTVEQ	SALMRD	VEDVM	MERESQ	FEKQBEQ	ARLLDEL	1380
DB	1342	PNSTVEQ	SALMRD	VEDVM	MERESQ	FEKQBEQ	ARLLDEL	1401
QY	1381	PGASCS	TECG	PGNCR	TDEGER	KCGPG	CGGLV	1440
DB	1402	PGASCS	TECG	PGNCR	TDEGER	KCGPG	CGGLV	1461
QY	1441	SKVSEAK	LRADEAK	QSAED	ILLKTNAT	KEKMDK	NEELNLI	1500
DB	1462	SKVSEAK	LRADEAK	QSAED	ILLKTNAT	KEKMDK	NEELNLI	1521
QY	1501	EAVANEV	LKWM	PSTPQ	QLNLTED	IRRVES	LSQVEV	1560
DB	1522	EAVANEV	LKWM	PSTPQ	QLNLTED	IRRVES	LSQVEV	1581
QY	1561	SKSATD	VKTAD	VMVEAL	EEAEK	QAAEKA	IKQADE	1620
DB	1582	SKSATD	VKTAD	VMVEAL	EEAEK	QAAEKA	IKQADE	1641
QY	1621	FNASQ	RISE	LRNVEL	KEKAAQ	NSGEAEY	IEKVVT	1680
DB	1642	FNASQ	RISE	LRNVEL	KEKAAQ	NSGEAEY	IEKVVT	1701
QY	1681	ENLIAK	TEESAD	ARRKAE	MLQNEAK	TLLAQA	NSKLQL	1740
DB	1702	ENLIAK	TEESAD	ARRKAE	MLQNEAK	TLLAQA	NSKLQL	1761
QY	1741	ARLEGE	VRSL	IKDISQ	KVAVYSTCL	1765		
DB	1762	ARLEGE	VRSL	IKDISQ	KVAVYSTCL	1786		



FT	DOMAIN	1028	1083	LAMININ EGF-LIKE 11.
FT	DOMAIN	1084	1131	LAMININ EGF-LIKE 12.
FT	DOMAIN	1132	1178	LAMININ EGF-LIKE 13.
FT	DOMAIN	1179	1397	DOMAIN II.
FT	DOMAIN	1398	1430	DOMAIN ALPHA.
FT	DOMAIN	1431	1785	DOMAIN I.
FT	DOMAIN	1216	1315	COILED COIL (POTENTIAL).
FT	DOMAIN	1368	1385	COILED COIL (POTENTIAL).
FT	DOMAIN	1448	1778	COILED COIL (POTENTIAL).
FT	DISULFID	271	280	BY SIMILARITY.
FT	DISULFID	273	298	BY SIMILARITY.
FT	DISULFID	300	309	BY SIMILARITY.
FT	DISULFID	312	332	BY SIMILARITY.
FT	DISULFID	335	344	BY SIMILARITY.
FT	DISULFID	337	362	BY SIMILARITY.
FT	DISULFID	365	374	BY SIMILARITY.
FT	DISULFID	377	395	BY SIMILARITY.
FT	DISULFID	398	411	BY SIMILARITY.
FT	DISULFID	400	426	BY SIMILARITY.
FT	DISULFID	428	437	BY SIMILARITY.
FT	DISULFID	440	455	BY SIMILARITY.
FT	DISULFID	458	472	BY SIMILARITY.
FT	DISULFID	460	479	BY SIMILARITY.
FT	DISULFID	481	490	BY SIMILARITY.
FT	DISULFID	493	507	BY SIMILARITY.
FT	DISULFID	773	795	BY SIMILARITY.
FT	DISULFID	775	782	BY SIMILARITY.
FT	DISULFID	794	803	BY SIMILARITY.
FT	DISULFID	806	818	BY SIMILARITY.
FT	DISULFID	821	833	BY SIMILARITY.
FT	DISULFID	823	840	BY SIMILARITY.
FT	DISULFID	842	851	BY SIMILARITY.
FT	DISULFID	854	864	BY SIMILARITY.
FT	DISULFID	867	876	BY SIMILARITY.
FT	DISULFID	869	883	BY SIMILARITY.
FT	DISULFID	886	895	BY SIMILARITY.
FT	DISULFID	898	914	BY SIMILARITY.
FT	DISULFID	917	933	BY SIMILARITY.
FT	DISULFID	919	944	BY SIMILARITY.
FT	DISULFID	946	955	BY SIMILARITY.
FT	DISULFID	958	973	BY SIMILARITY.
FT	DISULFID	976	990	BY SIMILARITY.
FT	DISULFID	978	997	BY SIMILARITY.
FT	DISULFID	1000	1009	BY SIMILARITY.
FT	DISULFID	1012	1025	BY SIMILARITY.
FT	DISULFID	1084	1096	BY SIMILARITY.
FT	DISULFID	1086	1103	BY SIMILARITY.
FT	DISULFID	1105	1114	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1132	1144	BY SIMILARITY.
FT	DISULFID	1134	1151	BY SIMILARITY.
FT	DISULFID	1153	1162	BY SIMILARITY.
FT	DISULFID	1165	1176	BY SIMILARITY.
FT	DISULFID	1179	1191	INTERCHAIN (PROBABLE).
FT	DISULFID	1182	1182	INTERCHAIN (PROBABLE).
FT	DISULFID	1785	1785	INTERCHAIN (PROBABLE).
FT	CARBOHYD	120	120	N-LINKED (GLCNAC. .)
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. .)
FT	CARBOHYD	519	519	N-LINKED (GLCNAC. .)
FT	CARBOHYD	677	677	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1041	1041	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1195	1195	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1279	1279	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1336	1336	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1343	1343	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1487	1487	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1533	1533	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1542	1542	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1643	1643	N-LINKED (GLCNAC. .)
FT	CONFLICT	1531	1534	N-LINKED (GLCNAC. .)
FT	CONFLICT	1749	1749	SGNA -> MEMP (IN REF. 2).
FT	CONFLICT	1796	1796	D -> N (IN REF. 2).
FT	SEQUENCE	1796	1796	MM: 846671B7F41A474 CRC64;

Query Match	94.2%;	Score 9092;	DB 1;	Length 1786;	
Best Local Similarity	93.0%;	Pred. No. 0;			
Matches 1642;	Conservative	71;	Mismatches 52;	Indels 0;	Gaps 0;
QY	1	QBPEFSYGCAEGSCYPATGDLII	GRAQKLSVTSTCGLHKPEPYCIV	SHLQEDKCCFICNS	60
DB	22	QBPEFSYGCAEGSCYPATGDLII	GRAQKLSVTSTCGLHKPEPYCIV	SHLQEDKCCFICDS	81
QY	61	QDPYHETLNPDSHLIENVVTF	FAPNRLKIWQSENGENVNTIQ	LDLEAEFFHFLHMTFK	120
DB	82	RDYHETLNPDSHLIENVVTF	FAPNRLKIWQSENGENVNTIQ	LDLEAEFFHFLHMTFK	141
QY	121	TFPAAWLIRSSDFGKTGWYRYF	AYDCBASPGISTGPMKVD	DIICDSRYSDIEPST	180
DB	142	TFPAAWLIRSSDFGKTGWYRYF	AYDCBASPGISTGPMKVD	DIICDSRYSDIEPST	201
QY	181	EGEVI FRALDPAPKIEDYPR	QNLKITNLRIKFVKLHTLGN	LDLSRMEIREKYVA	240
DB	202	EGEVI FRALDPAPKIEDYPR	QNLKITNLRIKFVKLHTLGN	LDLSRMEIREKYVA	261
QY	241	YVDMVVRGNCFCYGHASECAP	VDGFNEEVGMVHCHMC	RHNTKGLNCELAMD FYHDLPW	300
DB	262	YVDMVVRGNCFCYGHASECAP	VDGFNEEVGMVHCHMC	RHNTKGLNCELAMD FYHDLPW	321
QY	301	RPAGEGRNSNACKCNCHES	ISCHFDMAVYLATGNVSGV	CCDDCOHNTWGRNCEQCKPFY	360
DB	322	RPAGEGRNSNACKCNCHES	SSCHFDMAVFLATGNVSGV	CNCOHNTWGRNCEQCKPFY	381
QY	361	YQHPERIDRPNFCERTCD	PAGSQNEGICDSYTFSTGL	IAGOCRCKLNVGEHCDVCK	420
DB	382	FQHPERIDRPNFCERTCD	PAGSENGHICDGYTFPSV	GLIAGOCRCKLNVGEHCDVCK	441
QY	421	EGFVDSLSEDPFGCKSCA	CNPLGTIPGNPCDSTGHCY	CKRLVTGQCHQCCLPEHMGLS	480
DB	442	EGFVDSLSEDPFGCKSCA	CNPLGTIPGNPCDSTGHCY	CKRLVTGQCHQCCLPEHMGLS	501
QY	481	NLDGCRPCDDLGALNNS	CSFASQSCRPMTGROCN	VEPGYYFATLDHYLYEABE	540
DB	502	NLDGCRPCDDLGALNNS	CSDESQSCPLPHMGRQ	CNEVEPGYYFETLDDHYLYEABE	561
QY	541	ANLPGVSVIRQVITODR	IPSWTGAQFVRUPEGAYL	EFFIDNIPYSMEYDILIRYEQLP	600
DB	562	ANLPGVSVIRQVITODR	IPSWTGAQFVRUPEGAYL	EFFIDNIPYSMEYELIRYEQLP	621
QY	601	DHWEKAVITVORPGR	IPTSSRCGNTIPDDNQV	SLSPGSRVYVLPVPCFEXGNTYTVR	660
DB	622	DHWEKAVITVORPGR	KIPASSRCGNTIPDDNQV	SLSPGSRVYVLPVPCFEXGNTYTVR	681
QY	661	LELPQYTSDDVSPYTL	DSLVMPCYKSLDIFTV	GSGDGVVWNSAMETFORYRCLE	720
DB	682	LELPQYTSDDVSPYTL	DSLVLMPYCKSLDIFT	VGGSGDGVVWNSAMETFORYRCLE	741
QY	721	NSRSVVKTPMTDVCN	IIIFSALHQTGLACECD	POGSLSSVCDPNGGOCQCRPNVVGR	780
DB	742	NSRSVVKTPMTDVCN	IIIFSALIHOTGLACECD	POGSLSSVCDPNGGOCQCRPNVVGR	801
QY	781	TNCRCAPGTGFGSGCK	PCHECHLQGSVNAFNPV	TQCHCFQGVYARQDCRLPGHWGF	840
DB	802	TNCRCAPGTGFGSGCK	PCDCHLQGSASAFCD	AITGQCHCFQGIYARQDCRLPGYWG	861
QY	841	PSCQPCQNGHADD	CDPVTGELCNCODYTM	GHNCERCLAGVYGDPIIGSGDHCRPCPCPD	900
DB	862	PSCQPCQNGHADD	CDVITGELCSCODYT	GHNCERCLAGVYGDPIIGSGDHCRPCPCPD	921
QY	901	GPDSGRQFARSQYQDP	VTQLACVCDPGYIGSR	CCDPCGIFGPNPSEVGSQCQCHHN	960
DB	922	GPDSGRQFARSQYQDP	VTQLACVCDPGYIGSR	CCDPCGIFGPNPSEVGSQCQCHHN	981
QY	961	IDTTPDPAKDETGKCL	KLYHTEGEHCQCFRFG	YGDALRODKCKVCNVLGTVOEHCN	1020
DB	982	IDTTPDPAKDETGKCL	KLYHTEGEHCQCLQ	QYGYGDALRODKCKVCNVLGTVKHCN	1041
QY	1021	GSDCCQCDKATGQCL	PLPNVIGQNCDCR	CAPNTWQLASGTGCDPCN	CNNAHSGFSPSCNEFTG 1080

	BY SIMILARITY.			
FT	DISULFID	352	377	BY SIMILARITY.
FT	DISULFID	380	389	BY SIMILARITY.
FT	DISULFID	392	410	BY SIMILARITY.
FT	DISULFID	413	426	BY SIMILARITY.
FT	DISULFID	415	441	BY SIMILARITY.
FT	DISULFID	443	452	BY SIMILARITY.
FT	DISULFID	455	470	BY SIMILARITY.
FT	DISULFID	473	487	BY SIMILARITY.
FT	DISULFID	475	494	BY SIMILARITY.
FT	DISULFID	496	505	BY SIMILARITY.
FT	DISULFID	508	522	BY SIMILARITY.
FT	DISULFID	786	798	BY SIMILARITY.
FT	DISULFID	788	805	BY SIMILARITY.
FT	DISULFID	807	816	BY SIMILARITY.
FT	DISULFID	819	831	BY SIMILARITY.
FT	DISULFID	834	846	BY SIMILARITY.
FT	DISULFID	836	853	BY SIMILARITY.
FT	DISULFID	855	864	BY SIMILARITY.
FT	DISULFID	867	877	BY SIMILARITY.
FT	DISULFID	880	889	BY SIMILARITY.
FT	DISULFID	882	896	BY SIMILARITY.
FT	DISULFID	899	908	BY SIMILARITY.
FT	DISULFID	911	927	BY SIMILARITY.
FT	DISULFID	930	946	BY SIMILARITY.
FT	DISULFID	932	957	BY SIMILARITY.
FT	DISULFID	959	968	BY SIMILARITY.
FT	DISULFID	971	986	BY SIMILARITY.
FT	DISULFID	989	1003	BY SIMILARITY.
FT	DISULFID	991	1010	BY SIMILARITY.
FT	DISULFID	1013	1022	BY SIMILARITY.
FT	DISULFID	1025	1038	BY SIMILARITY.
FT	DISULFID	1098	1110	BY SIMILARITY.
FT	DISULFID	1100	1117	BY SIMILARITY.
FT	DISULFID	1119	1128	BY SIMILARITY.
FT	DISULFID	1131	1143	BY SIMILARITY.
FT	DISULFID	1146	1158	BY SIMILARITY.
FT	DISULFID	1148	1165	BY SIMILARITY.
FT	DISULFID	1167	1176	BY SIMILARITY.
FT	DISULFID	1179	1190	BY SIMILARITY.
FT	DISULFID	1193	1193	INTERCHAIN (PROBABLE).
FT	DISULFID	1196	1196	INTERCHAIN (PROBABLE).
FT	DISULFID	1800	1800	INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. .)
FT	CARBOHYD	371	371	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1098	1098	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1311	1311	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1351	1351	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1502	1502	N-LINKED (GLCNAC. .)
SQ	SEQUENCE	1801 AA;	196473 MM; 97AEF32F8F31FA7S CRC64;	(POTENTIAL).
	Query Match	52.7%;	Score 5084; DB 1; Length 1801;	(POTENTIAL).
	Best Local Similarity	51.5%;	Pred. No. 1.3e-182;	(POTENTIAL).
	Matches 910;	Conservative 303;	Mismatches 534; Indels 20; Gaps 8;	(POTENTIAL).
				(POTENTIAL).
QY		8	GCAEGSCYPATGDLILLGRAOKLSTVTCTGLHKHPYCIVSVHLQRDKKCFICNSODPYHET 67	
DB		44	GCGRSCCYPATGDLLVGRADRLTASTTCGLHSPPCYIVSHLQEKKCFCDSSRRPFSA 103	
QY		68	LNPOSHLENTVVTFAPNRLKIWMQSNGENVNTIQLDLEAFHFHTLMITFKTRPAAM 127	
DB		104	DNPNSHRIQNVTVSPAPORTAWQSENGVPWMTVIQLDLEAFHFHTLMITFKTRPAAM 163	
QY		128	LTERSDDGKTGWGVVRFPAYDCEASFPGISGTGPWKKVDDDIICDSRYSDIBPSTEGEVIFR 187	
DB		164	LVERSADFGRWVRVRFYSYDCGADFPGIPLAPRRWDVVVCESRYSEIEBSTEGEVIYR 223	
QY		188	ALDPAKTEDIPYSPIQNLIKTNLRKFVKLHTLGDNLDLSRMVEIREKYIYYAVDMVVR 247	
DB		224	VLDPAIRPIDPYSGRIQNLIKTNLRVNLTSLHTLGNDLDPREIREKYIYYALVELVIR 283	
QY		248	GNCFYCGHASCAPVDGFNEEVGMVGHWCHWCNRINTKGLNCCLCWDYFDHLPWFPAEGRN 307	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 47.8797 Seconds

(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-8

Perfect score: 9654

Sequence: 1 QEPFSGYCAEGSCYPATGD.....EVRSLKDISQKVAVYSTCL 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_plant.\*
- 10: sp\_phage.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp Vertebrate.\*
- 14: sp Unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6794	70.4	1785	13 Q8JHV7	Q8jlv7 brachydanio
2	5808	60.2	1086	4 Q8TAS6	Q8tas6 homo sapien
3	5321	55.1	1792	13 Q57484	Q57484 gallus gall
4	5069	52.5	1799	11 Q8ROY0	Q8roy0 mus musculus
5	4891	50.7	984	11 Q8K271	Q8k271 mus musculus
6	4527	46.9	911	11 Q9CRX6	Q9crx6 mus musculus
7	3832.5	39.7	1761	4 Q86XN2	Q86xn2 homo sapien
8	3785.5	39.2	1827	13 Q8JHV6	Q8jlv6 brachydanio
9	3625.5	37.6	1631	4 Q9Y6U6	Q9y6u6 homo sapien
10	2835	29.4	1067	5 Q44565	Q44565 caenorhabdi
11	2297.5	23.8	1168	5 Q96788	Q96788 schistocerc
12	2034	21.1	761	4 Q9UHI2	Q9uhi2 homo sapien
13	1921	19.9	1026	5 Q8SWY0	Q8swy0 drosophila
14	1847	19.1	1069	5 Q8BP22	Q8bp22 bombyx mori
15	1729.5	17.9	3704	5 P91904	P91904 caenorhabdi
16	1684.5	17.4	1593	13 Q8JHV8	Q8jlv8 brachydanio

17	1674.5	17.3	1623	5 Q9U3U7	Q9u3u7 anopheles g
18	1633	16.9	3712	5 Q9VRW0	Q9vrw0 drosophila
19	1564.5	16.2	3695	4 Q8TDF8	Q8tdf8 homo sapien
20	1491.5	15.4	1168	11 Q91V90	Q91v90 mus musculus
21	1380	14.3	1007	13 Q90ZN3	Q90zn3 gallus gall
22	1307.5	13.5	3102	5 Q45614	Q45614 caenorhabdi
23	1217	12.6	2731	5 Q9VJTS	Q9vjt5 drosophila
24	1217	12.6	3367	5 Q9XZC9	Q9xzc9 drosophila
25	1217	12.6	3375	5 Q8IP51	Q8ip51 drosophila
26	1101.5	11.4	1546	4 Q8NS27	Q8ns27 homo sapien
27	1093.5	11.4	1546	4 Q75445	Q75445 homo sapien
28	1064	11.0	1486	4 Q14637	Q14637 homo sapien
29	1041.5	10.8	1461	11 Q9JLP3	Q9jlp3 mus musculus
30	1040	10.8	750	4 Q86TF7	Q86tf7 homo sapien
31	1001.5	10.4	616	4 Q15483	Q15483 homo sapien
32	1001	10.4	628	11 Q9J133	Q9j133 mus musculus
33	993	10.3	628	4 Q8HB63	Q8hb63 homo sapien
34	991	10.3	628	4 Q8E2P1	Q8e2p1 homo sapien
35	975	10.1	605	4 Q7Z5B6	Q7z5b6 homo sapien
36	964	10.0	1512	11 Q8K3K1	Q8k3k1 rattus norv
37	889	9.2	1190	6 Q8HZ19	Q8hzi9 equus caball
38	880	9.1	1196	6 Q8E7A2	Q8e7a2 canis famli
39	695.5	7.2	604	11 Q924Z9	Q924z9 rattus norv
40	680	7.0	1664	5 Q9TV02	Q9tvq2 caenorhabdi
41	678.5	7.0	569	13 Q57339	Q57339 xenopus lae
42	678	7.0	602	13 Q42203	Q42203 brachydanio
43	675.5	7.0	529	4 Q8N2D6	Q8n2d6 homo sapien
44	674	7.0	603	13 Q42140	Q42140 brachydanio
45	669.5	6.9	1574	11 Q88281	Q88281 rattus norv

#### ALIGNMENTS

RESULT 1

Q8JHV7

ID Q8JHV7 PRELIMINARY; PRT; 1785 AA.

AC Q8JHV7;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Laminin beta 1.  
GN LAMB1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22065263; PubMed=12070089;

RA Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,

RA Hirst E.M., Stemple D.L.;

RT "Zebrafish mutants identify an essential role for laminins in

RT notochord formation.";

RL Development 129:3137-3146(2002).

DR EMBL; AF468049; AAM61767.1; .

DR GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006209; EGF-like

DR InterPro; IPR002049; Laminin\_EGF.

DR InterPro; IPR008211; LamNT.

DR Pfam; PF00053; laminin\_EGF; 13.

DR Pfam; PF00055; laminin\_Nterm; 1.

DR PRINTS; PR00011; EGFLAMIN.

DR SMART; SM00180; EGF\_Lam; 13.

DR SMART; SM00136; LamNT; 1.

DR PROSITE; PS00022; EGF\_1; 10.

DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.

KW Laminin EGF-like domain.

KW SEQUENCE 1785 AA; 197279 MW; 1BD338A0B6AB9F26 CRC64;

Query Match			70.4%;	Score 6794;	DB 13;	Length 1785;
Best Local Similarity			67.3%;	Pred. No. 1.4e-288;		
Matches 1189;			Conservative 253;	Mismatches 319;	Indels 6;	Gaps 6;
QY	3	PEPSYGCAAGSCYPATGDLIGRAQKLSVTSTGCLHKPEPCYCVSHLQEDKKCFICNSQD	62			
DB	20	PELGDVTEGSCYPATGDLIGRAQQLLATSTCGVHKPEPFCVSHLQEEKKCFVCDSRQ	79			
QY	63	PYHETLNP-DSHLIENVVTFAPNRLKIWQSENGENVVTIQLDLAEFPHTLIMTFKT	121			
DB	80	AYNETAHQVTSHTSIENVVTFAPNRLKIWQSENGLENVTIQLDLAEFPHTLIMTFKT	139			
QY	122	FRPAAMLIERSDFGKTGWVRYFAYDCEASFPQISTGPMKKVDDIICDSRYSDIEPSTE	181			
DB	140	FRPAAMVIERADFGNTQWVRYFAYDCESSPFSVSHGPMTKVDVVICDTRYSDIEPSTE	199			
QY	182	GEVIFRALDPFKIEDPSPRIQNLKITLIRKIFVKLHTLGNLLDSRMEIREKYYIYAV	241			
DB	200	GEVIFRVLDPAFRIDEPSPRIQNLKITLIRVKFTKLHTLGNLLDSRIEIKYYIYAI	259			
QY	242	YDMVVRGNCFCYGHASECAPVDGNEVEGVHGHCMCRHNTKGLNCELCHMDFYHDLFWR	301			
DB	260	YDMVVRGNCFCYGHASECAPVDGTGEAVEGVHGHCMCNHTIIGLNCERCQDFYHDLFWR	319			
QY	302	PABGRNSNACKKCNKNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTWGRNCEQCKPFY	361			
DB	320	PABGRNTNACKKCHNHHSSCHFDMAVYRASGNVSGVCDCCOHNMTWGRNCEQCKPFH	379			
QY	362	QHPERDIRDPNFCBRCCTCDPAGSQNGICDSYTFSTGLIAGQCRCKLANVEGHCDDVCKE	421			
DB	380	QHPEKDIRDPNICEPNCNDPVLGSLNGVCDPMTDVSILISGGQCRCKPNVBERCDDQCKQ	439			
QY	422	GFYDLSSDDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQCDCLPEHGWLSN	481			
DB	440	GHYGL-SEDPGLGQPCCTCNALGTVPGGSPCDDTSGNCYCKRLVTGRNCDCLPQHWGLSN	498			
QY	482	DLDCRCPDCLGALNNSCFABSGQSCSRPHMIGRCQNEVEPGYFATLDHLYEABEA	541			
DB	499	DMDGCRPCDCHGGAINNCSFVSGQCCQCRHFGRCQVSGFGFYFIALDHYEABEA	558			
QY	542	NLGPVGSIVERQYIQDRIPSWTAGFVRVPEGAYLEFFIDINIPYSMEYDILIRYEPQLPD	601			
DB	559	KFGPGVTVVRNHPQDRSPWTGTGIVNVPEGAFLFFSIDINIPYSMEYDILIRYEPQLPE	618			
QY	602	HWEKAVITVQRGRIPTSSRCGNTIPDDNQVSLSPGSRVYVLPFPRVCFEKGNTYVRL	661			
DB	619	QWEEVMTVIRPVITADSRCAANTPDDNQVSLSPGSRVYVLPFPRVCFEGLANTYRL	678			
QY	662	ELPQVTSDDSVESPYTLIDSLVLMPCYSKSIDIFTVGGSGDGVVTHNSAWEITFORVRCLE	720			
DB	679	SLSLY-SALSDVQSPYTLIDSLVLMPCCKNLDIFSGSGTEGGLNLTNSAWENFORVRCLE	737			
QY	721	NRSRVVKTPTMTDVCNRIIFISALLHOTGLACECDPQGSLSVCDPPNGGQCCQCRPNVGR	780			
DB	738	NSQAVVKTPTMTDVCNRIIFSVALLHQGVKACQCDPQGSLSVCDPPNGGQCCQCRPNVGR	797			
QY	781	TCNRCAPTGFPGSGCKPCBCHLQGSVNAPFNVPVGTQCHCFQGVYARQCDRCCLPGHWGF	840			
DB	798	NCDCRCAPTGFPGSGCKPCBCHLQGSVNAPFNVPVGTQCHCFQGVYARQCDRCCLPGHWGF	857			
QY	841	PSCQPCQNGHADDQDPTVTEGLNCQDYTMGHNCERCLAGYVGDPIIGSGDHCRPCPCPD	900			
DB	858	PNCRCPTCNGHAEQCDPQTGQCLSCRDHTTGHNCERCLAGYVGDPIIGSGDHCRPCPCPD	917			
QY	901	GPDSGRQFARSCYQDPVTIQLACVCDPQYIGSRCDCCASGVFGNPSVGGSCQPCQCHNN	960			
DB	918	GPDSGRQFSGACYKSPDSSQVFCVNCQYKGRACECAPGYGPNHPHEVGEGRPCQCNNS	977			
QY	961	IDTTPDPAKDETRGCLKCLVHTEGHCQFCRFGYVGDALRQDCKRCKVCNLTGVQEH- 1019				
DB	978	IDMDPESCDARTGACVKCLVHTEGHCNRCRLGTYGNALQDCKRCKVCNMQGTVEWCP	1037			
QY	1020	NGSDCCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFT	1079			

DB	1038	SFGNCCNCLTSGQCLCLENVVGHQCDQCAPDTWNASGKCEDCDPNDHSGSCHEIM	1097
QY	1080	GQCQMPFGGRTCECQCELFWGDPPDECRACDCCDPRGIETPQCDQSTQCCVCEVGEVP	1139
DB	1098	GQCSKCPFGGRTCECHRELFWGNPEVKCHACDCCDPRGIAEQCNKVTGHCVCVGVSGP	1157
QY	1140	RCDKTRIGSVFDPDCTECHQCFALNDVIAELTNRTHRFLEKAKALISGIVGPIRYRTV	1199
DB	1158	RCDTCARGYTFEPPQECRCHQCFABWDIIVGDLTNQTHRLVQKNTIKATITGPIYQATI	1217
QY	1200	DSEVERKVEIADILAQSPAAPLKNIGLNFBEAEKLIKDVMTMMAQVEVKLSDDTTSQNS	1259
DB	1218	NNVENSANSIRNILAQNPAQPLTEIQGLLEQATALMAEMNSNLNLTBETLSEISSDNN	1277
QY	1260	FAKELDSLOTEABSLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNASTT	1319
DB	1278	TDTKLSLKEEAQLEQTVKDLREQVEFKNSDIRGARASVTRYIYEQONAEIRANASTT	1337
QY	1320	ENSTVETOSALMRDVEDVMMERESQFKEQEQARLLDELQAGKLSLDLAAAEMTCGT	1379
DB	1338	DFYNLVNQSATLRTTEELMNQTKKEFNQORDEFSKLDNLQAGQLETLDSLSEKTCGS	1397
QY	1380	PPGA-SCSETEGCGNCRDTEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLALAEVE	1438
DB	1398	PAGSENCADSRCCGLSCVDMQGRXCGGCGDGLTTLAHNAWQKAMDLDLEIISAEVEVD	1457
QY	1439	QLSKVVSRAKRADEAKOSAEEDILKTNAKEMKDSNEELNLTQIRNFLTQPSADLD	1498
DB	1458	KLSKWSKAKVADBAKNAQEVLAQTNKTRKVDSSNEELRQLIKQIRDFITQDGALE	1517
QY	1499	SIEAVANEVLQVMPSTPQQLQNLTEDIRRVERVSQVEVILQHSAAADIAEAEMLEAK	1558
DB	1518	SIEAVANEVLQVMPSTPQQLQNLTEDIRRVERVSQVEVILQHSAAADILAEISLEQAR	1577
QY	1559	RASKSATDVKVTADVMVKEALAEAKAQAQAEKIAQADEDIQGTQNLTLTSETEAASSE	1618
DB	1578	KARKASDVKSFAEMVKEALQHAERQNSVBAALQAAVDIKGTQDILLVSVSETSSEL	1637
QY	1619	TLFNASQRISELERNVVELKRAQAQNSGEAEYIEKVYTVTKQSAEDVKKTLDELDEKVK	1678
DB	1638	KLSNATRELLKESDVALLEKALNTSISANSTEXEASINALEAQKLDLDELKDKYS	1697
QY	1679	KYENLIATKTESADARRKAEMLQNEAKTLAQANSKQLQLKDLERKEDNORYLEDKQAQ	1738
DB	1698	TVLEELITQAEQVAGAEKGAELQBEARNLLQASEKQLLKNLEKNYDQNKLEEDKAN	1757
QY	1739	ELARLEGEVRSLLKDISQKAVYVSTCL	1765
DB	1758	ELVDLEKAVKELQELSHKVTYVSTCL	1784
RESULT 2			
ID	Q8TAS6	PRELIMINARY;	PRT; 1086 AA.
AC	Q8TAS6;		
DT	01-JUN-2002 (T-EMBLrel. 21, Created)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)		
DE	Similar to laminin, beta 1 (fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RA	Strausberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC026018; AAH26018.1; -		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006209; EGF-like		
DR	InterPro; IPR002049; Laminin_EGF.		

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 48.4494 Seconds

(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-10

Perfect score: 9758

Sequence: 1 MGLQVAFAGVIALWGTRVC.....EVRSLKDIKSEKAVVYSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1596107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9758	100.0	1786	3 AAB19799	Aab19799 Mouse lam
2	9758	100.0	1786	3 AAB48450	Aab48450 Mouse lam
3	9758	100.0	1786	5 ABB81592	Abb81592 Mouse lam
4	9692	99.3	1776	2 AAW50894	Aaw50894 Mouse lam
5	9517.5	97.5	1764	1 AAP91872	Aap91872 Primary a
6	9429	96.6	1725	3 AAB19800	Aab19800 Mouse lam
7	9429	96.6	1725	3 AAB48451	Aab48451 Mouse lam
8	9429	96.6	1725	5 ABB81593	Abb81593 Mouse lam
9	9144	93.7	1786	2 AAW50893	Aaw50893 Human lam
10	9144	93.7	1786	3 AAB16522	Aab16522 Human lam
11	9144	93.7	1786	3 AAB19797	Aab19797 Human lam
12	9144	93.7	1786	3 AAB48448	Aab48448 Human lam
13	9144	93.7	1786	4 AAB90788	Aab90788 Human she
14	9144	93.7	1786	5 ABB81590	Abb81590 Human lam
15	9131	93.6	1786	5 AAM48896	Aam48896 Laminin p
16	9108.5	93.3	1785	2 AAY15461	Aay15461 Human lam
17	9092	93.2	1765	3 AAB19798	Aab19798 Human lam
18	9092	93.2	1765	3 AAB48449	Aab48449 Human lam
19	9092	93.2	1765	5 ABB81591	Abb81591 Human lam
20	5087.5	52.1	1801	2 AAW50895	Aaw50895 Rat lamin
21	5087.5	52.1	1801	7 ADE60383	Ade60383 Rat Prote
22	5066.5	51.9	1799	5 AAW50359	Aaw50359 Mouse lam
23	5031.5	51.6	1798	5 AAW50896	Aaw50896 Human lam
24	5031.5	51.6	1798	7 ADE60385	Ade60385 Human Pro
25	4902	50.2	1798	5 AAB19801	Aab19801 Protein L

26	4902	50.2	1798	5 AAM50360	Aam50360 Human lam
27	3861.5	39.6	1788	4 ABB62995	Abb62995 Drosophil
28	3813.5	39.1	1761	2 AAY15457	Aay15457 Human lam
29	3616	37.1	822	5 AAM48897	Aam48897 Laminin p
30	3610	37.0	1670	7 ADE07851	Ade07851 Novel pro
31	3068.5	31.4	1101	7 ADE28641	Ade28641 Human NOV
32	3046.5	31.2	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2640	27.1	466	2 AAR07447	Aar07447 Human lam
34	2154	22.1	527	3 AAB58995	Aab58995 Breast an
35	1940	19.9	434	1 AAP60109	Aap60109 Human Bl
36	1708	17.5	1339	4 ABB59807	Abb59807 Drosophil
37	1681	17.2	315	6 ABU70520	Abu70520 Human adi
38	1671	17.1	3712	4 ABB64954	Abb64954 Drosophil
39	1661.5	17.0	1572	3 AAB19806	Aab19806 Mouse lam
40	1661.5	17.0	1572	3 AAB48455	Aab48455 Mouse lam
41	1661.5	17.0	1572	5 ABB81597	Abb81597 Mouse lam
42	1661.5	17.0	1605	3 AAB19805	Aab19805 Mouse lam
43	1661.5	17.0	1605	3 AAB48454	Aab48454 Mouse lam
44	1661.5	17.0	1605	5 ABB81596	Abb81596 Mouse lam
45	1651	16.9	1609	3 AAB19801	Aab19801 Human lam

## ALIGNMENTS

### RESULT 1

AAB19799

ID AAB19799 standard; protein; 1786 AA.

XX AAB19799;

AC XX

DT 05-MAR-2001 (first entry)

XX Mouse laminin 2 beta-1 chain.

DE Mouse laminin 2 beta-1 chain.

XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;

KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Mus musculus.

OS Mus musculus.

XX Key

FT Peptide

FT Peptide

FT Protein

FT Protein

XX WO200066730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.

PR 15-JUN-1999; 99US-0139198P.

PR 12-JUL-1999; 99US-0143289P.

PR 24-SEP-1999; 99US-0155945P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88899.

XX Purified laminin 2 protein, useful for research and therapeutic purposes

XX including peripheral nerve regeneration, treatment of degenerative muscle

XX disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 212-218; 305pp; English.

XX The present sequence is that of the beta-1 chain of mouse laminin 2.

XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1

XX (100 kDa) chains. It is thought to be specifically required for

CC stabilizing myotubes during skeletal muscle development, and for  
 CC preventing apoptosis. Genetic defects in human laminin 2 structure or  
 CC expression are associated with a major type of congenital muscular  
 CC dystrophy. Laminin 2 is also thought to be important in Schwann  
 CC cell/basal lamina interactions. The invention provides laminin 2 alpha-2,  
 CC beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the  
 CC polynucleotides encoding them (see AAB88891-906), methods for making  
 CC recombinant laminin 2, cells that express recombinant laminin 2, and  
 CC methods for using purified laminin 2 for research and therapeutic  
 CC purposes including peripheral nerve regeneration, treatment of  
 CC degenerative muscle disorders, angiogenesis regulation, promoting cell  
 CC attachment and migration, ex vivo cell therapy, improving the take of  
 CC grafts, improving the biocompatibility of medical devices and preparing  
 CC improved culture devices and media  
 XX  
 SQ Sequence 1786 AA;

Query Match 100.0%; Score 9758; DB 3; Length 1786;  
 Best Local Similarity 100.0%; Pred No. 0;  
 Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLQVAFGLVGLWTRVCAQPEPSYGCARGSCYPATGDLIIIGRAQKLSVTSTCGLHK 60  
 Db 1 MGLQVAFGLVGLWTRVCAQPEPSYGCARGSCYPATGDLIIIGRAQKLSVTSTCGLHK 60

Qy 61 PEPYCIUHLQEDKCFICDSRDPYHETLNPDSHLIENVVTPAPNRLKIWMQSENGVEN 120  
 Db 61 PEPYCIUHLQEDKCFICDSRDPYHETLNPDSHLIENVVTPAPNRLKIWMQSENGVEN 120

Qy 121 VTIQDLAEAFHFTLIMTEKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPFGISTG 180  
 Db 121 VTIQDLAEAFHFTLIMTEKTPRAAMLIERSDFGKTWGVYRYPAYDCESFPFGISTG 180

Qy 181 PMKVVDDIIICDSYSDIEPSTEGEIVFRALDPFAFKIEDPSPRIQNLKLTNRIKFVKL 240  
 Db 181 PMKVVDDIIICDSYSDIEPSTEGEIVFRALDPFAFKIEDPSPRIQNLKLTNRIKFVKL 240

Qy 241 HTLGDNLIDRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300  
 Db 241 HTLGDNLIDRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300

Qy 301 RHNTKGLNCELMDYFHDLPWRPAEGNSNACKKCNHSSCHDFDMAVFLATGNVSG 360  
 Db 301 RHNTKGLNCELMDYFHDLPWRPAEGNSNACKKCNHSSCHDFDMAVFLATGNVSG 360

Qy 361 VCDNCQHTWGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGESNGGICDGYTDFSVG 420  
 Db 361 VCDNCQHTWGRNCEQCKPFYQHPERDIRDPNLCEPCTCDPAGESNGGICDGYTDFSVG 420

Qy 421 LIAGQCRCKLHVEGERCDVCKEGFYDLASBDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480  
 Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLASBDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480

Qy 481 CKRLVTGQRCDQCIPOHWGLSNDLDGCRPCDCLGGALNNSCEDSQCSCLPHMIGROC 540  
 Db 481 CKRLVTGQRCDQCIPOHWGLSNDLDGCRPCDCLGGALNNSCEDSQCSCLPHMIGROC 540

Qy 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGVVRPEGAYLEFF 600  
 Db 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPFGVVRPEGAYLEFF 600

Qy 601 IDNPYSMEYELIRYEPQLPDHHEKAVITVQRPCKIPASSRCGNTVPDDNQVSLSPG 660  
 Db 601 IDNPYSMEYELIRYEPQLPDHHEKAVITVQRPCKIPASSRCGNTVPDDNQVSLSPG 660

Qy 661 SRYVVLPRPVCFEKGMYTVLELPQYTAGSDVSEPYTFIDSLVLMFYCKSLDIFTVGG 720  
 Db 661 SRYVVLPRPVCFEKGMYTVLELPQYTAGSDVSEPYTFIDSLVLMFYCKSLDIFTVGG 720

Qy 721 SGDEVTNSAWETFCRYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQS 780  
 Db 721 SGDEVTNSAWETFCRYRCLENSRSVVKTPMTDVCRNIIIFSISALIHQTGLACECDPQS 780

RESULT 2  
 AAB48450  
 ID AAB48450 standard; protein; 1786 AA.  
 XX

781 LSSVCDPNGQCCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840  
 Db 781 LSSVCDPNGQCCQCRPNVVGRTNRCAPGTFGFGPNCKPCDCHLQGSASAFCDAITGQC 840

Qy 841 HCFGGIYARQCDRLCPGYWGFPPSCQPCQCNHGLDCCDVTGECLSQCDYTTGHCERCLA 900  
 Db 841 HCFGGIYARQCDRLCPGYWGFPPSCQPCQCNHGLDCCDVTGECLSQCDYTTGHCERCLA 900

Qy 901 GYYGDPYIIGSDHCRPCPCPDGPDGSRQFARSQVDPVTIQLACVCDPVGIGRCDCCAS 960  
 Db 901 GYYGDPYIIGSDHCRPCPCPDGPDGSRQFARSQVDPVTIQLACVCDPVGIGRCDCCAS 960

Qy 961 GFFGNPDSFGSCQPCQCHHNIDTTPDEACDKTGRCLKLYHTEGDRCOLCQYGYGDA 1020  
 Db 961 GFFGNPDSFGSCQPCQCHHNIDTTPDEACDKTGRCLKLYHTEGDRCOLCQYGYGDA 1020

Qy 1021 LRQCRKVCNLYLTGVEHCNMGSDCHDKATGQCSCLPNVIGQNCDFCAPNTWOLASGTG 1080  
 Db 1021 LRQCRKVCNLYLTGVEHCNMGSDCHDKATGQCSCLPNVIGQNCDFCAPNTWOLASGTG 1080

Qy 1081 CGPCNCAHSGFSPSCNEFTGQCOCMPFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140  
 Db 1081 CGPCNCAHSGFSPSCNEFTGQCOCMPFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140

Qy 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
 Db 1141 TPQCDQSTGQCVCEGVEGPRCDKCTRGYSGVFPDCTPCHQCFALMDAIIIGELTNRTHKF 1200

Qy 1201 LEKAKALKISGVIQPYRETVDSEKKYNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260  
 Db 1201 LEKAKALKISGVIQPYRETVDSEKKYNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260

Qy 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELAPQLEFFIKNSDIQAGALDS 1320  
 Db 1261 TERMAQVEVKLTDTASQSNSTAGELGALQAEBSLDKTVKELAPQLEFFIKNSDIQAGALDS 1320

Qy 1321 ITKYPQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDIMLERESPEKEQOEQARLDE 1380  
 Db 1321 ITKYPQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDIMLERESPEKEQOEQARLDE 1380

Qy 1381 LAGKLQSLDLASAAQMTGCTPPGADCSSECGGPNCRDTDEGKKCGGPGGGLVTVAHSA 1440  
 Db 1381 LAGKLQSLDLASAAQMTGCTPPGADCSSECGGPNCRDTDEGKKCGGPGGGLVTVAHSA 1440

Qy 1441 WQKAMDFDRDVLALAEVEQLSKMWSEAKVPRADAKQNAQDVLLKTATKEKVDKSNEDL 1500  
 Db 1441 WQKAMDFDRDVLALAEVEQLSKMWSEAKVPRADAKQNAQDVLLKTATKEKVDKSNEDL 1500

Qy 1501 RNLIKQIENFLETDSADLDSIEAVANEVLKSGNSTPQOLQNLTERIRERVETLSQVEVI 1560  
 Db 1501 RNLIKQIENFLETDSADLDSIEAVANEVLKSGNSTPQOLQNLTERIRERVETLSQVEVI 1560

Qy 1561 LQOQSAADTARAELILLEAEKRAKSKATDVKVTADVMVKGALEAEAEKQVAAEKAIQOADEDI 1620  
 Db 1561 LQOQSAADTARAELILLEAEKRAKSKATDVKVTADVMVKGALEAEAEKQVAAEKAIQOADEDI 1620

Qy 1621 QGTQNLTSISETAASSETLTNASQISKLERNVEELKRAAONSGEAEYIEKVVSVK 1680  
 Db 1621 QGTQNLTSISETAASSETLTNASQISKLERNVEELKRAAONSGEAEYIEKVVSVK 1680

Qy 1681 QNADDDVKKTLDEGLDEKYYKVESLTAQTEESADARRKAEALLONEAKTLLAQANSKLQLL 1740  
 Db 1681 QNADDDVKKTLDEGLDEKYYKVESLTAQTEESADARRKAEALLONEAKTLLAQANSKLQLL 1740

Qy 1741 EDLERKYEDNQKLYEDKQAEQLVRLEGEVRSLLKQISEKVAVYSTCL 1786  
 Db 1741 EDLERKYEDNQKLYEDKQAEQLVRLEGEVRSLLKQISEKVAVYSTCL 1786



AAB48450;  
 02-WAR-2001 (first entry)  
 Mouse laminin 8 polypeptide, SEQ ID NO: 18.  
 Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
 antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
 vascular tissue injury; neural injury; angiogenesis regulation.  
 Mus musculus.  
 WO200066732-A2.  
 09-NOV-2000.  
 28-APR-2000; 2000WO-US011543.  
 30-APR-1999; 90US-0131720P.  
 21-AUG-1999; 90US-0149738P.  
 24-SEP-1999; 99US-0155945P.  
 11-FEB-2000; 2000US-0182012P.  
 (BIOS-) BIOSTRATUM INC.  
 Kortessaa J, Tryggvason K;  
 N-PSDB; AAC83711.  
 WPI; 2000-687539/67.  
 Purified laminin 8 protein, useful for research and therapeutic purposes  
 including peripheral nerve regeneration, treatment of degenerative muscle  
 disorders, angiogenesis regulation, and ex vivo cell therapy.  
 Claim 5; Page 176-182; 245pp; English.  
 The present sequence is a laminin 8 polypeptide chain. Laminins are a  
 family of heterotrimeric glycoproteins that function via binding  
 interactions with neighbouring cell receptors and by forming laminin  
 networks. They are signalling molecules which influence cellular  
 function. Laminin 8 is useful for treating injuries to tissue of  
 mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
 treating injuries to vascular tissue, promoting cell attachment and  
 migration, ex vivo cell therapy, improving the biocompatibility of  
 medical devices, and preparing improved cell culture devices and media.  
 Laminin 8 is also useful for promoting re-endothelialisation at the site  
 of vascular injuries, improving the take of grafts, improving the  
 biocompatibility of medical devices, treating neural injuries (neural  
 regeneration), regulating angiogenesis, and promoting cell attachment and  
 migration  
 Sequence 1786 AA;  
 Query Match 100.0%; Score 9758; DB 3; Length 1786;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MGLQVAFGLVLMGTRVCAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSGLHK 60  
 1 MGLQVAFGLVLMGTRVCAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSGLHK 60  
 61 PEPYCIVSHLOEDKKFCISRDYPHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
 61 PEPYCIVSHLOEDKKFCISRDYPHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
 121 VTIQDLEAEFHTLIMTFKTRPAAMLIERSDFGKTVGYRYFAYDCSSPFGISTG 180  
 121 VTIQDLEAEFHTLIMTFKTRPAAMLIERSDFGKTVGYRYFAYDCSSPFGISTG 180  
 181 PMKKVDDIICDSRYSDIEPSTGEVIFRALDPAFKIEDPSPRIQNLKINRIKFKVL 240  
 181 PMKKVDDIICDSRYSDIEPSTGEVIFRALDPAFKIEDPSPRIQNLKINRIKFKVL 240

241 HTLGDNLLDSRMEIRKYYIYAVDMVVRGNCFYGHASECAPVDGVNBEVEGHCHMC 300  
 241 HTLGDNLLDSRMEIRKYYIYAVDMVVRGNCFYGHASECAPVDGVNBEVEGHCHMC 300  
 301 RHTKGLNCELMDFYHDLFWRPAEGRNSNACKKNCNEHSSCHDFDMAVFLATGNVSG 360  
 301 RHTKGLNCELMDFYHDLFWRPAEGRNSNACKKNCNEHSSCHDFDMAVFLATGNVSG 360  
 361 VDNCOHNTMGRNCEOCKPFYFQHPERDIRDNLCCEPCTCDPAGSENGGICDGYTDFSVG 420  
 361 VDNCOHNTMGRNCEOCKPFYFQHPERDIRDNLCCEPCTCDPAGSENGGICDGYTDFSVG 420  
 421 LIAQCRCKLHVGERCDYCKGFDLSAEDPVGCKSCACNPLGTIPGGNPCDSEGYCY 480  
 421 LIAQCRCKLHVGERCDYCKGFDLSAEDPVGCKSCACNPLGTIPGGNPCDSEGYCY 480  
 481 CKELVTGQRCDQCLPQHWGLSNDLDCRCPDCLGALANNSCEDSGQCSCLPHMTGRQC 540  
 481 CKELVTGQRCDQCLPQHWGLSNDLDCRCPDCLGALANNSCEDSGQCSCLPHMTGRQC 540  
 541 NEVESGYFTLTDHYIYEAEANLGPVVVVERQYIQRIPSWTGPVVRPEGAYLEFF 600  
 541 NEVESGYFTLTDHYIYEAEANLGPVVVVERQYIQRIPSWTGPVVRPEGAYLEFF 600  
 601 IDNIPYSMEYEIILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPG 660  
 601 IDNIPYSMEYEIILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNQVSLSPG 660  
 661 SRVVLPRPVCPEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCSLDIDFTVGG 720  
 661 SRVVLPRPVCPEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVLMPCSLDIDFTVGG 720  
 721 SGGEVNTSAWETFORVRCLENSRVVKTPTMTDVCNIIIFSALIHQTLGACEDCPQGS 780  
 721 SGGEVNTSAWETFORVRCLENSRVVKTPTMTDVCNIIIFSALIHQTLGACEDCPQGS 780  
 781 LSSVCDPNQGCQCRPNVVGRTNRCAPGTFGPGNGCKPCDCHLOGSASAFCDAITGQC 840  
 781 LSSVCDPNQGCQCRPNVVGRTNRCAPGTFGPGNGCKPCDCHLOGSASAFCDAITGQC 840  
 841 HCFQGIYAROCRLCPGYWGFPSQPCQNGHALDCDVTGCLSCQDVTTHGNCERCLA 900  
 841 HCFQGIYAROCRLCPGYWGFPSQPCQNGHALDCDVTGCLSCQDVTTHGNCERCLA 900  
 901 GYGDPFIIGSDHRCPCPCPDGPDGRQFARSCYQDPVTLQALACVCDPVGIGSRCDCCAS 960  
 901 GYGDPFIIGSDHRCPCPCPDGPDGRQFARSCYQDPVTLQALACVCDPVGIGSRCDCCAS 960  
 961 GFGNPSDFGSGCQPCQCHNIDTTPDPAKDTGTCLKCLVHTGHDHCOLCOGYGYGDA 1020  
 961 GFGNPSDFGSGCQPCQCHNIDTTPDPAKDTGTCLKCLVHTGHDHCOLCOGYGYGDA 1020  
 1021 LRQDCRKCVCNVLGTVKEHCHNGSDCHCDKATGQCCLPNVIGQNCDCRCPNTWQLASGTG 1080  
 1021 LRQDCRKCVCNVLGTVKEHCHNGSDCHCDKATGQCCLPNVIGQNCDCRCPNTWQLASGTG 1080  
 1081 CGPCNMAHSFGPSCNEFTGQCCQCHPGGRTCSQBELFWGDDPVEACDCCDRGIE 1140  
 1081 CGPCNMAHSFGPSCNEFTGQCCQCHPGGRTCSQBELFWGDDPVEACDCCDRGIE 1140  
 1141 TPQCDOSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKF 1200  
 1141 TPQCDOSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDAIIGELTNRTHKF 1200  
 1201 LEKAKALKISGIVGPRTVDSVEKKVNEIKDILAQSPAEPKNGIILFEAEKLTQDV 1260  
 1201 LEKAKALKISGIVGPRTVDSVEKKVNEIKDILAQSPAEPKNGIILFEAEKLTQDV 1260  
 1261 TEKMAOEVKLTDTASQNSSTAGELCALQAEASLDKTVKELAEQLEFKNSDIQALDS 1320  
 1261 TEKMAOEVKLTDTASQNSSTAGELCALQAEASLDKTVKELAEQLEFKNSDIQALDS 1320  
 1321 ITKYFQMSLEAEKRVNASSTTDPNSTVEQSALTDRVEDLMLESFPKQEQEQAALLDE 1380

Db 1321 ITKIFOMLEAEKRVNASTTDPNSTVEQALTRDRVEDMLERSEPFKEQEQEQLLDE 1380  
Qy 1381 LAGKLOSLDLASAAQMTCTGPPGADCSSESCGPNCRTEDEGKKCGGPGCGGLVTVAHSA 1440  
Db 1381 LAGKLOSLDLASAAQMTCTGPPGADCSSESCGPNCRTEDEGKKCGGPGCGGLVTVAHSA 1440  
Qy 1441 WQKAMPDRDVLASALAEVQLSNWSEAKVRADKONADVLTKTNATKEKVDKSNEDL 1500  
Db 1441 WQKAMPDRDVLASALAEVQLSNWSEAKVRADKONADVLTKTNATKEKVDKSNEDL 1500  
Qy 1501 RNLIKQIRNELTSDADLSIEAVANEVLKSGNASTPQOLQNLTERIRVETLSQVEVI 1560  
Db 1501 RNLIKQIRNELTSDADLSIEAVANEVLKSGNASTPQOLQNLTERIRVETLSQVEVI 1560  
Qy 1561 LOQSAADIAAEILLBEAKGASKSATDVKVTADWKEALEEAEKQAVAEKAKQADEDI 1620  
Db 1561 LOQSAADIAAEILLBEAKGASKSATDVKVTADWKEALEEAEKQAVAEKAKQADEDI 1620  
Qy 1621 QGTQNLITSTESATASEETLTNASORISKLEENVEELKRAQNSGEAEYIEKVYVSK 1680  
Db 1621 QGTQNLITSTESATASEETLTNASORISKLEENVEELKRAQNSGEAEYIEKVYVSK 1680  
Qy 1681 QNADDDVKTTDGBELDEKYYKVESLIAQKTEESADARKEALLQNEAKTLLAQANSKLQLL 1740  
Db 1681 QNADDDVKTTDGBELDEKYYKVESLIAQKTEESADARKEALLQNEAKTLLAQANSKLQLL 1740  
Qy 1741 EDLERKYEDNOKYLEDKAOELVLEGEVRSLLDKDISEKVAVYSTCL 1786  
Db 1741 EDLERKYEDNOKYLEDKAOELVLEGEVRSLLDKDISEKVAVYSTCL 1786

RESULT 3  
ABB81592  
ID ABB81592 standard; protein; 1786 AA.  
AC ABB81592;  
XX  
DT 19-SEP-2002 (first entry)  
DE Mouse laminin 10 second chain protein sequence SEQ ID NO:10.  
KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
OS Mus musculus.  
Key Location/Qualifiers  
FT Peptide 1..21  
FT Protein /label= signal  
FT /label= laminin\_10\_second\_chain  
WO200250111-A2.  
PD 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P.  
XX 28-MAR-2001; 2001US-0279282P.  
XX 13-NOV-2001; 2001US-00279282.  
XX (BTOS-) BIOTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
XX WPI; 2002-557650/59.  
XX N-PSDB; ABQ72910.  
XX New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX  
PS Claim 9; Page 140-145; 23pp; English.  
XX  
CC The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC encodes a second chain protein of laminin 10, from the present invention  
XX Sequence 1786 AA;  
SQ  
Query Match 100.0%; Score 9758; DB 5; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGLLQVPAFGVLAALWTRVCAQEPESYGAEGSCYPATGDLITGRAQKLSVTSTCGLHK 60  
Db 1 MGLLQVPAFGVLAALWTRVCAQEPESYGAEGSCYPATGDLITGRAQKLSVTSTCGLHK 60  
Qy 61 PEPYCIIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVTTPAPNRLKIWQSENGVEN 120  
Db 61 PEPYCIIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVTTPAPNRLKIWQSENGVEN 120  
Qy 121 VTIOLEAEFHFTHLIMTKTFRPAALMTERSSDFKWTGVVRYFAYDCESPPGISTG 180  
Db 121 VTIOLEAEFHFTHLIMTKTFRPAALMTERSSDFKWTGVVRYFAYDCESPPGISTG 180  
Qy 181 PMKXVDIIICDSRYSDIEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKTNRIKPVKL 240  
Db 181 PMKXVDIIICDSRYSDIEPSTEGEVIIFRALDPAPFKIEDPYSPIQNLLKTNRIKPVKL 240  
Qy 241 HTLGNLLDSMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300  
Db 241 HTLGNLLDSMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300  
Qy 301 RHNTKGLNCELAMDYHDLPRWPAEGNSNACKKNCNNEHSSCHFDMAVFLATGNVSGG 360  
Db 301 RHNTKGLNCELAMDYHDLPRWPAEGNSNACKKNCNNEHSSCHFDMAVFLATGNVSGG 360  
Qy 361 VCDNCHNTWGRNCEQCKPFYQHPERDIRDNPCLCEPCTCDPAGSENGGICDGYTDFSVG 420  
Db 361 VCDNCHNTWGRNCEQCKPFYQHPERDIRDNPCLCEPCTCDPAGSENGGICDGYTDFSVG 420  
Qy 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNPCDSETGYCY 480  
Db 421 LIAGQCRCKLHVEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGNPCDSETGYCY 480  
Qy 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSCQCSCLPHMIGRQC 540  
Db 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSCQCSCLPHMIGRQC 540  
Qy 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600  
Db 541 NEVESGYFTTLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGPGRVVRPEGAYLEFF 600  
Qy 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPGKIPASSRCQNTVPDDNQNVSISPG 660  
Db 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPGKIPASSRCQNTVPDDNQNVSISPG 660  
Qy 661 SRYVVLPEPVCFEKGMNVTRELPQYTAGSDVESPYTFIDSLVLMYPCKSLDIFTVGG 720  
Db 661 SRYVVLPEPVCFEKGMNVTRELPQYTAGSDVESPYTFIDSLVLMYPCKSLDIFTVGG 720  
Qy 721 SGDGEVNTNSAWETFORVRCLENSSVVKTPMTDVCNRIIFSISALIHQTGLACDCDQGS 780  
Db 721 SGDGEVNTNSAWETFORVRCLENSSVVKTPMTDVCNRIIFSISALIHQTGLACDCDQGS 780

QY 781 LSSVCDPNGGQCQCPNPNVGRTRNRCAPGTGFGPNGCKPCDCCHLQGSASAFCDAITGQC 840  
Db 781 LSSVCDPNGGQCQCPNPNVGRTRNRCAPGTGFGPNGCKPCDCCHLQGSASAFCDAITGQC 840  
QY 841 HCFQGIYARQCDRLCPGYWGPSPCOPCCNCHALDCTVTGCECLSCDYTTGHCNCRCLA 900  
Db 841 HCFQGIYARQCDRLCPGYWGPSPCOPCCNCHALDCTVTGCECLSCDYTTGHCNCRCLA 900  
QY 901 GYGDPIIIGSDHCRPCPCPDGSGRQFASCSYQDPVTLQACVDPGYTGSRCDDCAS 960  
Db 901 GYGDPIIIGSDHCRPCPCPDGSGRQFASCSYQDPVTLQACVDPGYTGSRCDDCAS 960  
QY 961 GFGNPSDFGSCQPCQCHNIDTTPDCAKDTGRCLKCLYHTEGDCQCLQYGYGDA 1020  
Db 961 GFGNPSDFGSCQPCQCHNIDTTPDCAKDTGRCLKCLYHTEGDCQCLQYGYGDA 1020  
QY 1021 LRQDCKVCNVLGTGKXHCNCSCHCDKATGQCSCLEPNVIGQNCDCRCPAPNTWOLASGTG 1080  
Db 1021 LRQDCKVCNVLGTGKXHCNCSCHCDKATGQCSCLEPNVIGQNCDCRCPAPNTWOLASGTG 1080  
QY 1081 CQPCNCAHSGPSCNEFTGQCQMPGFGGTCSCEQLFWGDDPVECRACDDCPRGIE 1140  
Db 1081 CQPCNCAHSGPSCNEFTGQCQMPGFGGTCSCEQLFWGDDPVECRACDDCPRGIE 1140  
QY 1141 TPQCDQSTGQCVGVGVEGPRCDKCTRGYSVGFPPDCTCHQCFAIWDALIIIGELTNRTHKF 1200  
Db 1141 TPQCDQSTGQCVGVGVEGPRCDKCTRGYSVGFPPDCTCHQCFAIWDALIIIGELTNRTHKF 1200  
QY 1201 LKAKALKISGIVGPIRETVDSVEKKVNEIKDILAQSPAAPLKNIGILFBEAEKLTNDV 1260  
Db 1201 LKAKALKISGIVGPIRETVDSVEKKVNEIKDILAQSPAAPLKNIGILFBEAEKLTNDV 1260  
QY 1261 TEKMAQVEVKLTDTASQSNSTAGELCALQAEASLDKTKVLAEOLEFIKNSDIOGALDS 1320  
Db 1261 TEKMAQVEVKLTDTASQSNSTAGELCALQAEASLDKTKVLAEOLEFIKNSDIOGALDS 1320  
QY 1321 ITKYFQMSLEAEKRVNASTDNPSTVEQSALTDRVEDLMLRESPPFKEQBEQARLLDE 1380  
Db 1321 ITKYFQMSLEAEKRVNASTDNPSTVEQSALTDRVEDLMLRESPPFKEQBEQARLLDE 1380  
QY 1381 LAGKLOSLDLASAAQMTCTPGADCSSECGGPNCRDTEGKKCGGCGGLVTVHA 1440  
Db 1381 LAGKLOSLDLASAAQMTCTPGADCSSECGGPNCRDTEGKKCGGCGGLVTVHA 1440  
QY 1441 WQKAMPFDRDLVLSALAEVQLSKMWSEAKVRADEAKQNAQDVLKTNATKKEKVDKSNEDL 1500  
Db 1441 WQKAMPFDRDLVLSALAEVQLSKMWSEAKVRADEAKQNAQDVLKTNATKKEKVDKSNEDL 1500  
QY 1501 RNLIKOIRNFLTSDADLSIEAVNEVLKSGNASTPQOLQNTDIRERVETLSQVEVI 1560  
Db 1501 RNLIKOIRNFLTSDADLSIEAVNEVLKSGNASTPQOLQNTDIRERVETLSQVEVI 1560  
QY 1561 LQQAADIAAELELLLEAEKRAKSAATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDI 1620  
Db 1561 LQQAADIAAELELLLEAEKRAKSAATDVKTADVMVKEALEEAEKAQVAEKAQKQADEDI 1620  
QY 1621 QGTQNLTSIESTASAEETLTNASQRIKSLERNVEELKRAQNSGEAEYIEKVVYSVK 1680  
Db 1621 QGTQNLTSIESTASAEETLTNASQRIKSLERNVEELKRAQNSGEAEYIEKVVYSVK 1680  
QY 1681 QNADDDVKTLQDGLDEKIKVVEGLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740  
Db 1681 QNADDDVKTLQDGLDEKIKVVEGLIAQKTEESADARRKAEALLQNEAKTLLAQANSKLQLL 1740  
QY 1741 EDLERYEDNQKYLEKQAEVLVEGEVRSLLKDISEKVAIVSTCL 1786  
Db 1741 EDLERYEDNQKYLEKQAEVLVEGEVRSLLKDISEKVAIVSTCL 1786

RESULT 4  
AAW50894  
ID AAW50894 standard; protein; 1776 AA.

XX AC AAW50894;  
XX DT 07-DEC-1998 (first entry)  
XX DE Mouse laminin B1 chain.  
XX KW Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
XX therapy.  
XX Mus sp.  
XX PN W09815179-A1.  
XX PD 16-APR-1998.  
XX PF 08-OCT-1997; 97WO-US018145.  
XX PR 08-OCT-1996; 96US-0027981P.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Castillo G, Snow AD;  
XX DR WPI; 1998-240534/21.  
XX PT Use of laminin and fragments - for developing products for use in the  
XX diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
XX CJD.  
XX PS Claim 15; Page 90-93; 132pp; English.  
XX CC This is the amino acid sequence of the mouse laminin B1 chain. The  
CC primary object of the invention is to use laminin, laminin-derived  
CC protein fragments and/or laminin-derived polypeptides as potent  
CC inhibitors of amyloid formation, deposition, accumulation and/or  
CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
CC products (see AAW50898-98) may include mouse or human laminin A or A1  
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
CC binding domain of the laminin A chain. A claimed method for treating an  
CC amyloid disease comprises administering a polypeptide having a  
CC conformational similarity to a fragment of a laminin protein. A method  
CC for diagnosing an amyloid disease involves determining levels of laminin  
CC in a sample. Production of laminin or its fourth globular repeat in vivo  
CC provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
CC products and methods can be used for the diagnosis, prognosis, monitoring  
CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
CC associated with chronic inflammation, various forms of malignancy and  
CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
CC prion diseases including Creutzfeldt-Jacob disease, Gertmann-Straussler  
CC prion disease, kuru and animal scrapie (PrP amyloid), the amyloidosis  
CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
CC transthyretin amyloid), and the amyloidosis associated with endocrine  
CC tumours such as medullary carcinoma of the thyroid (variant of  
XX procalcitonin)  
XX Sequence 1776 AA;

Query Match 99.3%; Score 9692; DB 2; Length 1776;

Best Local Similarity 99.8%; Pred. No. 0;		Matches 1776; Conservative	0; Mismatches	0; Indels	4; Gaps	1;
Qy	1	MGLQVAFGLVLMWTRVCAQBPESYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHK	60			
Db	1	MGLQVAFGLVLMWTRVCAQBPESYGCAGSCYPATGDLILIGRAQKLSVTSTCGLHK	60			
Qy	61	PEPYCIVSHLOEDKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVEN	120			
Db	61	PEPYCIVSHLOEDKCFICDSRDPYHETLNPDSHLIENVTTFAPNRLKIWMQSENGVEN	120			
Qy	121	VITQDLAEFFHTHLIMTKTPRPAAMLIERSDRGKTGWYRFPAYDCBSFGISGTG	180			
Db	121	VITQDLAEFFHTHLIMTKTPRPAAMLIERSDRGKTGWYRFPAYDCBSFGISGTG	180			
Qy	181	PMKVVDDIICDSYSIDIEPSTEVEVIFRALDPFKIEDPVSPIRQNLKILNLRKIFVKL	240			
Db	181	PMKVVDDIICDSYSIDIEPSTEVEVIFRALDPFKIEDPVSPIRQNLKILNLRKIFVKL	240			
Qy	241	HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGWGHCMC	300			
Db	241	HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGWGHCMC	300			
Qy	301	RHNTKGLNCLCNDFFVHDLPMRPAEGRNSNACKCNNEHSSCHPDMVAVFLATGNVSGG	360			
Db	301	RHNTKGLNCLCNDFFVHDLPMRPAEGRNSNACKCNNEHSSCHPDMVAVFLATGNVSGG	360			
Qy	361	VCNQCQNTWGRNCEQCKPFYQHPERDIRDPNLCPECTCDPAGSENGICDGYTDFSVG	420			
Db	361	VCNQCQNTWGRNCEQCKPFYQHPERDIRDPNLCPECTCDPAGSENGICDGYTDFSVG	420			
Qy	421	LIAGQCRKLVHGERCDVCEGFDLSAEDPYGCKSCACNPLGTIPGGNCPDSEGTGYCY	480			
Db	421	LIAGQCRKLVHGERCDVCEGFDLSAEDPYGCKSCACNPLGTIPGGNCPDSEGTGYCY	480			
Qy	481	CKRLVQRCQDCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGROC	540			
Db	481	CKRLVQRCQDCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQCSCLPHMIGROC	540			
Qy	541	NEVESGYFTTLDHYIYBAEANLPGVWVVERQYIQDRIPSWTGFVRVPEGAYLEFF	600			
Db	541	NEVESGYFTTLDHYIYBAEANLPGVWVVERQYIQDRIPSWTGFVRVPEGAYLEFF	600			
Qy	601	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVSLSPG	660			
Db	601	IDNIPYSMEYEILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDDNQVSLSPG	660			
Qy	661	SRVYVLPKPCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGG	720			
Db	661	SRVYVLPKPCFEKGMNVTVRLELPQYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGG	720			
Qy	721	SGDGEVNTSAWETFORVRCLENSRSVVKTPMTDVCNRIIFSIQALIHQTGLACECDPQGS	780			
Db	721	SGDGEVNTSAWETFORVRCLENSRSVVKTPMTDVCNRIIFSIQALIHQTGLACECDPQGS	780			
Qy	781	LSSVCDPENGQCCRPNVVGRTCNRCAPGTFGFGPKGCKPCDCHLQGSASAFCDATGQC	840			
Db	781	LSSVCDPENGQCCRPNVVGRTCNRCAPGTFGFGPKGCKPCDCHLQGSASAFCDATGQC	840			
Qy	841	HCFOGIVARQCDRLPGYWGPPSCQPCQNGHALDCDVTGECISQDYTTGHCERCLA	900			
Db	841	HCFOGIVARQCDRLPGYWGPPSCQPCQNGHALDCDVTGECISQDYTTGHCERCLA	900			
Qy	901	GYGDPITIGSDHCRPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPVGIGRCDDCAS	960			
Db	901	GYGDPITIGSDHCRPCPDGPDGSGRQFARSCYQDPVTLQLACVCDPVGIGRCDDCAS	960			
Qy	961	GFFGNPSDFGSCQPCQCHNIDTTPDPEACDKDGRCLKLYHTEGDHCOLCOGYGYGDA	1020			
Db	961	GFFGNPSDFGSCQPCQCHNIDTTPDPEACDKDGRCLKLYHTEGDHCOLCOGYGYGDA	1020			
Qy	1021	LRODCRKVCNLYGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTG	1080			

Db	1021	LRODCRKVCNLYGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTG	1080			
Qy	1081	CGFCNCAHSPGSCNFTGQCQCMPPGFGTSCQELFWGDPDVECRACDCDPPGIE	1140			
Db	1081	CGFCNCAHSPGSCNFTGQCQCMPPGFGTSCQELFWGDPDVECRACDCDPPGIE	1140			
Qy	1141	TPQCDOSTQCQCVGEGPRCDKCTRGYGVFPDCTPHQCQFALWDIAIIGELNTRTHKF	1200			
Db	1141	TPQCDOSTQCQCVGEGPRCDKCTRGYGVFPDCTPHQCQFALWDIAIIGELNTRTHKF	1200			
Qy	1201	LEXAKALKISGVIQPVRETVDSEKKNVEIKDILAQSPAAEPKNIKIGILFEAEKLTQDV	1260			
Db	1201	LEXAKALKISGVIQPVRETVDSEKKNVEIKDILAQSPAAEPKNIKIGILFEAEKLTQDV	1260			
Qy	1261	TERMAQVEVKLTDTASQSNSTAGELGALQABAEISDKTVKELAEQLEFIKNSDIQGALDS	1320			
Db	1261	TERMAQVEVKLTDTASQSNSTAGELGALQABAEISDKTVKELAEQLEFIKNSDIQGALDS	1320			
Qy	1321	ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLERSPFKQEQQEQRLLDE	1380			
Db	1321	ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLERSPFKQEQQEQRLLDE	1380			
Qy	1381	LAKGLQSLDLSAAAQMTCTGTPGADCSSECCGPNCRDDEGEKKCGGPGCGGLVTVAHSA	1440			
Db	1381	LAKGLQSLDLSAAAQMTCTGTPGADCSSECCGPNCRDDEGEKKCGGPGCGGLVTVAHSA	1440			
Qy	1441	WQAMDFDRDVLASALAEVQLSKMVSEAKVRADAEAKQNAQDVLLKTNAKTKVDSNEDL	1500			
Db	1441	WQAMDFDRDVLASALAEVQLSKMVSEAKVRADAEAKQNAQDVLLKTNAKTKVDSNEDL	1500			
Qy	1501	RNLIKQIRNFLTSDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI	1560			
Db	1501	RNLIKQIRNFLTSDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI	1560			
Qy	1561	LQSAADIAIRAEALLLEAEKASKSATDVKTADVMKEALEBAEKAQVAEKAIKQADEDI	1620			
Db	1561	LQSAADIAIRAEALLLEAEKASKSATDVKTADVMKEALEBAEKAQVAEKAIKQADEDI	1620			
Qy	1621	QGTQNLTSIESTASAEETLTNASQISKLERNVBEELKRAKAQNSGEAEYIEKVVYSVK	1680			
Db	1621	QGTQNLTSIESTASAEETLTNASQISKLERNVBEELKRAKAQNSGEAEYIEKVVYSVK	1680			
Qy	1681	QNADVVKTLGDGLDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLAQANSKLQLL	1740			
Db	1681	-----DVVKTLGDGLDEKYYKVESLIAQKTEESADARRKAEALLQNEAKTLAQANSKLQLL	1740			
Qy	1741	EDLERKYEDNQYLEPKAQELVLEGEVRSLLKDISEKVA	1780			
Db	1737	EDLERKYEDNQYLEPKAQELVLEGEVRSLLKDISEKVA	1776			
RESULT 5						
ID	AAP91672 standard; protein; 1764 AA.					
XX	AAP91672;					
AC	AAP91672;					
DT	25-MAR-2003 (revised)					
DT	31-OCT-2002 (revised)					
DT	29-JUN-1990 (first entry)					
DE	Primary amino acid sequence of B1 chain of laminin.					
XX	Laminin B1 chain fragment; heparin; prosthetic devices;					
KW	cell culture substrates; cell adhesion promoter; nerve regeneration;					
KW	wound healing; implant acceptance; cell attachment; metastasis inhibitor.					
OS	Mus musculus.					
OS	Synthetic.					
XX	Key					
PH	Location/Qualifiers					
FT	641..660					
FT	/note= "designated F9"					

Db	1021	LRODCRKVCNLYGTVKEHNGSDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTG	1080			
Qy	1081	CGPCNCAHSPGSCNENFTGQCQCMFPGGRTCSCEQLFWGDDPDPVECRACDCDPRGIE	1140			
Db	1081	CGPCNCAHSPGSCNENFTGQCQCMFPGGRTCSCEQLFWGDDPDPVECRACDCDPRGIE	1140			
Qy	1141	TPQCDQSTGQCVCEGVGEGPRCDKTRGYSVGFDPDCTPCHQCEALWDALIGELTNRTHKF	1200			
Db	1141	TPQCDQSTGQCVCEGVGEGPRCDKTRGYSVGFDPDCTPCHQCEALWDALIGELTNRTHKF	1200			
Qy	1201	LEKAKALKISGVIGPYRETVDVSEKKNWEIKDILAQSPAAEPKKNIGILFEEAEKLTQKV	1260			
Db	1201	LEKAKALKISGVIGPYRETVDVSEKKNWEIKDILAQSPAAEPKKNIGILFEEAEKLTQKV	1260			
Qy	1261	TEKMAQVEVKLTDTASOSNSTAGELGALQABASLQKTVKELAEQLEFINKSDIOGALDS	1320			
Db	1261	TEKMAQVEVKLTDTASOSNSTAGELGALQABASLQKTVKELAEQLEFINKSDIOGALDS	1320			
Qy	1321	ITTKYFQNSLAERKVNASTTDPNSTVQSALTRDRVEDLMLESPPFKSQEQAARLDE	1380			
Db	1321	ITTKYFQNSLAERKVNASTTDPNSTVQSALTRDRVEDLMLESPPFKSQEQAARLDE	1380			
Qy	1381	LAGKQLSLDLSAAQMTCCGTPPGADCSSESCGGPNCRDTDEGKCKCGGPGGGLVTVVHSA	1440			
Db	1381	LAGKQLSLDLSAAQMTCCGTPPGADCSSESCGGPNCRDTDEGKCKCGGPGGGLVTVVHSA	1440			
Qy	1441	WQKAWDFDRDVLASAEVOLSKMVSEAKYRDEAKQNAQDVLKTNATKEKVDKSNEDL	1500			
Db	1441	WQKAWDFDRDVLASAEVOLSKMVSEAKYRDEAKQNAQDVLKTNATKEKVDKSNEDL	1500			
Qy	1501	RNLKIQIRNFUTEDSADLSTIEAVANVLKSGNASTPQQLQNTEDIRERVETLSQVEVI	1560			
Db	1501	RNLKIQIRNFUTEDSADLSTIEAVANVLKSGNASTPQQLQNTEDIRERVETLSQVEVI	1560			
Qy	1561	LOQSAADIRARELLEAKGASKSATDVKYTDVMKEALBEAEKAQVAAEKAQKQADEDI	1620			
Db	1561	LOQSAADIRARELLEAKGASKSATDVKYTDVMKEALBEAEKAQVAAEKAQKQADEDI	1620			
Qy	1621	QGTQNLTSISETAASEETLTNASQISKLERNVEELKRAAQNQSGEAYIEKVVYSVK	1680			
Db	1621	QGTQNLTSISETAASEETLTNASQISKLERNVEELKRAAQNQSGEAYIEKVVYSVK	1680			
Qy	1681	QNAADDVKTLGDELDEKVKVKSIAQKTESADARBAKELLQNEAKTLAQANSKLQLL	1740			
Db	1681	QNAADDVKTLGDELDEKVKVKSIAQKTESADARBAKELLQNEAKTLAQANSKLQLL	1740			
Qy	1741	EDLERKYEDNOKYLEDKAEQELVRLGEVRSLLKDISEKVA	1780			
Db	1737	EDLERKYEDNOKYLEDKAEQELVRLGEVRSLLKDISEKVA	1776			
RESULT 5						
AAP91672						
ID	AAP91672 standard; protein; 1764 AA.					
XX	AAP91672;					
XX	25-MAR-2003 (revised)					
DT	31-OCT-2002 (revised)					
DT	29-JUN-1990 (first entry)					
XX	Primary amino acid sequence of B1 chain of laminin.					
XX	Laminin B1 chain fragment; heparin; prosthetic devices;					
KW	cell culture substrates; cell adhesion promoter; nerve regeneration;					
KW	wound healing; implant acceptance; cell attachment; metastasis inhibitor.					
XX	Mus musculus.					
OS	Synthetic.					
XX	Key					
XX	Location/Qualifiers					
FT	Peptide					
FT	641..660					
FT	/note= "designated F9"					

FT Peptide 1171. .1188  
FT /note= "designated F13"  
XX W08901493-A.  
XX 23-FEB-1989.  
XX 19-AUG-1987; 87US-00087157.  
XX 19-AUG-1987; 87US-00087157.  
XX (MINU ) MINNESOTA UNIVERSITY.  
XX Charonis A, Furcht LT;  
PI WPI; 1989-068855/09.  
XX New laminin B1 chain polypeptide(s) - for promoting heparin binding and  
XX cell adhesion.  
XX Disclosure, Page ?; 42pp; English.  
XX The new polypeptides have an amino acid sequence corresp. to a laminin B1  
CC chain fragment having specific binding capacity for heparin. Specifically  
CC mentioned are the two polypeptides F9 and F13 (see FT). The polypeptides  
CC may be used to promote binding of heparin to synthetic substrates and  
CC promote cell adhesion, eg endothelial, melanoma, fibrosarcoma, glioma and  
CC rheochromocytoma cells. They may be useful for assisting nerve  
CC regeneration, promoting wound healing, implant acceptance, cell  
CC attachment to culture substrates and inhibiting metastasis of malignant  
CC cells. They may be prep'd. by conventional Merrifield solid-phase  
CC synthesis. Also claimed are prosthetic devices and cell culture  
CC substrates coated with the new polypeptides. (Updated on 31-OCT-2002 to  
CC add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX Sequence 1764 AA;

Query Match 97.5%; Score 9517.5; DB 1; Length 1764;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1746; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 22 QPEFSGYGAEGSCYPATGDLIGRAQLSVTSGLHKPEPYCIIVSHLQEDKKCFICDS 81  
DB 1 QPEFSGYGAEGSCYPATGDLIGRAQLSVTSGLHKPEPYCIIVSHLQEDKKCFICDS 60  
QY 82 RDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVENVTIQLDEAFHFTHLIMTFK 141  
DB 61 RDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVENVTIQLDEAFHFTHLIMTFK 120  
QY 142 TFRPAAMLIERSDDPKTGVYFRAYDCESPPGISTGPMKVVDDIICDSYSIDIEPST 201  
DB 121 TFRPAAMLIERSDDPKTGVYFRAYDCESPPGISTGPMKVVDDIICDSYSIDIEPST 180  
QY 202 EGEVIFRALDPAPFKIEDPYSPRIQNLKITNRIKFKVLHTLGDNLDSRMEIREKYIYA 261  
DB 181 EGEVIFRALDPAPFKIEDPYSPRIQNLKITNRIKFKVLHTLGDNLDSRMEIREKYIYA 240  
QY 262 VYDMVVRGNCFCYGHASCAPVDGVNEVEGVHGHCMCRHNTKGLNCELQMDFFVHDLFW 321  
DB 241 VYDMVVRGNCFCYGHASCAPVDGVNEVEGVHGHCMCRHNTKGLNCELQMDFFVHDLFW 300  
QY 322 RPAEGRSNACKKCNKNEHSSSCHFDMAVFLATGNVSGVGVCDNCQHTMTGRNCEQCKPXY 381  
DB 301 RPAEGRSNACKKCNKNEHSSSCHFDMAVFLATGNVSGVGVCDNCQHTMTGRNCEQCKPXY 360  
QY 382 FOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441  
DB 361 FOHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 420  
QY 442 EGFYDLSAEDPYGCKSCACNPLGTITGGNPNCPDSETCYCYCKLVTGQRCDQCLPQHWGLS 501  
DB 421 EGFYDLSAEDPYGCKSCACNPLGTITGGNPNCPDSETCYCYCKLVTGQRCDQCLPQHWGLS 480

QY 502 NDLGGRPCDDIAGGALNNSCSDSQCSCLPHMIGRCQNEVESGYFTTLDHYIEAEE 561  
DB 481 NDLGGRPCDDIAGGALNNSCSDSQCSCLPHMIGRCQNEVESGYFTTLDHYIEAEE 540  
QY 562 ANLGPGVVVVERQYIQDRIPSWTGPQFVRVPEGAYLEFFIDNIPYSMEVAILIRYEPQLP 621  
DB 541 ANLGPGVVVVERQYIQDRIPSWTGPQFVRVPEGAYLEFFIDNIPYSMEVAILIRYEPQLP 600  
QY 622 DHWEKAVITVORBGKIPASSRCGNTVDDNQVVSISPGSRVYVVLPRPVCFEKGMNVTVR 681  
DB 601 DHWEKAVITVORBGKIPASSRCGNTVDDNQVVSISPGSRVYVVLPRPVCFEKGMNVTVR 660  
QY 682 LELPQYTAGSGDVESPYTFIDSLVLMYPYCKSLDIFTVGGSGDGEVNTNSAWETFORVRCLE 741  
DB 661 LELPQYTAGSGDVESPYTFIDSLVLMYPYCKSLDIFTVGGSGDGEVNTNSAWETFORVRCLE 720  
QY 742 NSRSVWVTMTDVCNRIIFISALIHQTGLACEDPQGSLSVSCDNGGOCQCRPNVVG 801  
DB 721 NSRSVWVTMTDVCNRIIFISALIHQTGLACEDPQGSLSVSCDNGGOCQCRPNVVG 780  
QY 802 TCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRLPGYWG 861  
DB 781 TCNRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCHCFQGIYARQCDRLPGYWG 840  
QY 862 PSQPCQCNHGLDCTVTGECILSCQDYTTGHCNRCERCLAGYGDPIIGSDHCRPCPCPD 921  
DB 841 PSQPCQCNHGLDCTVTGECILSCQDYTTGHCNRCERCLAGYGDPIIGSDHCRPCPCPD 900  
QY 922 GPSGRGFARSCYQDPVTLQACVCPGVIYSGSCDCCASGFFGNPSPFSGSCQPCQCHN 981  
DB 901 GPSGRGFARSCYQDPVTLQACVCPGVIYSGSCDCCASGFFGNPSPFSGSCQPCQCHN 960  
QY 982 IDTTDPACDKDGTGRCLKLYHTGHDHCLQCYGYGDALRQCRKVCNLYGTVEHCN 1041  
DB 961 IDTTDPACDKDGTGRCLKLYHTGHDHCLQCYGYGDALRQCRKVCNLYGTVEHCN 1020  
QY 1042 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWOLASGTGCGPCNCAHAFSGSCNEFTG 1101  
DB 1021 GSDCHCDKATGQCSCLPNVIGQNCDCRCAPNTWOLASGTGCGPCNCAHAFSGSCNEFTG 1080  
QY 1102 QCQCMPPGFGRTCSQCELFWGDPPVECRACDCCDPRIETPQCDQSTGQCVCVEGVEGPR 1161  
DB 1081 QCQCMPPGFGRTCSQCELFWGDPPVECRACDCCDPRIETPQCDQSTGQCVCVEGVEGPR 1140  
QY 1162 CDKCTRGYGVFPDCTPCHOCFALWDAIIGELTNRTHKLEKAKALKISVIGTRETVD 1221  
DB 1141 CDKCTRGYGVFPDCTPCHOCFALWDAIIGELTNRTHKLEKAKALKISVIGTRETVD 1200  
QY 1222 SVEKKVNEIKDILAQSPAAEPFLKNIGILFEEAEKLTNDVTERKMAQVEVKLTDTASQSNST 1281  
DB 1201 SYKKVANKIKDILAQIPAAEPFLKNIGILFEEAEKLTNDVTERKMAQVEVKLTDTASQSNST 1260  
QY 1282 AGEGLQAQAEBSLDKTVKELAEQLEFIKNSDTQGGALDSITKYFQMSLEAEKRVNASTTD 1341  
DB 1261 AGEGLQAQAEBSLDKTVKELAEQLEFIKNSDTQGGALDSITKYFQMSLEAEKRVNASTTD 1320  
QY 1342 PNSTVQESALTDRVEDLMLERESPPEQEQEQLDELQGLQSLDLSAAAQMTGCTP 1401  
DB 1321 PNSTVQESALTDRVEDLMLERESPPEQEQEQLDELQGLQSLDLSAAAQMTGCTP 1380  
QY 1402 PGADCSSECGGNCRTRTEGEKKCGPGCGGLVTVAHSAWQKAMDPRDVLALAEVEQL 1461  
DB 1381 PGADCSSECGGNCRTRTEGEKKCGPGCGGLVTVAHSAWQKAMDPRDVLALAEVEQL 1440  
QY 1462 SKWVSEAKVRADAKQNAQDVLLKTNATKEVKSNEDELNLIKOIRNFUTEDSADLDSI 1521  
DB 1441 SKWVSEAKVRADAKQNAQDVLLKTNATKEVKSNEDELNLIKOIRNFUTEDSADLDSI 1500  
QY 1522 EAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVILQQAADIARAEILLLEAKRA 1581  
DB 1501 EAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVILQQAADIARAEILLLEAKRA 1560  
QY 1582 SKSITDVKVTADMVKEALEAEKAAQVAEAKAIQKQADEDIQGTQNLITSISEETAASEETL 1641

1561 SKSATDVKTADVMKGALEAEAKAQAQAQEDIDQGTQNLTSIESETAASEETL 1620  
1642 TNASQISKLERNVEELKRAAONSGEAEYIEKVYVSVKONADDVKKTLDGELDEKVKV 1701  
1621 TNASQISKLERNVEELKRAAONSGEAEYIEKVYVSVKONADDVKKTLDGELD-KYKKV 1679  
1702 ESLIAQTEESADARRKAEILLONEAKTLLAQAANSKLOLLEDLERYEDNOKYLEKAQEL 1761  
1680 ESLIAQTEESADARRKAEILLONEAKTLLAQAANSKLOLLEDLERYEDNOKYLEKAQEL 1739  
1762 VRLEGEVRSLLKDISEKVAVYSTCL 1786  
1740 VRLEGEVRSLLKDISEKVAVYSTCL 1764

RESULT 6  
AAB19800  
ID AAB19800 standard; protein; 1725 AA.

XX AAB19800;  
XX 05-MAR-2001 (first entry)

XX Mouse laminin 2 mature beta-1 chain.  
XX Laminin 2; mouse; nerve regeneration; angiogenic; cell adhesion;  
XX degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Mus musculus.  
XX WO200066730-A2.

XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
XX 12-JUL-1999; 99US-0143289P.  
XX 24-SEP-1999; 99US-0155945P.

XX (UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX Yurchenco P;  
XX WPI; 2000-687537/67.  
XX N-PSDB; AAA88900.

Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.  
Claim 5; Page 226-232; 305pp; English.  
The present sequence is that of the mouse laminin 2 beta-1 chain mature protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in human laminin 2 structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA8891-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media

SQ	Sequence	1725 AA;
Query Match	96.6%; Score 9429; DB 3; Length 1725;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1725; Conservative	0; Mismatches	0; Gaps
0;		
QY	62 EPCIVSHLQBDKCFICDSRDPYHETLNPDSHLIENAVTTPAPNRUKIKWQSENGVENV	121
DB	1 EPCIVSHLQBDKCFICDSRDPYHETLNPDSHLIENAVTTPAPNRUKIKWQSENGVENV	60
QY	122 TIQDLAEAFHFTLIMTFTFRPAAMLIERSSDFGKTGWYRYFYAYDCSSFFGISTGP	181
DB	61 TIQDLAEAFHFTLIMTFTFRPAAMLIERSSDFGKTGWYRYFYAYDCSSFFGISTGP	120
QY	182 MKYVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLKLTNLRKFKVKLH	241
DB	121 MKYVDDIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPRIQNLKLTNLRKFKVKLH	180
QY	242 TLGDNLLDSRMEIREKYYVAYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCR	301
DB	181 TLGDNLLDSRMEIREKYYVAYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVGHCMCR	240
QY	302 HNTKGLNCELMDPYHDL PWRPAEGRNSNACKKCNHEHSSCHFDMAVFLATGNVSGGV	361
DB	241 HNTKGLNCELMDPYHDL PWRPAEGRNSNACKKCNHEHSSCHFDMAVFLATGNVSGGV	300
QY	362 CDNQHNTMGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	421
DB	301 CDNQHNTMGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL	360
QY	422 IAGQCRCKLHVEGRDVCKEGFDYLSAEDPYGCKSCACNPLGTIPGNCNCDSETGYCYC	481
DB	361 IAGQCRCKLHVEGRDVCKEGFDYLSAEDPYGCKSCACNPLGTIPGNCNCDSETGYCYC	420
QY	482 KRLVTGQRCDQCLPQHNLGSLNDLDCRCPDCDGLGALNNSCEDSGSCCLPHMIGRQCN	541
DB	421 KRLVTGQRCDQCLPQHNLGSLNDLDCRCPDCDGLGALNNSCEDSGSCCLPHMIGRQCN	480
QY	542 EVESGYFTTLDHYIYEAEEANLQPGVVVERQYIQRIPSWTQPGFVRVPEGYLBEFFI	601
DB	481 EVESGYFTTLDHYIYEAEEANLQPGVVVERQYIQRIPSWTQPGFVRVPEGYLBEFFI	540
QY	602 DNI PYSMEYEILIRYEPOLPDHWEKAVITVORPKIPASSRCGNTPVDDNQVVSLSFGS	661
DB	541 DNI PYSMEYEILIRYEPOLPDHWEKAVITVORPKIPASSRCGNTPVDDNQVVSLSFGS	600
QY	662 RYVLPVRPVCPEKGMNYTVRLLEPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGG	721
DB	601 RYVLPVRPVCPEKGMNYTVRLLEPQYTAGSDVESPYTFIDSLVLMPCYKSLDIFTVGG	660
QY	722 GDGEVTSNASETFORRYCLNRSRVKTPMTDVCNIIIFSALIHQTLGACEDPOGSL	781
DB	661 GDGEVTSNASETFORRYCLNRSRVKTPMTDVCNIIIFSALIHQTLGACEDPOGSL	720
QY	782 SSVCDPNGGQCCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITGQCH	841
DB	721 SSVCDPNGGQCCRPNVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASAFCDAITGQCH	780
QY	842 CFQGIYARQCDRCCLPGYWGFFSCPCQCNHGLCDTIVTGECLSCDYTTGHCNRCCLAG	901
DB	781 CFQGIYARQCDRCCLPGYWGFFSCPCQCNHGLCDTIVTGECLSCDYTTGHCNRCCLAG	840
QY	902 YGDFPIIGSGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG	961
DB	841 YGDFPIIGSGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG	900
QY	962 PFGNPSDFGGSCQPCQCHNITDTPDPAECDKTGRCLKLTHTGHDHQLQCYGYGSDAL	1021
DB	901 PFGNPSDFGGSCQPCQCHNITDTPDPAECDKTGRCLKLTHTGHDHQLQCYGYGSDAL	960
QY	1022 RODCRKVCNVLGTIVKEHCNCGSDCHCDKATQCSCLPNVIGONCDRCAPNTWQLASGTGC	1081
DB	961 RODCRKVCNVLGTIVKEHCNCGSDCHCDKATQCSCLPNVIGONCDRCAPNTWQLASGTGC	1020

1082 GPCNNAHSGPSCNEFTGQCQMPGGRGRTSCQELFWGDPDVECRACDPRGIET 1141  
Db 1021 GPCNNAHSGPSCNEFTGQCQMPGGRGRTSCQELFWGDPDVECRACDPRGIET 1080  
Qy 1142 PQDQSTQCVCVEGPRCDKCTRGYSVFPDCTPCHQCFALWDAIIGELTNRHKFL 1201  
Db 1081 PQDQSTQCVCVEGPRCDKCTRGYSVFPDCTPCHQCFALWDAIIGELTNRHKFL 1140  
Qy 1202 EKAKALKISGIVGPRVETVDSVEKKVNEIKDILAQSPAAEPKKNIGILFEEAEKLTVDVT 1261  
Db 1141 EKAKALKISGIVGPRVETVDSVEKKVNEIKDILAQSPAAEPKKNIGILFEEAEKLTVDVT 1200  
Qy 1262 EKMAQVEKLTDTASQNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1321  
Db 1201 EKMAQVEKLTDTASQNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIOGALDSI 1260  
Qy 1322 TKYFOMSLAEKRVNASTTDPNSTVEQSALTRDRVEDLMLRESPPFEQEQEQLARLDEL 1381  
Db 1261 TKYFOMSLAEKRVNASTTDPNSTVEQSALTRDRVEDLMLRESPPFEQEQEQLARLDEL 1320  
Qy 1382 AGKQSLDLSAAQMTCTPGADCSSECGPNCRTDEGEKKCGPGCGGLVTVASAW 1441  
Db 1321 AGKQSLDLSAAQMTCTPGADCSSECGPNCRTDEGEKKCGPGCGGLVTVASAW 1380  
Qy 1442 QKAMPFDRDVLASAEVQLSKWSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1501  
Db 1381 QKAMPFDRDVLASAEVQLSKWSEAKVRADEAKQNAQDVLLKTNATKEKVDKSNEDLR 1440  
Qy 1502 NLIKQIRNFTEDSADLDSIEAVANEVLKSGNASTPQQLNLTDIRRVETLSQVEVIL 1561  
Db 1441 NLIKQIRNFTEDSADLDSIEAVANEVLKSGNASTPQQLNLTDIRRVETLSQVEVIL 1500  
Qy 1562 QOSADIAAEALLLEAEKASKSATDVKVTADVKEALEAEKAEKAKOADEIDQ 1621  
Db 1501 QOSADIAAEALLLEAEKASKSATDVKVTADVKEALEAEKAEKAKOADEIDQ 1560  
Qy 1622 GTQNLLTSIESETAASEETLTNASORISKLERNVEELKRAKAAQNSGEAEYIEKVYVSQ 1681  
Db 1561 GTQNLLTSIESETAASEETLTNASORISKLERNVEELKRAKAAQNSGEAEYIEKVYVSQ 1620  
Qy 1682 NADDVKLTLDGELDEKYKVFESLIAQKTESADARRKAEILLONEAKTLLAQAANSKLOLLE 1741  
Db 1621 NADDVKLTLDGELDEKYKVFESLIAQKTESADARRKAEILLONEAKTLLAQAANSKLOLLE 1680  
Qy 1742 DLERKYEDNQKYLEDAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786  
Db 1681 DLERKYEDNQKYLEDAQELVRLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 7  
ID AAB48451  
AC AAB48451; standard; protein; 1725 AA.  
XX AAB48451;  
XX 02-MAR-2001 (first entry)  
DT Mouse laminin 8 polypeptide, SEQ ID NO: 20.  
DE Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW anticarcinogenic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
OS Mus musculus.  
XX WO2000066732-A2.  
PN 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011543.  
PF 30-APR-1999; 99US-0131720P.  
PR

21-AUG-1999; 99US-0149738P.  
24-SEP-1999; 99US-0155945P.  
11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
XX WPI; 2000-687539/67.  
XX N-PSDB; AAC83712.  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 189-194; 245pp; English.  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment and  
CC migration  
XX Sequence 1725 AA;

Query Match 96.6%; Score 9429; DB 3; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 62 EPYCVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 121  
Db 1 EPYCVSHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVNV 60  
Qy 122 TIQDLEAFHFTHLINTFTFRPAAMLIERSDFGKTGWVRYFAYDCESSFPFGISTGP 181  
Db 61 TIQDLEAFHFTHLINTFTFRPAAMLIERSDFGKTGWVRYFAYDCESSFPFGISTGP 120  
Qy 182 MKKVDDIIICDSYSDIEPSTEGEVIFFRALDPFKIEDPSPRIQNLKITNLRKFVKLH 241  
Db 121 MKKVDDIIICDSYSDIEPSTEGEVIFFRALDPFKIEDPSPRIQNLKITNLRKFVKLH 180  
Qy 242 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVMHGHCMCR 301  
Db 181 TLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVEGVMHGHCMCR 240  
Qy 302 HNTKGLNCELMDYHDLFWRPAEGNSNACKKCNHSSCHSPDMVFLATGNVSGGV 361  
Db 241 HNTKGLNCELMDYHDLFWRPAEGNSNACKKCNHSSCHSPDMVFLATGNVSGGV 300  
Qy 362 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 421  
Db 301 CDNCQHTMGRNCEQCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
Qy 422 IAQCCKLHVGEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGPNPCDSETCYCYC 481  
Db 361 IAQCCKLHVGEGERCDVCKEGFYDLSEADPYGCKSCACNPLGTIPGPNPCDSETCYCYC 420  
Qy 482 KRLVTQRCQDCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSQSCCLPHMIGRCQN 541  
Db 421 KRLVTQRCQDCLPQHWGLSNDLDGCRPCDCLGGALNNSCSDSQSCCLPHMIGRCQN 480  
Qy 542 EVESGYFTTLDHYIYEAEANLPGCVVVERQYQIDRIPSWTGPQGVVRPVGAYLEPFI 601  
Db 481 EVESGYFTTLDHYIYEAEANLPGCVVVERQYQIDRIPSWTGPQGVVRPVGAYLEPFI 540



QY 602 DNIPISEYELLIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDNQVLSLSPGS 661  
Db 541 DNIPISEYELLIRYEPQLPDHWEKAVITVORPGKIPASSRCGNTPVDDNQVLSLSPGS 600  
QY 662 RYVVLPRPVCFBKGMNVTYRLELPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGGS 721  
Db 601 RYVVLPRPVCFBKGMNVTYRLELPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGGS 660  
QY 722 GDEVTNSAWETPQVRCLNSVSVKTPMTDVCNRNIIFSIISALHQTGLACEDCPQSL 781  
Db 661 GDEVTNSAWETPQVRCLNSVSVKTPMTDVCNRNIIFSIISALHQTGLACEDCPQSL 720  
QY 782 SSVCDENGOCOCRPNVVGTNRCAPTGFGENGCKPCDCHLOGSASAFCDALITGOCH 841  
Db 721 SSVCDENGOCOCRPNVVGTNRCAPTGFGENGCKPCDCHLOGSASAFCDALITGOCH 780  
QY 842 CFQGIYARQCDRLPGYWGPPSCQPCQNGHALDCTVTGECLSQDYTTGNCRCRLAG 901  
Db 781 CFQGIYARQCDRLPGYWGPPSCQPCQNGHALDCTVTGECLSQDYTTGNCRCRLAG 840  
QY 902 YGDPPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG 961  
Db 841 YGDPPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG 900  
QY 962 FFGNPSDFGSCQPCQCHNIDITDPEACDKDTRGCLKCLYHTEGHDHCOLCOYGYGDAL 1021  
Db 901 FFGNPSDFGSCQPCQCHNIDITDPEACDKDTRGCLKCLYHTEGHDHCOLCOYGYGDAL 960  
QY 1022 RQCRKVCNLYGTVKEHNGSDCHDKATGQSCCLPNVIGQNCDCRCAPTWQLASGTGC 1081  
Db 961 RQCRKVCNLYGTVKEHNGSDCHDKATGQSCCLPNVIGQNCDCRCAPTWQLASGTGC 1020  
QY 1082 GPCNCAAHFGFSCNEFTQCCQCMFGFGRTCEQQLFWGDPDVECRACDCDPRGIE 1141  
Db 1021 GPCNCAAHFGFSCNEFTQCCQCMFGFGRTCEQQLFWGDPDVECRACDCDPRGIE 1080  
QY 1142 PQCDQSTGQCVVEGVEGRCDKTRGYSVFPDCTPCHQCFALWDALIGELNTRHKL 1201  
Db 1081 PQCDQSTGQCVVEGVEGRCDKTRGYSVFPDCTPCHQCFALWDALIGELNTRHKL 1140  
QY 1202 EKAKALISGVIGYRTRTVDSVEKKNIEKDILAQSPAAPLKNIGILFEEAEKLTQDVT 1261  
Db 1141 EKAKALISGVIGYRTRTVDSVEKKNIEKDILAQSPAAPLKNIGILFEEAEKLTQDVT 1200  
QY 1262 EKMAQVEVGLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFIKNSDIQGLDSI 1321  
Db 1201 EKMAQVEVGLTDTASQSNSTAGELGALQAEASLDKTVKELAQLEFIKNSDIQGLDSI 1260  
QY 1322 TKYFQMSLEAKRYNASTTDPNSTVEQSALTRVEDLMLERESPKEQSEQARLLDEL 1381  
Db 1261 TKYFQMSLEAKRYNASTTDPNSTVEQSALTRVEDLMLERESPKEQSEQARLLDEL 1320  
QY 1382 AGKLSLDLSAAQWTCGTPPGADCSSECGPNCRTEGEXKCGPGCGGLVTVHSAW 1441  
Db 1321 AGKLSLDLSAAQWTCGTPPGADCSSECGPNCRTEGEXKCGPGCGGLVTVHSAW 1380  
QY 1442 QKAMDFRDVLSALAEVQLSKMVSBAKRYADEAKQNAQDVILKTNATKEKVDKSNEDLR 1501  
Db 1381 QKAMDFRDVLSALAEVQLSKMVSBAKRYADEAKQNAQDVILKTNATKEKVDKSNEDLR 1440  
QY 1502 NLIKQIRNFTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1561  
Db 1441 NLIKQIRNFTEDSADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVIL 1500  
QY 1562 QQSAADIPARALLIEEAKRSKATDVKVTDAMVKEALEEAEKQVAAEKAIAQADEDIQ 1621  
Db 1501 QQSAADIPARALLIEEAKRSKATDVKVTDAMVKEALEEAEKQVAAEKAIAQADEDIQ 1560  
QY 1622 GTONLLTSESETAASEETLTNASORISKLRNVEELKRAQNSGAEVIEKVVYSVKQ 1681  
Db 1561 GTONLLTSESETAASEETLTNASORISKLRNVEELKRAQNSGAEVIEKVVYSVKQ 1620

QY 1682 NADVVKTLDELDEKYKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKQLLE 1741  
Db 1621 NADVVKTLDELDEKYKVESLIAQKTESADARRKAEALLQNEAKTLLAQANSKQLLE 1680  
QY 1742 DLRKYEDNOKYLEDKAEQELVRLEGEVRSLLKDOISEKVAIVYSTCL 1786  
Db 1681 DLRKYEDNOKYLEDKAEQELVRLEGEVRSLLKDOISEKVAIVYSTCL 1725  
RESULT 8  
ABB81593  
ID ABB81593 standard; protein; 1725 AA.  
XX ABB81593;  
AC 19-SEP-2002 (first entry)  
DT XX  
XX Mouse laminin 10 second chain protein sequence SEQ ID NO:12.  
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
XX tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX Mus musculus.  
OS WO200250111-A2.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P.  
PR 28-MAR-2001; 2001US-0279282P.  
PR 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
PI WPI; 2002-557650/59.  
XX N-PSDB; ASQ72911.  
DR New human laminin-10 proteins, useful for accelerating the healing of  
XX vascular tissue, improving the biocompatibility of grafts, or for  
XX promoting re-endothelialization at the site of vascular injuries.  
PS Claim 9; Page 153-158; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
XX an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
XX useful in maintaining cell/tissue phenotype as well as promoting cell  
XX growth and differentiation in tissue repair development. Specifically,  
XX laminin 10 can be used for accelerating the healing injuries of vascular  
XX tissue, improving the biocompatibility of grafts useful for treating such  
XX injuries, for promoting re-endothelialisation at the site of vascular  
XX proliferation, and promote cell attachment and subsequent cell stasis,  
XX proliferation, differentiation, and/or migration. The present sequence  
XX represents a second chain protein of laminin 10, from the present  
XX invention.  
SQ Sequence 1725 AA;  
Query Match 96.6%; Score 9429; DB 5; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 62 EBYCVISHLOEDKKCFICDSRDPYHETINPDHSHLIENVVTFAPNRLKIWQSENGENV 121  
Db 1 EBYCVISHLOEDKKCFICDSRDPYHETINPDHSHLIENVVTFAPNRLKIWQSENGENV 60  
QY 122 TIQLDLEAFHFHTLIMTKTFRPAAMLIERSDDPGKWTGVRYPAYCCSPGISTGP 181

Db 61 TIQLDLBAEFHFTLIMFTKTRPAAMLIERSSDFGKTWGVYRFAVDCSSFFPISTGP 120  
Qy 182 MKKVDDIIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPSPRIQNLKLTNLRKFKVKLH 241  
Db 121 MKKVDDIIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPSPRIQNLKLTNLRKFKVKLH 180  
Qy 242 TLGNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNEVEGVHGHCMCR 301  
Db 181 TLGNLLDSRMEIREKYYIAYVDMVVRGNCFCYGHASECAPVDGVNEVEGVHGHCMCR 240  
Qy 302 HNTKGLNCELQWDFVHDLPRWPAEGRNSNACKNCNEHSSCHFDMAVFLATCNVSGGV 361  
Db 241 HNTKGLNCELQWDFVHDLPRWPAEGRNSNACKNCNEHSSCHFDMAVFLATCNVSGGV 300  
Qy 362 CDNCOHNTMGRNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGL 421  
Db 301 CDNCOHNTMGRNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGL 360  
Qy 422 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 481  
Db 361 IAGQCRCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 420  
Qy 482 KRLVTGQRCDQCLPOHWGLSNDLQCRPCDCLGGALNNSCEDSGQSCCLPHMIGRQCN 541  
Db 421 KRLVTGQRCDQCLPOHWGLSNDLQCRPCDCLGGALNNSCEDSGQSCCLPHMIGRQCN 480  
Qy 542 EVESGYFTTLDHYIYEAEANLGPVVVVRQYIQDRIPSWTGPFGVVRPEGAYLEFFI 601  
Db 481 EVESGYFTTLDHYIYEAEANLGPVVVVRQYIQDRIPSWTGPFGVVRPEGAYLEFFI 540  
Qy 602 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 661  
Db 541 DNIPIYSMEYEILIRYEPQLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSPGS 600  
Qy 662 RYVVLPRVPCBEKGMNVTRELPOYTASGSDVSPYTFIDSLVLMPCYKSLDIFTVGG 721  
Db 601 RYVVLPRVPCBEKGMNVTRELPOYTASGSDVSPYTFIDSLVLMPCYKSLDIFTVGG 660  
Qy 722 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRNIIFSALIHQTGLACECDPQGL 781  
Db 661 GDGEVNTSAWETFORYRCLENSRSVVKTPMTDVCNRNIIFSALIHQTGLACECDPQGL 720  
Qy 782 SSVCDPNGQOCQCRNVVGRNCRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 841  
Db 721 SSVCDPNGQOCQCRNVVGRNCRCAPGTFGFGNGCKPCDCHLQGSASAFCDAITGQCH 780  
Qy 842 CFOGIYARQCRCCLPGYWGFFSCQPCQCNHGLDCDVTGECCLSCQDVTTHNCERCLAG 901  
Db 781 CFOGIYARQCRCCLPGYWGFFSCQPCQCNHGLDCDVTGECCLSCQDVTTHNCERCLAG 840  
Qy 902 YYGDPPIIGSDHCRPCPCPDGPDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 961  
Db 841 YYGDPPIIGSDHCRPCPCPDGPDGRQFARSCYQDPVTLQACVCDPGYIGSRCDDCASG 900  
Qy 962 FFGNPSDFGSGCOPCQCHNITDTPDCACDKDTGRCLKCLVHTGSDHCOLCQYGVGDAL 1021  
Db 901 FFGNPSDFGSGCOPCQCHNITDTPDCACDKDTGRCLKCLVHTGSDHCOLCQYGVGDAL 960  
Qy 1022 RQDCRKCVCNVLGTVKEHCNGSDCHCDKATQCSCLPNVIGQNCDCRCPNTWQLASGTGC 1081  
Db 961 RQDCRKCVCNVLGTVKEHCNGSDCHCDKATQCSCLPNVIGQNCDCRCPNTWQLASGTGC 1020  
Qy 1082 GPCNNAHSGPSCNEETGOCQMPGFGGTCSECOELFWGDPDVECRACDDPRGIET 1141  
Db 1021 GPCNNAHSGPSCNEETGOCQMPGFGGTCSECOELFWGDPDVECRACDDPRGIET 1080  
Qy 1142 PQCDQSTGQCVGEVGEPRCDKCTRGYSGVFPDCTPCHQCFAWDAIIGELTNRHKFL 1201  
Db 1081 PQCDQSTGQCVGEVGEPRCDKCTRGYSGVFPDCTPCHQCFAWDAIIGELTNRHKFL 1140  
Qy 1202 EKAKALKISGVIGPRTVDSVEKKVNEIKOILAQSPAEPKXGILFEEAEKLTVDVT 1261  
Db 1141 EKAKALKISGVIGPRTVDSVEKKVNEIKOILAQSPAEPKXGILFEEAEKLTVDVT 1200

Qy 1262 EKMAQVVEVLTDTASOSNSTAGELGALQAEABSLDKTVKELAEQLEFIKNSDIQALDSI 1321  
Db 1201 EKMAQVVEVLTDTASOSNSTAGELGALQAEABSLDKTVKELAEQLEFIKNSDIQALDSI 1260  
Qy 1322 TKYFQMSLEAEKRVNASTTDPNSTVQESALTDRDRVEDLMLERESPFEKQOEQARLLDEL 1381  
Db 1261 TKYFQMSLEAEKRVNASTTDPNSTVQESALTDRDRVEDLMLERESPFEKQOEQARLLDEL 1320  
Qy 1382 AGKLQSLDLSAAQMTCTGTPPGADCESECCGPNCRTEDEGEKKCGGPGCGGLVTVHAWSA 1441  
Db 1321 AGKLQSLDLSAAQMTCTGTPPGADCESECCGPNCRTEDEGEKKCGGPGCGGLVTVHAWSA 1380  
Qy 1442 OKAMDPRDVLGALAEVOLSKMWSEAKVRADAEKQACQVLLKTNATKEKVDKSNEDLR 1501  
Db 1381 OKAMDPRDVLGALAEVOLSKMWSEAKVRADAEKQACQVLLKTNATKEKVDKSNEDLR 1440  
Qy 1502 NLIKQIRNFELTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1561  
Db 1441 NLIKQIRNFELTSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVIL 1500  
Qy 1562 QQSAADIAEABILLBEAKSKSATDVKTADMVKEALEBEAKQVAAEKAIKQADEDIQ 1621  
Db 1501 QQSAADIAEABILLBEAKSKSATDVKTADMVKEALEBEAKQVAAEKAIKQADEDIQ 1560  
Qy 1622 GTQNLITSIETSEATASEETLTNASQRIKSLERNVSELKKAQNSGEAEYIEKVVYSVKQ 1681  
Db 1561 GTQNLITSIETSEATASEETLTNASQRIKSLERNVSELKKAQNSGEAEYIEKVVYSVKQ 1620  
Qy 1682 NADDVKITLDGELDEKVKVKSIIAQKTESADARAKKELLONEAKTLLAQANSKLQILLE 1741  
Db 1621 NADDVKITLDGELDEKVKVKSIIAQKTESADARAKKELLONEAKTLLAQANSKLQILLE 1680  
Qy 1742 DLERKYEDNOKYLEDKAQBLVLEGEVRSLLKDISEKVAVYSTCL 1786  
Db 1681 DLERKYEDNOKYLEDKAQBLVLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 9  
AAW50893  
ID AAW50893 standard; protein; 1786 AA.  
XX  
AC AAW50893;  
XX  
DT 07-DEC-1998 (first entry)  
XX  
DE Human laminin B1 chain.  
XX  
KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma; CJD;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertmann-Strausler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9815179-A1.  
XX  
PD 16-APR-1998.  
XX  
PP 08-OCT-1997; 97WO-US018145.  
XX  
PR 08-OCT-1996; 96US-0027981P.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Castillo G, Snow AD;  
XX  
DR WPI; 1998-240534/21.  
XX

PT Use of laminin and fragments - for developing products for use in the  
 PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
 PT CUD.  
 XX  
 XX  
 XX  
 XX  
 CC Claim 15; Page 86-89; 132pp; English.  
 CC This is the amino acid sequence of the human laminin B1 chain. The  
 CC primary object of the invention is to use laminin, laminin-derived  
 CC protein fragments and/or laminin-derived polypeptides as potent  
 CC inhibitors of amyloid formation, deposition, accumulation and/or  
 CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
 CC products (see AAW50888-98) may include mouse or human laminin A or A1  
 CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
 CC chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
 CC binding domain of the laminin A chain. A claimed method for treating an  
 CC amyloid disease comprises administering a polypeptide having a  
 CC conformational similarity to a fragment of a laminin protein. A method  
 CC for diagnosing an amyloid disease involves determining levels of laminin  
 CC in a sample. Production of laminin or its fourth globular repeat *in vivo*  
 CC provides a method for *in vivo* inhibition of beta-amyloid amyloidosis. The  
 CC products and methods can be used for the diagnosis, prognosis, monitoring  
 CC and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
 CC and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
 CC (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
 CC associated with chronic inflammation, various forms of malignancy and  
 CC Familial Mediterranean Fever (AA amyloid or inflammation-association  
 CC amyloidosis), the amyloidosis associated with multiple myeloma and other  
 CC B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
 CC II diabetes (amylin or islet amyloid), the amyloidosis associated with  
 CC prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler  
 CC syndrome, kuru and animal scrapie (prp amyloid), the amyloidosis  
 CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
 CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
 CC amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or  
 CC transthyretin amyloid), and the amyloidosis associated with endocrine  
 CC tumours such as medullary carcinoma of the thyroid (variant of  
 CC procalcitonin)  
 XX  
 SQ Sequence 1786 AA;  
 Query Match 93.7%; Score 9144; DB 2; Length 1786;  
 Best Local Similarity 92.7%; Pred. No. 0;  
 Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
 QY 1 MGLQVAFGLVWTRVCAQPEPSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
 DB 1 MGLQLLAFSLALCARVRAQPEPSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
 QY 61 PEPYCVSHQEDKKCFICDSDROPYHETLNPDSHLIENVVTPAPNRLKIWQSENGVEN 120  
 DB 61 PEPYCVSHQEDKKCFICDSDROPYHETLNPDSHLIENVVTPAPNRLKIWQSENGVEN 120  
 QY 121 VTIQDLEAFHFHLLIMTKTRPAAAMLIERSDFGKTGWVYRYFAYDCESFPQISTG 180  
 DB 121 VTIQDLEAFHFHLLIMTKTRPAAAMLIERSDFGKTGWVYRYFAYDCESFPQISTG 180  
 QY 181 PMKVVDDIIICDSYSDIEPSTEGEVIFRALDPFKIEDPSPRIQNLKITNLRIKFVKL 240  
 DB 181 PMKVVDDIIICDSYSDIEPSTEGEVIFRALDPFKIEDPSPRIQNLKITNLRIKFVKL 240  
 QY 241 HTLGDNLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300  
 DB 241 HTLGDNLDSRMEIREKYYAVYVDMVVRGNCFCYGHASECAPVDGVNEEVEGVHGHCMC 300  
 QY 301 RHNTKGLNCLCMLDFHDLFWRPAEGNSNACKKCNNEHSSCHSDPMAVFLATGNVSGG 360  
 DB 301 RHNTKGLNCLCMLDFHDLFWRPAEGNSNACKKCNNEHSSCHSDPMAVFLATGNVSGG 360  
 QY 361 VCDNCQNTWGRNCEQCKPFYQHPERDIRDPNLCPCTCDPAGSNGGICDGYTDFSVG 420  
 DB 361 VCDNCQNTWGRNCEQCKPFYQHPERDIRDPNLCPCTCDPAGSNGGICDGYTDFSVG 420  
 QY 421 LIAGQCRCKLVHGEGRCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNCPCSETHCY 480

DB 421 LIAGQCRCKLVHGEGRCDVCKEGFYDLSSDPFGCKSCACNPLGTIPGNCPCSETHCY 480  
 QY 481 CKRLVTQCRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSQCSCLPHMTGRQC 540  
 DB 481 CKRLVTQCRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCFAESQCSCLPHMTGRQC 540  
 QY 541 NEVESGYFTTLDHYIYEAEANLPGVWVVRQYIQDRIPSWTGPQFVRVPEGAYLEFF 600  
 DB 541 NEVESGYFTTLDHYIYEAEANLPGVWVVRQYIQDRIPSWTGPQFVRVPEGAYLEFF 600  
 QY 601 IDNTPYMEVEILLIRYEPQIPDHWEKAVITVQRPKIPASSRCQNTVDDNDNQVLSLPG 660  
 DB 601 IDNTPYMEVEILLIRYEPQIPDHWEKAVITVQRPKIPASSRCQNTVDDNDNQVLSLPG 660  
 QY 661 SRYVVLPRPVCFEKGMNVTYRLLELPQYTAGSDVESPYTIDSLVLMYPYCKSLDIFTVGG 720  
 DB 661 SRYVVLPRPVCFEKGMNVTYRLLELPQYTAGSDVESPYTIDSLVLMYPYCKSLDIFTVGG 720  
 QY 721 SGDEVTNSAWETPQRYRCLENSRSVVKTPMTDVCRNIIFSIISALIHQTGLACECDPQGS 780  
 DB 721 SGDEVTNSAWETPQRYRCLENSRSVVKTPMTDVCRNIIFSIISALIHQTGLACECDPQGS 780  
 QY 781 LSSVCDPNGGOCQCRPNVGRTCNRCAPGTFGFGPNCKPCDCHLOGSAGAFCDATGQC 840  
 DB 781 LSSVCDPNGGOCQCRPNVGRTCNRCAPGTFGFGPNCKPCDCHLOGSAGAFCDATGQC 840  
 QY 841 HCFQGIYARQCDRLPGYWGFPSPQPCQCNHGLDCDVTGECLSQDYTTGNCERCLA 900  
 DB 841 HCFQGIYARQCDRLPGYWGFPSPQPCQCNHGLDCDVTGECLSQDYTTGNCERCLA 900  
 QY 901 GYGDPIIGSDHCRPCPCDGDPSGRQPARSCVQDPVTIQLACVDPGVIGSRCDCCAS 960  
 DB 901 GYGDPIIGSDHCRPCPCDGDPSGRQPARSCVQDPVTIQLACVDPGVIGSRCDCCAS 960  
 QY 961 GFGNPNDFGSGCOPCQCHNIDTDTPEACDKTGRCLKCLYHTEGDHCOLQCYGYGDA 1020  
 DB 961 GFGNPNDFGSGCOPCQCHNIDTDTPEACDKTGRCLKCLYHTEGDHCOLQCYGYGDA 1020  
 QY 1021 LRQCRKVCNLYGTVEHNGSDCHCKATGQCSCLPNVIGQNCDCRCAFNWOLASGTG 1080  
 DB 1021 LRQCRKVCNLYGTVEHNGSDCHCKATGQCSCLPNVIGQNCDCRCAFNWOLASGTG 1080  
 QY 1081 CGPCNCAAHSGFSCNEFTGQCOCMPFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140  
 DB 1081 CGPCNCAAHSGFSCNEFTGQCOCMPFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140  
 QY 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIAIIGELNTRHKF 1200  
 DB 1141 TPQCDQSTGQCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFALWDVIAIIGELNTRHKF 1200  
 QY 1201 LEKAKALKISGIVGYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260  
 DB 1201 LEKAKALKISGIVGYRETVDVSVEKKVNEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260  
 QY 1261 TERMAQVEVKLTDTASQNSSTAGELQALQABASLDTKTVKELABQLBFINKNSDIQOALDS 1320  
 DB 1261 TERMAQVEVKLTDTASQNSSTAGELQALQABASLDTKTVKELABQLBFINKNSDIQOALDS 1320  
 QY 1321 ITKYPQMSLEAEKRYNASTTDPNSTVEQSALTDRDVEDLMLERESPFKEQOEQARLLDE 1380  
 DB 1321 ITKYPQMSLEAEKRYNASTTDPNSTVEQSALTDRDVEDLMLERESPFKEQOEQARLLDE 1380  
 QY 1381 LAGKQLSLDLASAAQMTCGTTPPGADCSSECGGPNCTDEGEKKCGGPGCGGLVTVAHSA 1440  
 DB 1381 LAGKQLSLDLASAAQMTCGTTPPGADCSSECGGPNCTDEGEKKCGGPGCGGLVTVAHSA 1440  
 QY 1441 WQKAMDPRDVLALAEVEQLSKWVSEAKVRADEAKONADVLLKTNATKEKVDKSNEDL 1500  
 DB 1441 WQKAMDPRDVLALAEVEQLSKWVSEAKVRADEAKONADVLLKTNATKEKVDKSNEDL 1500  
 QY 1501 RNLIKQINFUTEDSADLDSIEAVANVLKSGNASTPQQLQNLTFEDIRERVTLSQVEVI 1560

1501 RNLIKQINFLTQDADLSDIEAVANEVLKXMPSTPQOLQNLTDIERVESLSQVEVI 1560  
1561 LQSSAADIAEAELEAEKRAKSAATDVKVTADVMYKEALEBAEKAQVAEKAQAEDEI 1620  
1561 LQSSAADIAEAELEAEKRAKSAATDVKVTADVMYKEALEBAEKAQVAEKAQAEDEI 1620  
1621 QCTONLLTSIESETAASEETLNASORISKLEENVEELKRAAQNAGAEVIEKVVYSVK 1680  
1621 QCTONLLTSIESETAASEETLNASORISELERNVEELKRAAQNAGAEVIEKVVYTVK 1680  
1681 QNADVDKKTLDGELDEKYYKVESLIAQKTESADARRKAELLQNEAKTLQAQNSKLQLL 1740  
1681 QSAEDVKKTLDGELDEKYYKVENLIAKTESADARRKAEMLQNEAKTLQAQNSKLQLL 1740  
1741 EDLEKRYEDNQYLEDKQAEVLRLSGEVRSLIKDISEKVAVYSTCL 1786  
1741 KDLERKYEDNQYLEDKQAEVLRLSGEVRSLIKDISEKVAVYSTCL 1786

RESULT 10

AAB16522  
ID AAB16522 standard; protein; 1786 AA.

XX AAB16522;

XX 27-OCT-2000 (first entry)

XX Human laminin protein sequence.

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiotensin;  
XX endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
XX psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
XX cerebral collateral; arteriovenous malformation; rubecosis; cancer;  
XX diabetic retinopathy; arthritis; wound healing; peptic ulcer;  
XX Helicobacter related disease; fracture; cat scratch fever.

XX Homo sapiens.

XX WO200032631-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028897.

XX 04-DEC-1998; 98US-00206059.

XX (ENTR-) ENTREMED INC.

XX Macdonald N7, Sim KL;

XX WPI; 2000-412290/35.

XX New angiogenesis-inhibiting protein receptors, useful in methods for  
XX treating diseases and processes that are mediated by angiogenesis, such  
XX as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.

XX Claim 1; Fig 6A; 100pp; English.

XX This invention relates to angiogenesis-inhibiting protein receptors, and  
XX the DNA sequences encoding them. Angiogenesis is the generation of new  
XX blood vessels into a tissue, and normally occurs in wound healing, foetal  
XX and embryonal development and the formation of the corpus luteum,  
XX endometrium and placenta. Angiostatin is a protein (see AAB16450 and  
XX AAB68202) involved in angiogenesis, and has an amino acid sequence  
XX similar to that of a plasminogen fragment (see murine plasminogen  
XX AAB16490). Angiostatin has the ability to inhibit angiogenesis.  
XX Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and  
XX AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein  
XX sequences of human laminin. Laminin is an angiostatin binding protein,  
XX and some of the peptides of the invention share homology with regions of  
XX laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the  
XX angiogenesis-inhibiting protein receptor fragments of the invention. The  
XX peptides bind either angiotensin or endostatin and can be used in methods

CC for treating diseases and processes that are mediated by angiogenesis,  
CC such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis,  
CC Crohn's disease, cerebral collaterals, arteriovenous malformations,  
CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,  
CC Helicobacter related diseases, fractures, placental and cat scratch  
CC fever. They are useful for the detection and prognosis of cancer. DNA  
CC sequences A628204-A628241 encode the peptides of the invention

XX Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 3; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLLOVFAFGVLTALMGTRVCAQSPESYGCAGESCYPATGDLILGRAQKLSVTSTCGLHK 60  
DB 1 MGLLQLLAFSLFALCRARVRAQEPESYGCAGESCYPATGDLILGRAQKLSVTSTCGLHK 60  
QY 61 PEPYCVSHLQEDKCFICDSRDYHETLNPDSHLIENVVTFPAPNRLKIWQSENGVEN 120  
DB 61 PEPYCVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFPAPNRLKIWQSENGVEN 120  
QY 121 VTQLDLAEAFHETHLIMTFKTPAPAMLIERSDFGKTGWYRYFAYDCESFPGISG 180  
DB 121 VTQLDLAEAFHETHLIMTFKTPAPAMLIERSDFGKTGWYRYFAYDCESFPGISG 180  
QY 181 PMKKVDDIICDSRYSDIEPSTEGEVIFFRALDPFAKIEDPYSPIQNLKITNLRIKFVKL 240  
DB 181 PMKKVDDIICDSRYSDIEPSTEGEVIFFRALDPFAKIEDPYSPIQNLKITNLRIKFVKL 240  
QY 241 HTLGDNLLDSRMIREKYYIYAVDMVGRNCFYGHASECAPVDGYNVEEGMVHGHCMC 300  
DB 241 HTLGDNLLDSRMIREKYYIYAVDMVGRNCFYGHASECAPVDGYNVEEGMVHGHCMC 300  
QY 301 RHNTKGLNCELMDYFDHDLFWPRAEGRNSNACKKCNENHSSCHDFDMVFLATGNVSGG 360  
DB 301 RHNTKGLNCELMDYFDHDLFWPRAEGRNSNACKKCNENHSSCHDFDMVFLATGNVSGG 360  
QY 361 VCNCQHTNMGRCNCEQCKPFYFOHPRDIRDPNLCEPTCDPAGSNGGICDYTFESVG 420  
DB 361 VCDDCQHTNMGRCNCEQCKPFYOHPRDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420  
QY 421 LIAGQCRCKLHVGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNCPDSEGTGYC 480  
DB 421 LIAGQCRCKLHVGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGGNCPDSEGTGYC 480  
QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDCRCDLGGALANNSCEDSGQCSCLPHMIGRQC 540  
DB 481 CKRLVTGQRCDQCLPQHWGLSNDLDCRCDLGGALANNSCEDSGQCSCLPHMIGRQC 540  
QY 541 NEVESGYFTLDDHYIYEAEEANLGPVVVVERQYIQDRIPSWTGPQVVRVPGAYLEFF 600  
DB 541 NEVEPGYFFATLDHYLYEAEEANLGPVSVIVERQYIQDRIPSWTGPQVVRVPGAYLEFF 600  
QY 601 IDNIPYSMEYELLIRYEPQLPDHWEKAVITVQPGKIPASSRCGNTVPDDNOWNVSLSPG 660  
DB 601 IDNIPYSMEYDILLIRYEPQLPDHWEKAVITVQPGRIPTSSRCGNTIPDDNOWNVSLSPG 660  
QY 661 SRYVLPVPVCFKGMNVTYRLLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720  
DB 661 SRYVLPVPVCFKGMNVTYRLLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720  
QY 721 SGDEVTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIPFISALIHQTGLACECDPQGS 780  
DB 721 SGDGVTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIPFISALIHQTGLACECDPQGS 780  
QY 781 LSSVCDPNGGQCCQCRPNVGRTCNRCAPGTFGFGNGKCPDCDCHLOGSASAFCDATGQC 840  
DB 781 LSSVCDPNGGQCCQCRPNVGRTCNRCAPGTFGFGSPGCKPCECHLOGSVNAFCNPVTGQC 840  
QY 841 HCFQGIYAROCDCRLPGYWGFPSCQCCQNGHALDCDVTGECLSQCDYTTGHCNRCCLA 900  
DB 841 HCFQGIYAROCDCRLPGYWGFPSCQCCQNGHALDCDVTGECLSQCDYTTGHCNRCCLA 900

QY 901 GYGDPPIIGSGHRCPCPCPDGPDGROFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960  
 Db 901 GYGDPPIIGSGHRCPCPCPDGPDGROFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960  
 QY 961 GFGNPSDFGSCPCQCHNITDTPDPCADKOTGRCLKCLYHTGHDHCLQCYGYVGDA 1020  
 Db 961 GFGNPSDFGSCPCQCHNITDTPDPCADKOTGRCLKCLYHTGHDHCLQCYGYVGDA 1020  
 QY 1021 LRQDCRKCVCNLTGTVKECHGSDCHCDKATGQSCCLPNVIGQNCDCRCAPTNQLASGTG 1080  
 Db 1021 LRQDCRKCVCNLTGTVKECHGSDCHCDKATGQSCCLPNVIGQNCDCRCAPTNQLASGTG 1080  
 QY 1081 CQPCNCAHSGPSCNFTGQCCQCPGPGGRTSCCELEFWGDDPVECRACDCDPRGIE 1140  
 Db 1081 CQPCNCAHSGPSCNFTGQCCQCPGPGGRTSCCELEFWGDDPVECRACDCDPRGIE 1140  
 QY 1141 TPQDCQSTQCCVCGVEGPRCDKCTRGYGVFPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
 Db 1141 TPQDCQSTQCCVCGVEGPRCDKCTRGYGVFPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
 QY 1201 LEKAKALKISGIVGPRETVDSVEKKNVEIKDILAQSPAAPLKNIGILFEAEKLTQV 1260  
 Db 1201 LEKAKALKISGIVGPRETVDSVEKKNVEIKDILAQSPAAPLKNIGILFEAEKLTQV 1260  
 QY 1261 TEMAQVEVKLTDTASQSNSTAGELGALQAEASLDTVKELABQLEFINKSDIQGALDS 1320  
 Db 1261 TEMAQVEVKLTDTASQSNSTAGELGALQAEASLDTVKELABQLEFINKSDIQGALDS 1320  
 QY 1321 ITKYFQMSLEAEKRYNAETDPSNVEQSAITRVEDLMLERSPKQEQEQAARLIDE 1380  
 Db 1321 ITKYFQMSLEAEKRYNAETDPSNVEQSAITRVEDLMLERSPKQEQEQAARLIDE 1380  
 QY 1381 LAGKLSQDLSDLSAAQWTCGTPPGDCSECEGPGNCRDTEGKCGGPGGGLVVAHSA 1440  
 Db 1381 LAGKLSQDLSDLSAAQWTCGTPPGDCSECEGPGNCRDTEGKCGGPGGGLVVAHSA 1440  
 QY 1441 WQKAMDFRDVLSALAEVQSLKMWSEAKVPADEAKQNAQDVLLKTNATKVKDKNEEL 1500  
 Db 1441 WQKAMDFRDVLSALAEVQSLKMWSEAKVPADEAKQNAQDVLLKTNATKVKDKNEEL 1500  
 QY 1501 RNLIQKIRNFLTQSDADLSIEAVANEVLMKMPSTPQQLNLTEDIRERVETLSQVEVI 1560  
 Db 1501 RNLIQKIRNFLTQSDADLSIEAVANEVLMKMPSTPQQLNLTEDIRERVETLSQVEVI 1560  
 QY 1561 LQCSAADTARAEELLEAKRASKATDVKTADVMVKEALAEAKQAQAEKAIKQADEDI 1620  
 Db 1561 LQCSAADTARAEELLEAKRASKATDVKTADVMVKEALAEAKQAQAEKAIKQADEDI 1620  
 QY 1621 QCTONLLTSISETAASBETLTFNASQISKLERNVEELKKAQNSGEAEYIEKVVYSVK 1680  
 Db 1621 QCTONLLTSISETAASBETLTFNASQISKLERNVEELKKAQNSGEAEYIEKVVYSVK 1680  
 QY 1681 QNADDVKTLDGELDEKYYKVESLIAQKTESADARBAELLQNEAKTLIAQANSKLQLL 1740  
 Db 1681 QNADDVKTLDGELDEKYYKVESLIAQKTESADARBAELLQNEAKTLIAQANSKLQLL 1740  
 QY 1741 EDLEKEDNOKYLEDKAQELVRLGEVRSLLKDISKAVYSTCL 1786  
 Db 1741 EDLEKEDNOKYLEDKAQELVRLGEVRSLLKDISKAVYSTCL 1786

RESULT 11  
 AAB19797 standard; protein; 1786 AA.

AC AAB19797;  
 XX AAB19797;  
 DT 05-MAR-2001 (first entry)  
 XX Human laminin 2 beta-1 chain.  
 DE Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
 XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;

degenerative muscle disorder; muscular dystrophy; cell therapy.  
 Homo sapiens.  
 Key Location/Qualifiers  
 Peptide 1..21  
 /label= Signal\_peptide  
 Protein 22..1786  
 /label= Mature\_protein  
 WO200066730-A2.  
 09-NOV-2000.  
 28-APR-2000; 2000WO-US011378.  
 30-APR-1999; 99US-0131720P.  
 15-JUN-1999; 99US-0139198P.  
 12-JUL-1999; 99US-0143289P.  
 24-SEP-1999; 99US-0155945P.  
 (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 Yurchenco P;  
 WPI; 2000-687537/67.  
 N-PSDB; AAA88897.  
 Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.  
 Claim 5; Page 186-191; 305pp; English.  
 The present sequence is that of the beta-1 chain of human laminin 2. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding them (see AAA88991-906), methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using purified laminin 2 for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the take of grafts, improving the biocompatibility of medical devices and preparing improved culture devices and media  
 Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 3; Length 1786;  
 Best Local Similarity 92.7%; Pred. No. 0;  
 Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
 QY 1 MGLQVFAFGVLAWGTRVCAQPEPSYCAEGSCYPATGDLIGRAQKLSVTTCGLHK 60  
 Db 1 MGLQLLAFSFLACRARVFAQPEPSYCAEGSCYPATGDLIGRAQKLSVTTCGLHK 60  
 QY 61 PEPYIVSHLQEDKKCFICSDRDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVEN 120  
 Db 61 PEPYIVSHLQEDKKCFICSDRDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVEN 120  
 QY 121 VTIOLEAEAFHFTLIMTKFPRPAAMLIERSDPFGKTGWVRYFAYDCESFPFGISTG 180  
 Db 121 VTIOLEAEAFHFTLIMTKFPRPAAMLIERSDPFGKTGWVRYFAYDCESFPFGISTG 180  
 QY 181 PMKVVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKLTNRIRKFKVL 240  
 Db 181 PMKVVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKLTNRIRKFKVL 240

1321 ITKYFQMSLEAKRVNASTTDPNSTVQSAITRDRVEDIMLEREFKEQEQEQLLDE 1380  
1321 ITKYFQMSLEAKRVNASTTDPNSTVQSAITRDRVEDIMLEREFKEQEQEQLLDE 1380  
1381 LAGKLOSLDLASAAQMTCTPPGADCSBSCGPGNCRDDEGKCKGPGCGGLVTVHSA 1440  
1381 LAGKLOSLDLASAAQMTCTPPGADCSBSCGPGNCRDDEGKCKGPGCGGLVTVHSA 1440  
1441 WQKAMPDQDVLASALAEVQSLKQVSEAKVRADEAKQADVLLKTNAKKEKVDKSNEDL 1500  
1441 WQKAMPDQDVLASALAEVQSLKQVSEAKVRADEAKQADVLLKTNAKKEKVDKSNEDL 1500  
1501 RNLIKQIRNPLTEDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRRVETLSQVEVI 1560  
1501 RNLIKQIRNPLTEDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRRVETLSQVEVI 1560  
1561 LQSAADIAAEELLLLEAKRASKSATDVKTADWKEALEEAEKQVAAEAKIQAQADEI 1620  
1561 LQSAADIAAEELLLLEAKRASKSATDVKTADWKEALEEAEKQVAAEAKIQAQADEI 1620  
1621 QGTQNLTSIESSTAASEETLNASQRIKSLERNVEELKRAAQNSEAEYIEKVYTVK 1680  
1621 QGTQNLTSIESSTAASEETLNASQRIKSLERNVEELKRAAQNSEAEYIEKVYTVK 1680  
1681 QNADDVKKTLDGELDEKYYKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLL 1740  
1681 QNADDVKKTLDGELDEKYYKVESLIAQKTEESADARRKAEILLQNEAKTLLAQANSKLQLL 1740  
1741 EDLERKYEDNQKYLEKQAEELVRLEGEVRSLLKDISEKAVVYSTCL 1786  
1741 EDLERKYEDNQKYLEKQAEELVRLEGEVRSLLKDISEKAVVYSTCL 1786  
1741 KDLERKYEDNQKYLEKQAEELVRLEGEVRSLLKDISEKAVVYSTCL 1786  
1741 KDLERKYEDNQKYLEKQAEELVRLEGEVRSLLKDISEKAVVYSTCL 1786  
RESULT 12  
AAB48448  
ID AAB48448 standard; protein; 1786 AA.  
XX AAB48448;  
AC AAB48448;  
XX AAB48448;  
DT 02-MAR-2001 (first entry)  
XX Human laminin 8 polypeptide, SEQ ID NO: 14.  
DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX Homo sapiens.  
XX WO2000066732-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011543.  
XX 30-APR-1999; 99US-0131720P.  
XX 21-AUG-1999; 99US-0149738P.  
XX 24-SEP-1999; 99US-0155945P.  
XX 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOSTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
XX WPI; 2000-687539/67.  
XX N-PSDB; AAC83709.  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 150-155; 245pp; English.  
XX

241 HTLGNLLDSRMEIREKYYAYVDMVVEGNCFCYGHASECAPDGVNEVEGMVHGCMC 300  
241 HTLGNLLDSRMEIREKYYAYVDMVVEGNCFCYGHASECAPDGVNEVEGMVHGCMC 300  
301 RHNTKGLNCELCEMDPYHDLPRPABGRNSNACKKCNNEHSSSCHFDMAVELATGNVSGG 360  
301 RHNTKGLNCELCEMDPYHDLPRPABGRNSNACKKCNNEHSSSCHFDMAVELATGNVSGG 360  
361 VCDNCHNTMGRCNQCQKPFYFQHPERDIRPNLCEPCTCDPASSENGICDGTDFSVG 420  
361 VCDNCHNTMGRCNQCQKPFYFQHPERDIRPNLCEPCTCDPASSENGICDGTDFSVG 420  
421 LIAGOCRCKLHVEGRCDVCEGFFDLSEADPYGCKSCACNPLGTIPGNCPCDSEYCY 480  
421 LIAGOCRCKLHVEGRCDVCEGFFDLSEADPYGCKSCACNPLGTIPGNCPCDSEYCY 480  
481 CKRLVTGRCOCLPQHGLNSDLDCRCPDCLGALNNSCSEDSGQCSCLPHMIGRCQ 540  
481 CKRLVTGRCOCLPQHGLNSDLDCRCPDCLGALNNSCSEDSGQCSCLPHMIGRCQ 540  
541 NEVESGYFTLLDHYTYEABEANLPGVAVVERQVIQDRIPSWTGPGRVPEGAYLEFF 600  
541 NEVESGYFTLLDHYTYEABEANLPGVAVVERQVIQDRIPSWTGPGRVPEGAYLEFF 600  
601 IDNIPYSMEYELLIRYEQLPDPHNEKAVITVORPGKIPASSRCGNTPDDNQVVSLSGP 660  
601 IDNIPYSMEYELLIRYEQLPDPHNEKAVITVORPGKIPASSRCGNTPDDNQVVSLSGP 660  
661 SRYVLPVPVCEKGMNTVRLLEPYTASGDVESPFTFIDSLVMPYCKSLDFTVGG 720  
661 SRYVLPVPVCEKGMNTVRLLEPYTASGDVESPFTFIDSLVMPYCKSLDFTVGG 720  
721 SDGGEVTSANETFORRYCLNSRSVWKTPTMDVCRNIIFSISALIHQTLGACDPOGS 780  
721 SDGGEVTSANETFORRYCLNSRSVWKTPTMDVCRNIIFSISALIHQTLGACDPOGS 780  
781 LSSVCDPNQGGQCCRPNVVGRTCNRCAPGTGFGNGKPCDCHLOGSASFCAITGQC 840  
781 LSSVCDPNQGGQCCRPNVVGRTCNRCAPGTGFGNGKPCDCHLOGSASFCAITGQC 840  
841 HCFQGIYARQCDRLPLGFWGFPSCPCQCNHALDCDVTGECISQDQYTTGHCNCRCLA 900  
841 HCFQGIYARQCDRLPLGFWGFPSCPCQCNHALDCDVTGECISQDQYTTGHCNCRCLA 900  
901 GYGDPIIGSGDHCRPCPCDGPDSGROFARSQYQDPVTLQACVDPGYIGSRCDCCAS 960  
901 GYGDPIIGSGDHCRPCPCDGPDSGROFARSQYQDPVTLQACVDPGYIGSRCDCCAS 960  
961 GFPGNPSDFGSCQPCQCHNIDTTPACDKDTGRCCLKLYHTBGRHCLQCOVGYGDA 1020  
961 GFPGNPSDFGSCQPCQCHNIDTTPACDKDTGRCCLKLYHTBGRHCLQCOVGYGDA 1020  
1021 LRQDCRKVCNLYGTVKEHNGSDCHCDKATQCCSCLPNVIGQNCDCRCAPTWOLASGTG 1080  
1021 LRQDCRKVCNLYGTVKEHNGSDCHCDKATQCCSCLPNVIGQNCDCRCAPTWOLASGTG 1080  
1081 CGPCNNAHSGPSCNFTGOCQMPGFGHTCSCQELFWGDPDVECRACDCCDPRGIE 1140  
1081 CGPCNNAHSGPSCNFTGOCQMPGFGHTCSCQELFWGDPDVECRACDCCDPRGIE 1140  
1141 TPQCQOSTGQCVVGVGVEPRCDKTRGVSGVFPDCTCHQCQFALWDIAIIGELTNRTHKF 1200  
1141 TPQCQOSTGQCVVGVGVEPRCDKTRGVSGVFPDCTCHQCQFALWDIAIIGELTNRTHKF 1200  
1201 LKAKALKISGVIGYRETVDSVEKYNKDIKDLAQSPAAPLKNIGILFEEAKLTKDV 1260  
1201 LKAKALKISGVIGYRETVDSVEKYNKDIKDLAQSPAAPLKNIGILFEEAKLTKDV 1260  
1261 TEKMAQVEKLTDTASQSNSTAGELCALQAAESLDKTVKELAEQLEFIKNSDIQCALDS 1320  
1261 TEKMAQVEKLTDTASQSNSTAGELCALQAAESLDKTVKELAEQLEFIKNSDIQCALDS 1320

CC The present sequence is a laminin 8 polypeptide chain. Laminins are a  
CC family of heterotrimeric glycoproteins that function via binding  
CC interactions with neighbouring cell receptors and by forming laminin  
CC networks. They are signalling molecules which influence cellular  
CC function. Laminin 8 is useful for treating injuries to tissue of  
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
CC treating injuries to vascular tissue, promoting cell attachment and  
CC migration, ex vivo cell therapy, improving the biocompatibility of  
CC medical devices, and preparing improved cell culture devices and media.  
CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
CC of vascular injuries, improving the take of grafts, improving the  
CC biocompatibility of medical devices, treating neural injuries (neural  
CC regeneration), regulating angiogenesis, and promoting cell attachment  
CC migration  
XX  
SQ Query Match 93.7%; Score 9144; DB 3; Length 1786;  
Best Local Similarity 92.7%; Pred. NO. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY	1	MGLQVFAFGVLWTRVCAQEPFSGYCAAGSCYVATGDLIGRAQKLSVTSICGLHK	60
DB	1	MGLQLLAFSLFALCARVTAQEPFSGYCAAGSCYVATGDLIGRAQKLSVTSICGLHK	60
QY	61	PEPYCIVSHLQEDKCFICSDRDPYHETLNPDSHLIENVVVTFAPNRLKIMWQSENGVEN	120
DB	61	PEPYCIVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVVTFAPNRLKIMWQSENGVEN	120
QY	121	VITQLDEAFPHFLIMTFKTRPAAULIERSDFGKTWGVYFAYDCEASFPGISTG	180
DB	121	VITQLDEAFPHFLIMTFKTRPAAULIERSDFGKTWGVYFAYDCEASFPGISTG	180
QY	181	PMKVVDDIICDSRYSIDIEPTEGEVIFRALDPAFKIEDPYSRIQNLKITNLRIKFVKL	240
DB	181	PMKVVDDIICDSRYSIDIEPTEGEVIFRALDPAFKIEDPYSRIQNLKITNLRIKFVKL	240
QY	241	HTLGDNLLSRMBIREKYYAVDMVVRGNCFCYGHASECAPVDGWNEVEGWVGHCHC	300
DB	241	HTLGDNLLSRMBIREKYYAVDMVVRGNCFCYGHASECAPVDGWNEVEGWVGHCHC	300
QY	301	RHNTKGLNCLMDVFDHLPWRPAEGNSNACKCNCNEHSSCHFDMAVFLATGNVSGG	360
DB	301	RHNTKGLNCLMDVFDHLPWRPAEGNSNACKCNCNEHSSCHFDMAVFLATGNVSGG	360
QY	361	VCNCOHNTMGRNCEQCKPPYFOHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG	420
DB	361	VCDDCOHNTMGRNCEQCKPPYQHPERDIRDNPFCERCTCDPAGSQNEGICDSTDFSTG	420
QY	421	LIAGQCRKLVGEBCDVCKEGFDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCY	480
DB	421	LIAGQCRKLVGEBCDVCKEGFDLSSEDDPFCSCACNPLGTIPGNPCDSETGHY	480
QY	481	CKBLVTGQRCDQCLPQHWGLSNDLDCRCDLGGALANSCEDSGQSCCLPHMIGROC	540
DB	481	CKBLVTGQRCDQCLPEHWGLSNDLDCRCDLGGALANSCEDSGQSCSCRPHMIGROC	540
QY	541	NEVESGYFTTLDHYLYEAEANLGPQVWVVERQYIQDRIPSWTGPVVRPEGAYLEFF	600
DB	541	NEVEPGYFTTLDHYLYEAEANLGPQVSVVERQYIQDRIPSWTGPVVRPEGAYLEFF	600
QY	601	IDNIPYSMEYIILIRYEPQLPDHEKAVITVQRPKIPASSRCGNTVPDDDNQVSLSPG	660
DB	601	IDNIPYSMEYIILIRYEPQLPDHEKAVITVQRPGRIPTSRRCGNTIPDDDNQVSLSPG	660
QY	661	SRVVLPRPVCFEKGMNVTYRLPQVYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGG	720
DB	661	SRVVLPRPVCFEKGMNVTYRLPQVYTAGSDVESPYTFIDSLVMPYCKSLDIFTVGG	720
QY	721	SGDGEVNTSAWEITPQRYRCLNSRSVVKTPMTDVCRNIIIFSISALIHQTLGACECDPQGS	780
DB	721	SGDGVNTSAWEITPQRYRCLNSRSVVKTPMTDVCRNIIIFSISALLHQTLGACECDPQGS	780

RESULT 13  
AAB90788  
ID AAB90788 standard; protein; 1786 AA.  
XX

QY	781	LSSVCDPNGGQCCOCRRNVWVGRTCNRCAPGTGFGPNGCKPCDCHLQSSASAFCDAITGQC	840
DB	781	LSSVCDPNGGQCCOCRRNVWVGRTCNRCAPGTGFGPNSGCKPCCECHLQSSYNFACNPTVGTQC	840
QY	841	HCFGGYAROCDCRLCYGWFPGSPCCQCNHGLDCDVTGBCLSQDVTTHGNCERCLA	900
DB	841	HCFGGYAROCDCRLCYGWFPGSPCCQCNHGLDCDVTGBCLNQDVTMGNCERCLA	900
QY	901	GYGDPPIIGSDHCRPCPCPDGDSGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAS	960
DB	901	GYGDPPIIGSDHCRPCPCPDGDSGRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAS	960
QY	961	GFFGNPSDFGSCQPCQCHNIDITDPEACDKDGTGRLKCLYHTEGDHQLCOYGYGDA	1020
DB	961	GFFGNPSDFGSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGHCQFCFGYGDA	1020
QY	1021	LRQDCRKCVCNLYGTVKEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTG	1080
DB	1021	LRQDCRKCVCNLYGTVQEHNCNGSDCCQDKATGQCLCLPNVIGQNCRCAPNTWQLASGTG	1080
QY	1081	CGPCNCAHSGFSCNBEFTGQCQCMFPGFGRTCSECBELFWGDPPDVECRACDCDPRGIE	1140
DB	1081	CDPCNCAHSGFSCNBEFTGQCQCMFPGFGRTCSECBELFWGDPPDVECRACDCDPRGIE	1140
QY	1141	TPQCDQSTGQCVGVGEGPRCDKTRGYSGVPPDCTPCHQCFALMDAIIIGELTNRTHKF	1200
DB	1141	TPQCDQSTGQCVGVGEGPRCDKTRGYSGVPPDCTPCHQCFALMDVIIAELTNRTHF	1200
QY	1201	LEKAKALKISGVIPYRETVDSEKKVNEIKDILAQSPAAEPLKNTIGILFEEAEKTKDV	1260
DB	1201	LEKAKALKISGVIPYRETVDSEKRVSEIKDILAQSPAAEPLKNTGNLFEAEKLIKDV	1260
QY	1261	TEKMAQVEVKLTDTASOSNSTAGELGALQAEASLQTKVLAEOLEFIKNSDIOGALDS	1320
DB	1261	TEKMAQVEVKLSTTSOSNSTAKELSLQTEASLQNTVKELAEQLEFIKNSDIOGALDS	1320
QY	1321	ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFEQCEQARLLDE	1380
DB	1321	ITKYFQMSLEAEKRVNASTTDPNSTVEQSALMDRVEDVMVERESQFKEQCEQARLLDE	1380
QY	1381	LAKGLQSLDLSAAQWTCGTPPGADCSBSCGPGNCRCTDEGEKKCGGPGGLVTVVAHSA	1440
DB	1381	LAKGLQSLDLSAAAEWTCGTPPGASCSBSCGPGNCRCTDEGERKCGGPGGLVTVVAHNA	1440
QY	1441	WQKAMDPRDVLALAEVEQLSKMVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDL	1500
DB	1441	WQKAMDLDQVLSALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTNATKEKMDKSNEL	1500
QY	1501	RNLIKQIRNFLETDSADLDSIEAVANEVLKSGNASIPQQLONTEDIRERVETLSQVEVI	1560
DB	1501	RNLIKQIRNFLETDSADLDSIEAVANEVLKXEMPSTPQQLONTEDIRERVESLSQVEVI	1560
QY	1561	LQQAADIAIAEALLLEBAKQASKSATDVKTADWVKEALBEAEKAQVAEAKAIKQADEDI	1620
DB	1561	LQHSADIAIAEALLLEBAKQASKSATDVKTADWVKEALBEAEKAQVAEAKAIKQADEDI	1620
QY	1621	QGTQNLITSIESETAASEETLTNASQRIKLERVNEELKRAAQNSEAEYIEKVYVSVK	1680
DB	1621	QGTQNLITSIESETAASEETLNFNASQRISELERVNEELKRAAQNSEAEYIEKVYVTVK	1680
QY	1681	QNAADVKTLDGELDEKVKYKVESLIAQKTESADARREKAEALLQNEAKTLAQANSKLQLL	1740
DB	1681	QSAEDVKTLDGELDEKVKYKVENLIAKTESADARREKAEALLQNEAKTLAQANSKLQLL	1740
QY	1741	EDLERKYEDNQKYLDEKAEQELVRLEGEVRSLLKDISEKJAVYSTCL	1786
DB	1741	KDLERKYEDNQRYLEDKAEQELVRLEGEVRSLLKDIISQKAVYSTCL	1786



AAB90788;  
 15-JUN-2001 (first entry)  
 Human shear stress-response protein SEQ ID NO: 76.  
 Human; shear stress-response protein; vascular disease; arteriosclerosis.  
 Homo sapiens.  
 WO200125427-A1.  
 12-APR-2001.  
 02-OCT-2000; 2000WO-JP006840.  
 01-OCT-1999; 99JP-00280976.  
 (KYOW ) KYOWA HAKKO KOGYO KK.  
 (NOJII) NOJIMA H.  
 Nojima H, Yoshieue H, Obayashi M, Ota T, Kawabata A, Sakurada K;  
 Kuga T, Sekine S, Nakamura Y, Sugano S;  
 WPI: 2001-266308/27.  
 N-PSDB; AAB02911.  
 DNA sequences, proteins encoded by them and antibodies against them  
 useful in diagnosis and treatment of vascular disease caused by  
 arteriosclerosis.  
 Claim 60; Page 440-449; 678pp; Japanese.  
 The present invention provides the protein and coding sequences of a  
 number of human shear stress response proteins. These are useful in the  
 diagnosis, treatment and screening of vascular diseases caused by  
 arteriosclerosis, including heart failure, post-PICA restenosis and  
 hypertension  
 Sequence 1786 AA;  
 Query Match 93.7%; Score 9144; DB 4; Length 1786;  
 Best Local Similarity 92.7%; Pred. No. 0;  
 Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
 QY 1 MGLQVAFGLVAGTVCQAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
 DB 1 MGLQLLAFSFLALCRANVRAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
 QY 61 PEPYCIIVSHLQDKKCFICDGRDPHETLNPDLSHLIENVVTTFAPNRLKIWQSENGVEN 120  
 DB 61 PEPYCIIVSHLQDKKCFICNSQDPYHETLNPDLSHLIENVVTTFAPNRLKIWQSENGVEN 120  
 QY 121 VTIQDLAEAFHFTLIMTKTFRAAMLIERSDFGKTGWYRYFAYDCSSPFGISTG 180  
 DB 121 VTIQDLAEAFHFTLIMTKTFRAAMLIERSDFGKTGWYRYFAYDCASFPFGISTG 180  
 QY 181 PMKKVDDIICDSRYSDIEPSTGEVIFRALDPAFKIEDPYSPRIQNLKINLRIKFVKL 240  
 DB 181 PMKKVDDIICDSRYSDIEPSTGEVIFRALDPAFKIEDPYSPRIQNLKINLRIKFVKL 240  
 QY 241 HTLGNLDSRMEIRBKYYAYVDMVRGNCFCYHASECAPVDGVNEEVGVHGHCMC 300  
 DB 241 HTLGNLDSRMEIRBKYYAYVDMVRGNCFCYHASECAPVDGVNEEVGVHGHCMC 300  
 QY 301 RENTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNCHSSCHDFMAVFLATGNVSGG 360  
 DB 301 RENTKGLNCELWDFYHDLPMRPAEGRNSNACKKCNCHSSCHDFMAVFLATGNVSGG 360  
 QY 361 VCDNCHQNTMGRNCQCKPFYQHEDIRDNLCPECTCDPASSENGICDGVYDTSVSG 420  
 DB 361 VCDNCHQNTMGRNCQCKPFYQHEDIRDNLCPECTCDPASSENGICDGVYDTSVSG 420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLISAEDPYGCKSCACNPLGTIPGNPCDSETGYCY 480  
 DB 421 LIAGQCRCKLHVEGERCDVCKEGFYDLISAEDPYGCKSCACNPLGTIPGNPCDSETGYCY 480  
 QY 481 CKELVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGALNNSCEDSGQSCCLPHMIGRQC 540  
 DB 481 CKELVTGQRCDQCLPQHGLSNDLDGCRPCDCDLGALNNSCEDSGQSCCLPHMIGRQC 540  
 QY 541 NEVESGYFTTLDHYIYAEAEANLGGVVVEROVIQDRIPSWTGGFVRVPEGAYLEFF 600  
 DB 541 NEVEPGYFATLDHYIYAEAEANLGGVVVEROVIQDRIPSWTGGFVRVPEGAYLEFF 600  
 QY 601 IDNIPYSMEYEILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDDDNVVSLSPG 660  
 DB 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGKIPASSRCGNTPVDDDDNVVSLSPG 660  
 QY 661 SRYVLPVPCFEKGMNVTYRLELQYTAGSGDVESPYTFIDSLVLMPCYKSLDFTVGG 720  
 DB 661 SRYVLPVPCFEKGMNVTYRLELQYTAGSGDVESPYTFIDSLVLMPCYKSLDFTVGG 720  
 QY 721 SGEVYTNASWTFORYRCLNSRSVVKPMTDVCNIIIFSIISALITHOTGLACECDPQGS 780  
 DB 721 SGEVYTNASWTFORYRCLNSRSVVKPMTDVCNIIIFSIISALITHOTGLACECDPQGS 780  
 QY 781 LSVCDPNGGQCCRPVNVVGRTCNRCAPOTFGFGNGCKPCDCHLOGSASAFCDALITGOC 840  
 DB 781 LSVCDPNGGQCCRPVNVVGRTCNRCAPOTFGFGNGCKPCDCHLOGSASAFCDALITGOC 840  
 QY 841 HCFQGYIARQCDRLCPGYWGFSPCCQCNHGLDCTVTGRCLSCDYTTGHNCERCLA 900  
 DB 841 HCFQGYIARQCDRLCPGYWGFSPCCQCNHGLDCTVTGRCLSCDYTTGHNCERCLA 900  
 QY 901 GYGGDPIIISGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPGYISGRCDCCAS 960  
 DB 901 GYGGDPIIISGDHCRPCPCPDGDSGRQFARSCYQDPVTLQACVCDPGYISGRCDCCAS 960  
 QY 961 GFNGNSDFGGSCOPCQCHNIDTTPDPCADKDTGRCLKCLYHTEGHDHCOLQCYGYGDA 1020  
 DB 961 GFNGNSDFGGSCOPCQCHNIDTTPDPCADKDTGRCLKCLYHTEGHDHCOLQCYGYGDA 1020  
 QY 1021 LRQDCRKCVCNLYGTVEKHCNCGSDCHCDKATQCCCLPNVIGQNCDCRCAPTNWLASGTG 1080  
 DB 1021 LRQDCRKCVCNLYGTVEKHCNCGSDCHCDKATQCCCLPNVIGQNCDCRCAPTNWLASGTG 1080  
 QY 1081 CGFCNCAHSGFSPSCNEFTGQCCWPGFGGRTCECOELFWGDDPVECRACDPRGTE 1140  
 DB 1081 CGFCNCAHSGFSPSCNEFTGQCCWPGFGGRTCECOELFWGDDPVECRACDPRGTE 1140  
 QY 1141 TPQCDSTGQCVCEVGEVGRCDKCTRGYSVGFPPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
 DB 1141 TPQCDSTGQCVCEVGEVGRCDKCTRGYSVGFPPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
 QY 1201 LERAKALKISGVIGPYRETVDVSVKRVNEIKOILAQSPAAEPLKNIGNLFEAEKLIKDV 1260  
 DB 1201 LERAKALKISGVIGPYRETVDVSVKRVNEIKOILAQSPAAEPLKNIGNLFEAEKLIKDV 1260  
 QY 1261 TERKAOVEKLTDTASQNSSTAGELGALCAEAESLDKTVKELAEQLEFKNSDIOGALDS 1320  
 DB 1261 TERKAOVEKLTDTASQNSSTAGELGALCAEAESLDKTVKELAEQLEFKNSDIOGALDS 1320  
 QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFKQSEBARLLDE 1380  
 DB 1321 ITKYFQMSLEAEKRVNASTTDPNSTVQSALTRDRVEDLMLERESPFKQSEBARLLDE 1380  
 QY 1381 LAGKLSLDLSAAQMTCTGTPGADCSSECGGPNCTDEGKCGCGGCGGIVTVAHSA 1440  
 DB 1381 LAGKLSLDLSAAQMTCTGTPGADCSSECGGPNCTDEGKCGCGGCGGIVTVAHSA 1440  
 QY 1441 WQXAMDFDRDLVSALAEVEQLSKWSEAKVRADKQNAQDVLTKTNATKVKYDKSNEDL 1500  
 DB 1441 WQXAMDFDRDLVSALAEVEQLSKWSEAKVRADKQNAQDVLTKTNATKVKYDKSNEDL 1500  
 QY 1501 RNLIKOIRNFLETSDSADLDSIEAVANEVLKSGNASTPQQLQNLNLTEDIRERVETLSQVEVI 1560

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Db 1501 RNIUKIRNPLTQDSADLSIEAVNEVLKMPSTPQQLMTEDIRVESLSQVEVI 1560
Qy 1561 LQOAAADIAFAEALLLEAEKASATDVKTADMKVKEALEAEKAAQVAAEKAQKQADEDI 1620
Db 1561 LQSAADIAFAEALLLEAEKASATDVKTADMKVKEALEAEKAAQVAAEKAQKQADEDI 1620
Qy 1621 QGTQNLTSIESTASAEETLTNASORISKLRNVEELKRAQNSGEAEYIEKVYVVK 1680
Db 1621 QGTQNLTSIESTASAEETLTNASORISELERNVEELKRAQNSGEAEYIEKVYVVK 1680
Qy 1681 QNADDVKKTLGDELDEKYYKVESLIAQKTEESADARRKAEELLQNEAKTLQAQNSKLQLL 1740
Db 1681 QSAEDVKKTLGDELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQLL 1740
Qy 1741 EDLERYEDNOKYLEDKAEQLVLEGEVRSLLKQISEKVAHVYSTCL 1786
Db 1741 KOLERYEDNORYLEDKAEQLVLEGEVRSLLKQISQKVAHVYSTCL 1786

```

## RESULT 14

ABB81590  
ID ABB81590 standard; protein; 1786 AA.

XX ABB81590;

DT 19-SEP-2002 (first entry)

DE Human laminin 10 second chain protein sequence SEQ ID NO:6.

XX Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein 22..1786

FT /label= laminin\_10\_second\_chain

XX W0200250111-A2.

XX 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

XX 28-MAR-2001; 2001US-0279282P.

XX 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Tryggvason K, Doi M, Thyboll J;

XX WPI; 2002-557650/59.

XX N-PSDB; ABQ72908.

XX New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 113-119; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a second chain protein of laminin 10, from the present  
XX invention

SQ Sequence 1786 AA;

Query Match 93.7%; Score 9144; DB 5; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

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Qy 1 MGLLOVAFGLVAMWGTRVCAQSPFSGYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Db 1 MGLLOLLAFSPALCARVRAQEPFSGYGAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60
Qy 61 PEPYCIVSHLQEDKKCFICSDRPYHETLNPDHSLINVTTPAPNRLKTKWQSENGVEN 120
Db 61 PEPYCIVSHLQEDKKCFICNSQDFYHETLNPDHSLINVTTPAPNRLKTKWQSENGVEN 120
Qy 121 VTIQDLLEAEFHFTHLIMTFTKTPAAPAMLIERSDFGKTWGVYRYFAYDCEASPPGISTG 180
Db 121 VTIQDLLEAEFHFTHLIMTFTKTPAAPAMLIERSDFGKTWGVYRYFAYDCEASPPGISTG 180
Qy 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPTQNLKLTNLRKFEVKL 240
Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVIFRALDPAPKIEDPYSPTQNLKLTNLRKFEVKL 240
Qy 241 HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEYGVHGHCMC 300
Db 241 HTLGNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEYGVHGHCMC 300
Qy 301 RHNTKGLNCELCHDFYHDLRPAEGNSNACKKCNCHESSSCHDFDMAYFLATGVNMSG 360
Db 301 RHNTKGLNCELCHDFYHDLRPAEGNSNACKKCNCHESSSCHDFDMAYFLATGVNMSG 360
Qy 361 VCDNCQHTMGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTFPSVG 420
Db 361 VCDNCQHTMGRNCEOCKPFYFQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTFPSVG 420
Qy 421 LIACQCRCKLHVEGERCDVCKEGFYDLSAEDPVGCKSCACNPLGTPGGNPCDSETHCY 480
Db 421 LIACQCRCKLHVEGERCDVCKEGFYDLSAEDPVGCKSCACNPLGTPGGNPCDSETHCY 480
Qy 481 CKRLVTGQRCDQCLPQHWGLSNLDLDCRCDCLGALNNSCEDSDSCQCLPHMIGRQC 540
Db 481 CKRLVTGQRCDQCLPQHWGLSNLDLDCRCDCLGALNNSCEDSDSCQCLPHMIGRQC 540
Qy 541 NEVSSGYFTTLDHYIYEAENLPGVWVVERQYIQDRIPSWTGPQFVRVPEGAYLEFF 600
Db 541 NEVSPGYFATLDHYIYEAENLPGVWVVERQYIQDRIPSWTGPQFVRVPEGAYLEFF 600
Qy 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPG 660
Db 601 IDNIPYSMEYDILLIRYEPQLPDHWEKAVITVQRPKIPASSRRCGNTVPDDDNQVVSLSPG 660
Qy 661 SRYVVLPRPVCFEKGMNYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFEKGMNYTVRLELPQYTAGSDVESPYTFIDSLVLMPYCKSLDIFTVGG 720
Qy 721 SGDGVNTNSAVETQRYRCLENSRSVVKTPMTDVCNRIIFPSIALIHQTGLACEDCPQS 780
Db 721 SGDGVNTNSAVETQRYRCLENSRSVVKTPMTDVCNRIIFPSIALIHQTGLACEDCPQS 780
Qy 781 LSSVCDPNNGGQCQRPNVVGTCNRCAPGTFPGFPGNGCKPCDCHLQGSASAFCDATGQC 840
Db 781 LSSVCDPNNGGQCQRPNVVGTCNRCAPGTFPGFPGNGCKPCDCHLQGSASAFCDATGQC 840
Qy 841 HCFQGIYARQCDRLCPGYWGPSPQPCQCNHADDCTVTGECILSCDQYTTGHCNCRCLA 900
Db 841 HCFQGIYARQCDRLCPGYWGPSPQPCQCNHADDCTVTGECILSCDQYTTGHCNCRCLA 900
Qy 901 GYIGDPIIGSDHCRPCPCPDGDSGQFARSCYQDPVTQLQACVCPGYIGSQCDDCAS 960

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D	b	901	GYGDPPIIGSDHCHPCPCPDGPDGSRQFARSCVQDPVTIQLACVCPGVIGSRCDCCAS	960
Q	y	961	GFFGNPSDFGSCQPCQCHNIDITDDEACDQUTGRCLKLYHTEGHCQLCQYGYGDA	1020
D	b	961	GYGNPSEVGGSCQPCQCHNIDITDDEACDQUTGRCLKLYHTEGHCQFCRFGYGDA	1020
Q	y	1021	LRQCRKVCNLYGTVEKHCNGSDCHDKATGQSCCLPNVIGQNCDCAPNTWQLASGTG	1080
D	b	1021	LRQCRKVCNLYGTVEKHCNGSDCHDKATGQSCCLPNVIGQNCDCAPNTWQLASGTG	1080
Q	y	1081	CGPCNCAHSGFSGSCNEFTQCCQCMFGFGGRTSCQELFWGDDPVECRACDPRGIE	1140
D	b	1081	CGPCNCAHSGFSGSCNEFTQCCQCMFGFGGRTSCQELFWGDDPVECRACDPRGIE	1140
Q	y	1141	TPQCDQSTGQCVGVGVGEGPCDCKTRGYSVFPDCTPCHQCFALWDIAIGELTNRTHF	1200
D	b	1141	TPQCDQSTGQCVGVGVGEGPCDCKTRGYSVFPDCTPCHQCFALWDIAIGELTNRTHF	1200
Q	y	1201	LEKAKALKISGVIPIGYRETVDVSEKKNVEIKDILAQSPAAEPLKNIIGILFEEAEKLTQV	1260
D	b	1201	LEKAKALKISGVIPIGYRETVDVSEKKNVEIKDILAQSPAAEPLKNIIGILFEEAEKLTQV	1260
Q	y	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEISLDTVKELARQLSEFIKNSDIOGALDS	1320
D	b	1261	TEKMAQVEVKLTDTASQSNSTAGELGALQAEISLDTVKELARQLSEFIKNSDIOGALDS	1320
Q	y	1321	ITKVFQMSLEAEKRVNASTTDPNSTVEQSALTRDVEDLMLESFPKEQEQEQLLDE	1380
D	b	1321	ITKVFQMSLEAEKRVNASTTDPNSTVEQSALTRDVEDLMLESFPKEQEQEQLLDE	1380
Q	y	1381	LAKGLQSLDLAAQMTCTGTPGADCSSECGGNCRTDEGEKCGGPGGGLVTVAHSA	1440
D	b	1381	LAKGLQSLDLAAQMTCTGTPGADCSSECGGNCRTDEGEKCGGPGGGLVTVAHSA	1440
Q	y	1441	WQKAMDFRDVLSALAEVQSLKMWSEAKVRADEAKQNAQVLLKTNATKEKVDKXNEDL	1500
D	b	1441	WQKAMDFRDVLSALAEVQSLKMWSEAKVRADEAKQNAQVLLKTNATKEKVDKXNEDL	1500
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Q	y	1561	LQQAADTARAEELLEAKRASKATDVKTADVMKEALEAEKAAQVAAEKAIQKQADEI	1620
D	b	1561	LQQAADTARAEELLEAKRASKATDVKTADVMKEALEAEKAAQVAAEKAIQKQADEI	1620
Q	y	1621	QGTQNLTSISETAASBETITNASQISKLERNVEELKRAAQNSEAEYIEKVYTVK	1680
D	b	1621	QGTQNLTSISETAASBETITNASQISKLERNVEELKRAAQNSEAEYIEKVYTVK	1680
Q	y	1681	QNAADVKTLOGELDEKVKYVESLIAQKTESADARRKAEELLQNEAKTLIAQANSKLQLL	1740
D	b	1681	QNAADVKTLOGELDEKVKYVESLIAQKTESADARRKAEELLQNEAKTLIAQANSKLQLL	1740
Q	y	1741	EDLERKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKAVYSTCL	1786
D	b	1741	EDLERKYEDNQYLEDKQAEVLRLGEVRSLLKDISEKAVYSTCL	1786

RESULT 15  
AAW48896  
ID AAW48896 standard; protein; 1786 AA.

XX AC AAW48896;  
XX DT 04-APR-2002 (first entry)  
XX DE Laminin protein.

XX Human; angioastatin; endostatin; angiogenesis; cancer; metastasis;  
KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;  
KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;  
KW gene therapy; angioastatin antagonist; endostatin antagonist;

KW antiangiogenic; cytostatic; antiarthritic; antiinflammatory;  
KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnery;

XX synaecological; cat scratch fever.  
XX Unidentified.

PN WO200193897-A2.  
XX 13-DEC-2001.

XX 04-JUN-2001; 2001WO-US017947.  
XX 02-JUN-2000; 2000US-0209065P.  
XX 08-MAY-2001; 2001US-0289387P.

XX (ENTR-) ENTREMED INC.  
XX Sim KL, Macdonald NJ;  
XX WPI; 2002-130569/17.  
XX N-PSDB; ABA97525.

XX Regulating angiogenesis and treatment of angiogenesis-mediated diseases,  
XX e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding  
XX compound or actin disrupting compound.

XX Example 11; Fig 6A; 95pp; English.  
XX The present invention relates to methods of regulating angiogenesis in an  
XX individual by administering an angiogenesis regulating composition  
XX comprising a tropomyosin binding compound or an actin disrupting  
XX compound. The compositions are useful for treating diseases and processes  
XX mediated by angiogenesis including haemangioma, solid tumours, blood  
XX borne tumours, leukaemia, metastasis, Crohn's disease, coronary or  
XX cerebral collaterals, arthritis, diabetic neovascularisation, macular  
XX degeneration, wound healing, Helicobacter related diseases, ovulation,  
XX menstruation, and cat scratch fever. The present sequence is a protein  
XX described in the exemplification of the invention

XX SQ Sequence 1786 AA;  
XX Query Match 93.6%; Score 9131; DB 5; Length 1786;  
XX Best Local Similarity 92.6%; Pred. No. 0;  
XX Matches 1654; Conservative 71; Mismatches 61; Indels 0; Gaps 0;

Qy 1 MGLQVFAFGVLAALMGTRVCAQSPFSYCAAGSCVPATGDLIGRAQKLSVTTCGLHK 60  
Db 1 MGLQLLAFSLALCRARVRAQEPFSYCAAGSCVPATGDLIGRAQKLSVTTCGLHK 60

Qy 61 PEYCIIVSHLQDKKCFICDSRDPYHETLNPSHLIENVVTFAPNRLKIWQSENGVEN 120  
Db 61 PEYCIIVSHLQDKKCFICNSQDPYHETLNPSHLIENVVTFAPNRLKIWQSENGVEN 120

Qy 121 VTITDLEAFHFHFLIMTFKTRPAAMLIERSDDGKTGWYVYFAYDCSSFPGISG 180  
Db 121 VTITDLEAFHFHFLIMTFKTRPAAMLIERSDDGKTGWYVYFAYDCSSFPGISG 180

Qy 181 PMKVVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKILTRIKFVKL 240  
Db 181 PMKVVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKILTRIKFVKL 240

Qy 241 HTLGNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEVEGMVHCHMC 300  
Db 241 HTLGNLLDSRMEIREKYYIYAVYDMVVRGNCFCYGHASECAPVDGVNEVEGMVHCHMC 300

Qy 301 RHNTKGLNCELQMDFYHDLPPWPAEGRNSNACKKNCNEHSSCHFDMAVFLATGVNSGG 360  
Db 301 RHNTKGLNCELQMDFYHDLPPWPAEGRNSNACKKNCNEHSSCHFDMAVFLATGVNSGG 360

Qy 361 VCDNCQHTMGRNCEQCKPFYQHPERDIRDNLCPTCDPAGSENGICDGYTDFSVG 420  
Db 361 VCDNCQHTMGRNCEQCKPFYQHPERDIRDNLCPTCDPAGSENGICDGYTDFSVG 420



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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 13.5107 Seconds  
(without alignments)  
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Title: US-10-037-182-10  
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Sequence: 1 MGLQVAFGVLMWTRVC.....EVRSLKDKISEKVAIVSTCL 1786

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9758	100.0	1786	4	US-09-562-702A-18
2	9758	100.0	1786	4	US-09-561-818A-18
3	9429	96.6	1725	4	US-09-562-702A-20
4	9429	96.6	1725	4	US-09-561-818A-20
5	9144	93.7	1786	4	US-09-562-702A-14
6	9144	93.7	1786	4	US-09-561-818A-14
7	9144	93.7	1786	4	US-09-561-709B-9
8	9092	93.2	1765	4	US-09-562-702A-16
9	9092	93.2	1765	4	US-09-561-818A-16
10	5697.5	58.4	1196	1	US-08-144-131-4
11	5697.5	58.4	1196	2	US-08-735-893-4
12	5066.5	51.9	1799	4	US-09-845-583A-6
13	4907	50.3	1798	4	US-09-561-709B-11
14	4902	50.2	1798	4	US-09-845-583A-8
15	3813.5	39.1	1761	4	US-09-561-709B-1
16	3068.5	31.4	1101	4	US-09-561-709B-5
17	2880.5	29.5	1342	4	US-09-561-709B-13
18	1661.5	17.0	1572	4	US-09-562-702A-32
19	1661.5	17.0	1572	4	US-09-561-818A-28
20	1661.5	17.0	1605	4	US-09-562-702A-30
21	1661.5	17.0	1605	4	US-09-561-818A-26
22	1651	16.9	1609	4	US-09-562-702A-22
23	1651	16.9	1609	4	US-09-561-818A-22
24	1651	16.9	1617	4	US-09-562-702A-26
25	1643	16.8	1576	4	US-09-562-702A-24
26	1643	16.8	1576	4	US-09-561-818A-24
27	1643	16.8	1584	4	US-09-562-702A-28

28	1619	16.6	271	1	US-08-152-019A-28	Sequence 28, Appl
29	1584	16.2	3635	4	US-09-845-583A-2	Sequence 2, Appl
30	1572.5	16.1	3075	2	US-08-460-309-5	Sequence 5, Appl
31	1572.5	16.1	3075	2	US-08-125-077-5	Sequence 5, Appl
32	1560.5	16.0	3111	2	US-08-460-309-4	Sequence 4, Appl
33	1560.5	16.0	3111	2	US-08-125-077-4	Sequence 4, Appl
34	1555	15.9	3110	4	US-09-562-702A-2	Sequence 2, Appl
35	1555	15.9	3110	4	US-09-562-702A-5	Sequence 6, Appl
36	1555	15.9	3110	4	US-09-561-709B-7	Sequence 7, Appl
37	1553.5	15.9	3088	4	US-09-562-702A-8	Sequence 8, Appl
38	1553.5	15.9	3089	4	US-09-562-702A-4	Sequence 4, Appl
39	1550.5	15.9	1172	4	US-09-919-172-16	Sequence 16, Appl
40	1548	15.9	279	1	US-08-152-019A-29	Sequence 29, Appl
41	1542	15.8	278	2	US-08-460-309-13	Sequence 13, Appl
42	1542	15.8	278	2	US-08-125-077-13	Sequence 13, Appl
43	1541.5	15.8	1170	4	US-09-561-709B-12	Sequence 12, Appl
44	1524	15.6	3106	4	US-09-562-702A-10	Sequence 10, Appl
45	1522.5	15.6	3084	4	US-09-562-702A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-562-702A-18  
; Sequence 18, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-18

Query Match	100.0%;	Score 9758;	DB 4;	Length 1786;	
Best Local Similarity	100.0%;	Pred	No. 0;		
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				Gaps	0;
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Db	61	PEPYCVSHLQEDKCCFICDSRDP	YHETLNPDHSHLIENVVTT	FAPNRLKIWMQSENGVEN	120
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Qy	181	PMKKVDDIICDSRYS	DIETSEGENVFRALDPAFKIED	PYSRIQNLKILTRIKFVKL	240
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Db 541 NEVESGYTYTLLDHYIYEAEANLPGVWVVERQYIQDRIPSWTGGFVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEYIILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSGP 660  
Db 601 IDNIPYSMEYIILIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTPVDDNQVVSLSGP 660  
QY 661 SRVVLPRPVCFBKGMNYVRLLEPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGG 720  
Db 661 SRVVLPRPVCFBKGMNYVRLLEPOYTASGSDVESPYTFIDSLVMPYCKSLDIFTVGG 720  
QY 721 SGGEVNTSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALHTOGLACECDPOGS 780  
Db 721 SGGEVNTSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALHTOGLACECDPOGS 780  
QY 781 LSSVCDPNGQCCRCRPNVVRGTCNRCAPGTFGPGNGCKPCDCHLOGSASAFCDITGQC 840  
Db 781 LSSVCDPNGQCCRCRPNVVRGTCNRCAPGTFGPGNGCKPCDCHLOGSASAFCDITGQC 840  
QY 841 HCFQGIYAROCRLPYGFPSCQCNHGLDCTVTGECSCODYTTGHCNERCLA 900  
Db 841 HCFQGIYAROCRLPYGFPSCQCNHGLDCTVTGECSCODYTTGHCNERCLA 900  
QY 901 GYTGDPITIGSDHRCRCPDGPDSGRQFARSQYQDPVTLQACVCDPGYIISGRCDCCAS 960  
Db 901 GYTGDPITIGSDHRCRCPDGPDSGRQFARSQYQDPVTLQACVCDPGYIISGRCDCCAS 960  
QY 961 GFNGNPSDFGSGQPCQCHNIDTTPDCAKDTGRLCLVHTGHDHCLQYGYGDA 1020  
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QY 1021 LRQDCRCVCNVLGTVKEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTG 1080  
Db 1021 LRQDCRCVCNVLGTVKEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTG 1080  
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Db 1081 CGPCNMAHSPGSCNEFTGQCCMPFGGRTCSCEQLFWGDPDVECRACDPRGIE 1140  
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Db 1261 TEKMAQVEVKLTDPASOSNSTAGELGALQAEASLDTKVKELAEQLEFKNSDIQCALDS 1320  
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Db 1321 ITKYFQMSLEAEKAVNSTTDPNSTVEQSALTRDRVEDLMLRESFPKQOEQARLLDE 1380  
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Db 1381 LAGKLSLDLSAAAAQMTCTGTPPGADCSSECGGNCRCTDEGEKKCGGPGGLVTVHAHA 1440  
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Db 1441 WQKAMDFDRVLSALAEVEOLSKWVSEAKVRADAEKQNAQDVLTKTNATKEKVDKSNEDL 1500  
QY 1501 RNLIKQIRNFLETSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560  
Db 1501 RNLIKQIRNFLETSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVI 1560  
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Db 1621 QGTQNLITSIESETAASEETLTNASQRIKSLERNVEELKEKAAQNSGEAEYIEKVVYSVK 1680  
QY 1681 QNADVVKTLDGELDEKVKVESLIAQTEESADARRKAEALLQNEAKTLAQAANSKLQLL 1740  
Db 1681 QNADVVKTLDGELDEKVKVESLIAQTEESADARRKAEALLQNEAKTLAQAANSKLQLL 1740  
QY 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLXDISEKVAVYSTCL 1786  
Db 1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLXDISEKVAVYSTCL 1786  
  
RESULT 2  
US-09-561-818A-18  
; Sequence 18, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561.818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-18  
  
Query Match 100.0%; Score 9758; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 PEPYCIYVSHLOEDKCKICDSRDYPHETLNPDSHLIENNVTTFAPNRLKTIWQSENGVEN 120  
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QY 121 VTIQLDLEAEFPHFTHLINTFKTFPAAMLIERSDDFGKTWGVYFYFAYDCESFPFGISTG 180  
Db 121 VTIQLDLEAEFPHFTHLINTFKTFPAAMLIERSDDFGKTWGVYFYFAYDCESFPFGISTG 180  
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Db 181 PMKKVDDIICDSRYSDDIESTEGEVIIFRALDPAPFKIEDPYSPIQNLLKITNLRIKFKVL 240  
QY 241 HTLGNLDSRWEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMC 300  
Db 241 HTLGNLDSRWEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVHGHCMC 300  
QY 301 RHNTKGLNCELMDYFHDLPWPAEGRNSNAKCKCNCHSHSSCHFDMAVPLATGNVSGG 360

301 RHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNCHSSCHFDMAVFLATGNVSGG 360  
361 VCDNCQHTWGRNCEQCKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVG 420  
361 VCDNCQHTWGRNCEQCKPFYFQHPERDIRDPNICEPCTCDPAGSENGGICDGYTDFSVG 420  
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601 IDNIPYSMEYILIRYEPQDPHWEKAVITVORPKIPASSRCNGTVPDDNQVVSLSPG 660  
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661 SRYVVLPRPVCFEKGMNTVLELPQYTAGSDVESPYTFIDSLVLMYPYCKSLDIFTVGG 720  
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1741 EDLERKYEDNQYLEDKQAEQVRLSEGEVRSLLKDISKAVVYSTCL 1786

## RESULT 3

US-09-562-702A-20  
; Sequence 20, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; PRIOR APPLICATION NUMBER: 2000-04-28  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-20

Query Match 96.6%; Score 9429; DB 4; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

62 EPCIVSHLOEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 121  
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181 TLGNLLDSRMEIREKYYVAVDMVVRGNCFCYGHASECAPVDGVNNEEVEGVHGHCMCR 240  
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301 CQNDQHTNMGRCCEQCKPFYQHPERDTRDNLCEPCTCDPAGSENGGICDGYTDFSVGL 360  
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361 IAQCRCKLVHGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTPGGNPGCDSETGYCYC 420  
482 KSLVGTQRCQDCLPOHGWGLSNDLDCRCDLGGALANNSCEDSGQCSCLPHMIGRCQN 541  
421 KSLVGTQRCQDCLPOHGWGLSNDLDCRCDLGGALANNSCEDSGQCSCLPHMIGRCQN 480  
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721 SVVCDPNGQCCRCRPNVGRTRCNRCAPGTGFGPNCKPCDCHLOQSASAFCDAITGQCH 780  
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781 CFQGIYARQCDCLPGYGFSCQCCQCNHALDCDVTGECSCQDYTTGHCNCRCLAG 840  
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1141 ERKAKALKISGVIPRETVDSVEKKVNEIKDILAQSPAAPLKNIGILFEEAEKLTQDVT 1200  
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1682 NADDVKKTLDCGELDEKVKVESLTAQKTESADARRKAEILLONEAKTLLAQANSKLQLE 1741  
1621 NADDVKKTLDCGELDEKVKVESLTAQKTESADARRKAEILLONEAKTLLAQANSKLQLE 1680  
1742 DLERKYEDNQYLEDKQAEVRLGEVRSLLKDISEKVAVYSTCL 1786  
1681 DLERKYEDNQYLEDKQAEVRLGEVRSLLKDISEKVAVYSTCL 1725

## RESULT 4

US-09-561-818A-20  
; Sequence 20, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jari  
; APPLICANT: Tytgvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99 274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-20

Query Match 96.6%; Score 9429; DB 4; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EPYCVIIVSHLODKKCFICDSRDPVHETLNPDSHLIENVVTTTAPNRLKIWQSENGENV 121  
DB 1 EPYCVIIVSHLODKKCFICDSRDPVHETLNPDSHLIENVVTTTAPNRLKIWQSENGENV 60  
QY 122 TIQLDLAEAFHFTLINTFTFPAAMLIERSSDFGKTGWVRYPAYDCSSFPGISTGP 181  
DB 61 TIQLDLAEAFHFTLINTFTFPAAMLIERSSDFGKTGWVRYPAYDCSSFPGISTGP 120  
QY 182 MKKYDDIICDSRSDIETSPTEGEVIFRALDPAPKIDPSPRIQNLKTLNRIKFKVLH 241  
DB 121 MKKYDDIICDSRSDIETSPTEGEVIFRALDPAPKIDPSPRIQNLKTLNRIKFKVLH 180  
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DB 181 TLGNLLDSMEIREKYYIAYVDMVTRGNCFCYGHASCECAPVDGVNNEVEGVMHGHCMCR 240  
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DB 241 HNTKGLNCELMDYFHDLPWRPAEGNSNACKKCNHSSSCHFDMAVFLATGNVSGV 300  
QY 362 CDNCQHTNMGRCCEQCKPFYQHPERDIRDPNLCPECTCDPAGSENGGICDGYTDFSVGL 421  
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Db 1681 DLERYEDNQKLEDKAQLVLEGEVRSLLKDISEKVAVYSTCL 1725

RESULT 5

US-09-562-702A-14  
; Sequence 14, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-14

Query Match 93.7%; Score 9144; DB 4; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

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Db 61 PEPCYIVSHLOEDKKCFICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120  
QY 121 VTIQDLEAEFHTLIMTFKTRPAAMLIERSDDFGKTGWYRVYFAYDCESFPGISG 180  
Db 121 VTIQDLEAEFHTLIMTFKTRPAAMLIERSDDFGKTGWYRVYFAYDCESFPGISG 180  
QY 181 PMKXVDIIICDSRYSIDIEPSTGEVIFRALDPAFKIEDPYSPIQNLKILTKLRKFVKL 240  
Db 181 PMKXVDIIICDSRYSIDIEPSTGEVIFRALDPAFKIEDPYSPIQNLKILTKLRKFVKL 240  
QY 241 HTLGDNLLDSRWEIREKYYAVYDMVVRNCFYGHASECAPVDGVNBEVEGWHGCHMC 300  
Db 241 HTLGDNLLDSRWEIREKYYAVYDMVVRNCFYGHASECAPVDGVNBEVEGWHGCHMC 300  
QY 301 RHNTKGLNCELMDYFDLPLWPAEGRNSNACKKCNNEHSSCHDFDPAVFLATQNVSGG 360

QY 422 IAGOCRKLHVEGRCVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 481  
Db 361 IAGOCRKLHVEGRCVCKEGFYDLSEAEDPYGCKSCACNPLGTIPGNPCDSETGYCYC 420  
QY 482 KRLVTGQRCDQCLPQHGLSNDLDCRCPDCDLGALNNSCEDSGQSCCLPHMIGRQCN 541  
Db 421 KRLVTGQRCDQCLPQHGLSNDLDCRCPDCDLGALNNSCEDSGQSCCLPHMIGRQCN 480  
QY 542 EVESGYFTTLDHVIYEAEBANLPGVWVVERQYIQRIIPSWTGPGRVVRPEGAYLEFFI 601  
Db 481 EVESGYFTTLDHVIYEAEBANLPGVWVVERQYIQRIIPSWTGPGRVVRPEGAYLEFFI 540  
QY 602 DNIPIYSMEYEILIRYEPQLPDHMEKAVITVORPGKIPASSRCNGNTVPDDNQVVSLSPGS 661  
Db 541 DNIPIYSMEYEILIRYEPQLPDHMEKAVITVORPGKIPASSRCNGNTVPDDNQVVSLSPGS 600  
QY 662 RYVVLPRPVCHEKGMNVTYRLLEILOYTASGSDVESPYTFIDSLVLMYPCKSLDIFTVGG 721  
Db 601 RYVVLPRPVCHEKGMNVTYRLLEILOYTASGSDVESPYTFIDSLVLMYPCKSLDIFTVGG 660  
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Db 721 SSVCDPNGGQCCRPVNVGRTCNRCAPGTGFGNGCKPCDCHLOGSASAFCAITQCH 780  
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Db 781 CFQGIYARQCDRCLPGYWGFFSPCCQCNHGLDCDVTGBCLSQDYTTGHCNRCERCLAG 840  
QY 902 YYGDPPIIGSDHCRPCPCDGPDSGRQPARSCYQDPVTLQACVCDPGYIGSRCDCCASG 961  
Db 841 YYGDPPIIGSDHCRPCPCDGPDSGRQPARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
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Db 901 FFGNPSDFGSGCOPCOCHNIDTTPDPCADKDTGRCLKCLVHTGEGHCOLCOYGYGDAL 960  
QY 1022 RQDCRKVCNVLGTVKHCNDSCHCDKATQCCSLPNVIGQNCDCRCAPNTWQLASGTC 1081  
Db 961 RQDCRKVCNVLGTVKHCNDSCHCDKATQCCSLPNVIGQNCDCRCAPNTWQLASGTC 1020  
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Db 1021 GPCNCAHSGFSPSCNFTGQCCMGFGGRTCSQCQLFWGDDPVECRACDCDPRGIET 1080  
QY 1142 POCDOSTGQCVGEVGPGRCDKCTRGYSYGVFPDCTPCHQCFALWDALIIIGELTNRHKFL 1201  
Db 1081 POCDOSTGQCVGEVGPGRCDKCTRGYSYGVFPDCTPCHQCFALWDALIIIGELTNRHKFL 1140  
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Db 1201 EKMAQVEVKLTDTASQSNSTAGELGALCAEASLDKTVKELAEOLFTKNSDIOGALDSI 1260  
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Db 1261 TKYFQMSLEAKRVNASTTDPNSTVEQSALTRDRVEDLMLRESPPFKEQOEQARLLDEL 1320  
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Db 361 VDDCOHNTWGRNCEOCKEYFQHPERDIRDNLPCEPCTCDPAGSENGGICDGYTDFSTG 420  
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Db 481 CKRLVTGQRCQDLCPHWHGLSNDLDCRCPDCCDLGGALNNSCSBDSGGCCLPHMIGRCQ 540  
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Db 601 IDNIPYSMEYELIRYEPOLPDHWEKAVITVQRGKIPASSRCGNVTTPDDNNQVVSLSPG 660  
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QY 1141 TPQCDQSTGQCVGVGVEGPRCDKTRGYSVFPDCTPCHQCFALMDAIIIGELTNRTHKF 1200  
Db 1141 TPQCDQSTGQCVGVGVEGPRCDKTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHRF 1200  
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Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTRDRVEDLMLERESPFKEQCEQOARLDE 1380  
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Db 1441 WQKAMDLDDQVLSALAEVEQLSKWVSEAKVRADEAKQNAQDVLTKTNATKEKVDKSNEDL 1500  
QY 1501 RNLIKQIRNFLTBDSDADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVELTSQVEVI 1560  
Db 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKSGNASTPQQLQNLTEDIRERVELTSQVEVI 1560  
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Db 1621 QGTQNLTSIESETAASEETLTNASORISIKLERVVELKRAAQAQNGSEAEYIEKVVYSVK 1680  
QY 1681 QNADDDVKKTLDDGELDEKVKVESLIQKTEESADARKKAEELLQNEAKTLQAQNSKLQLL 1740  
Db 1681 QNADDDVKKTLDDGELDEKVKVESLIQKTEESADARKKAEELLQNEAKTLQAQNSKLQLL 1740  
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## RESULT 6

US-09-561-818A-14  
; Sequence 14, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-14

Query Match 93.7%; Score 9144; DB 4; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

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QY 241 HTLGNLLDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGVNVEEGVMVHGCMC 300  
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DB 661 SRYVVLPRPVCPEKGMNTVRLLELPOYTASSDVESEPTTFDSLVLMPYCKSLDIFTVGG 720  
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DB 721 SDGCVTNSAWETFORYLENSRSVWKTPTMDVCRNIIFPSIALIHOTGLACEDCPGS 780  
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DB 1621 QGTQNLITSTESETAASEETLTNASORISKLERNVEELKRAAQNQSGEAEYIEKVVSYSK 1680  
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DB 1741 EDLERKVENOKYLEDKAOBLVRLEGEVRSLLKDISEKVVAVYSTCL 1786  
  
RESULT 7  
US-09-561-709B-9  
; Sequence 9, Application US/09561709B  
; Patent No. 6682311  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champiaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMINIS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; CURRENT FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-9  
  
Query Match 93.7%; Score 9144; DB 4; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
  
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DB 121 VTQDLDEAFHFTHLIMTKFRPAAMLIERSDDPGKTGWYRYPAYDCESFPFGISG 180  
QY 181 PMKQVDDIICDSRYSIEPSTEGEVI FRALDPAFKIEDPYSRIQNLKITNLRIFVKL 240  
DB 181 PMKQVDDIICDSRYSIEPSTEGEVI FRALDPAFKIEDPYSRIQNLKITNLRIFVKL 240  
QY 241 HTLGDNLDSRMEIRKYYIYAVDMVVRNCFCYGHASECAPVDGVNEEVEGWHGHCMC 300  
DB 241 HTLGDNLDSRMEIRKYYIYAVDMVVRNCFCYGHASECAPVDGVNEEVEGWHGHCMC 300

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Db 361 VCDNCOHNTMGRNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG 420
Qy 421 LIAGQCRCKLHVGEGERCDYCKEFGYDLSAEDPYGKSCACNPLGTIPGPNPCDSTGYCY 480
Db 421 LIAGQCRCKLHVGEGERCDYCKEFGYDLSAEDPYGKSCACNPLGTIPGPNPCDSTGYCY 480
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Db 481 CKRLVTGQRCDQCLPEHNGSLNDLDCRCDCLDGLALNNSCSEDSGOCCLPHMIGRQC 540
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Db 541 NEVESGYFTTLDHYIYZEAEANLGFVGVVVERQYIQDRIPSWTQPGFVRVPEGAYLEFF 600
Qy 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIPASSRCGNVTVPDDNQVYLSRG 660
Db 601 IDNIPYSMEYELIRYEPQLPDHWEKAVITVORPGKIPASSRCGNVTVPDDNQVYLSRG 660
Qy 661 SRVYVLPVPCPEKGMNYTVRLPQYTAGSDVESPVTYFIDSLVMPYCKSLDIFTVGG 720
Db 661 SRVYVLPVPCPEKGMNYTVRLPQYTAGSDVESPVTYFIDSLVMPYCKSLDIFTVGG 720
Qy 721 SGGEVYNSAWETFORVRCLENSRSVVKTPMTDVCNRIIFSIHALIHOTGLACECDPQGS 780
Db 721 SGGEVYNSAWETFORVRCLENSRSVVKTPMTDVCNRIIFSIHALIHOTGLACECDPQGS 780
Qy 781 LSSVCDPNNGQCCRCRCPGDPGSGROFARSCYQBPVTQLQACDPCYIGSRCDCCAS 900
Db 781 LSSVCDPNNGQCCRCRCPGDPGSGROFARSCYQBPVTQLQACDPCYIGSRCDCCAS 900
Qy 901 GYVGDPIIGSGDRCRCPGDPGSGROFARSCYQBPVTQLQACDPCYIGSRCDCCAS 960
Db 901 GYVGDPIIGSGDRCRCPGDPGSGROFARSCYQBPVTQLQACDPCYIGSRCDCCAS 960
Qy 961 GFFGNPSDFGSGSQPCQCHNHITDTPDCAKDTGRCLKLYHTEGDHQCQLQCYGYGDA 1020
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Db 1021 LRQDCRKVCNYLGTVEHNGNSDCHDKATGQCSCLPNVIGQNCDCRCAPINTWOLASGTG 1080
Qy 1081 CGPCNCAHNSFGPSCNEFTGQCCQMPFGGRTCSQBELFWGDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNCAHNSFGPSCNEFTGQCCQMPFGGRTCSQBELFWGDPDVECRACDCDPRGIE 1140
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Db 1141 TPQCDQSTGQCVCEGVGPRCDKTRGYSVGPDPCTPCHQCPALWDALIGELTNRTHKF 1200
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Db 1201 LEKAKALKISGVIGPVTRETVDSVEKKVNEIKDILAQSPAAEPUNKIGILFEAEKLTQDV 1260
Qy 1261 TEXMAQVEVKLTDTASQSNSTAGELGALQABASLDTKVELABOEFINKNSDIQALDS 1320
Db 1261 TEXMAQVEVKLTDTASQSNSTAGELGALQABASLDTKVELABOEFINKNSDIQALDS 1320
Qy 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDIMLWRESFPKQEQEQAALLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDIMLWRESFPKQEQEQAALLDE 1380
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Qy 1381 LAGKLOSLDLSAAAQWTCGTPPGADCSBSCGPGNCRTEGEKKCGPGCGGLVTVAHSA 1440
Db 1381 LAGKLOSLDLSAAAQWTCGTPPGADCSBSCGPGNCRTEGEKKCGPGCGGLVTVAHSA 1440
Qy 1441 WQAMDFDROVLISALAEVEQLSKWVSEAKVRADAEKQNAQDVLLKTNATKEKVDKSNEDL 1500
Db 1441 WQAMDFDROVLISALAEVEQLSKWVSEAKVRADAEKQNAQDVLLKTNATKEKVDKSNEDL 1500
Qy 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSNASTPQOLQNLNLTEDIRERAVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSNASTPQOLQNLNLTEDIRERAVETLSQVEVI 1560
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Db 1561 LQSAADIAAEALLLEBEAKRASKSATDVKTADWKEALEEAEKAAQVAAEKAIKQADEDI 1620
Qy 1621 QGTQNLNLTSTESETAASEETLTNASQIRSKLERNVBEELKRAAQNSEAEYIEKVYYSVK 1680
Db 1621 QGTQNLNLTSTESETAASEETLTNASQIRSKLERNVBEELKRAAQNSEAEYIEKVYYSVK 1680
Qy 1681 QNADVDVKTLDGELDEKVKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLOLL 1740
Db 1681 QNADVDVKTLDGELDEKVKVESLIAQKTESADARRKAEELLQNEAKTLLAQANSKLOLL 1740
Qy 1741 EDLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAIVYSTCL 1786
Db 1741 EDLERKYEDNQKYLEDKAQLVRLGEVRSLLKDISEKVAIVYSTCL 1786
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## RESULT 8

US-09-562-702A-16  
; Sequence 16, Application US/09562702A

; Patent No. 6632790

; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 1765

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-562-702A-16

Query Match 93.2%; Score 9092; DB 4; Length 1765;  
Best Local Similarity 93.0%; Pred. No. 0;  
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

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Qy 22 QEPFSGYCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCFICDS 81
Db 1 QEPFSGYCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCFICNS 60
Qy 82 RDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFHTHLIMTFK 141
Db 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFHTHLIMTFK 120
Qy 142 TFRPAAMLIERSSFGKWTGYRYFAYDCSSPFGISTGPMKKVDDIICDSRYSDIEPST 201
Db 121 TFRPAAMLIERSSFGKWTGYRYFAYDCSSPFGISTGPMKKVDDIICDSRYSDIEPST 180
Qy 202 EGEVIERALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTGLGNLLDSRWEIREKYYA 261
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181 EGEVIFRALDPFAFKIEDPSPRIQNLKITTNRKFKVHLTGLDNLDSRMEIREKYYA 240  
262 VYDMVVRGNCFCYGHASCAFPVGGNEVEGVHGHCHMCRNTKGLNCELQMDYHDLPW 321  
241 VYDMVVRGNCFCYGHASCAFPVGGNEVEGVHGHCHMCRNTKGLNCELQMDYHDLPW 300  
322 RPAEGRNACKKNCNBSCHPDMAVFLATNGVSGVCDNCOHNTMGRNCQCKPFY 381  
301 RPAEGRNACKKNCNBSCHPDMAVFLATNGVSGVCDNCOHNTMGRNCQCKPFY 360  
382 FOHPERDIRDNLCEPTCDPAGSNGGICDGYTDFVGLTAGOCRCCKLVHVEGRCDVCK 441  
361 FOHPERDIRDNLCEPTCDPAGSNGGICDGYTDFVGLTAGOCRCCKLVHVEGRCDVCK 420  
442 EGFYDLSAEDPYGCKSCACNPLGITPGNPNCDSETGYCYCKRLVTGQRCDQCLPQHWGLS 501  
421 EGFYDLSAEDPYGCKSCACNPLGITPGNPNCDSETGYCYCKRLVTGQRCDQCLPQHWGLS 480  
502 NDLDCRCPCDCLGALANNSCEDSGQCSCLPHMIGROCNEVSGYFTTLDHYIYBAES 561  
481 NDLDCRCPCDCLGALANNSCEDSGQCSCLPHMIGROCNEVSGYFTTLDHYIYBAES 540  
562 ANLPGVWVVERQYIQDRIIPSWTGPVVRPEGAYLEFFIDNIPYSMEYELIRYEPQLP 621  
541 ANLPGVWVVERQYIQDRIIPSWTGPVVRPEGAYLEFFIDNIPYSMEYELIRYEPQLP 600  
622 DHWEKAVITVQRPKIPASSRCGNTPDDNQVLSLSPGSRVVLPRVCFEKGMYTVR 681  
601 DHWEKAVITVQRPKIPASSRCGNTPDDNQVLSLSPGSRVVLPRVCFEKGMYTVR 660  
682 LELPOVTASGDSVESPYTFIDSLVLMYCKSLDIFTVGGSGDGEVTSAMWTFQYRCLE 741  
661 LELPOVTASGDSVESPYTFIDSLVLMYCKSLDIFTVGGSGDGEVTSAMWTFQYRCLE 720  
742 NSRSVVKPTMTDVCNRIIFTSALIHOTGLACEDPQGSLSVCDPNCGQCCQCPNVVGR 801  
721 NSRSVVKPTMTDVCNRIIFTSALIHOTGLACEDPQGSLSVCDPNCGQCCQCPNVVGR 780  
802 TCNRCAPGTFGPGNGKPCDCHLQGSASAFCDAITGCHCFQGIYARQCDRLCPGWGF 861  
781 TCNRCAPGTFGPGNGKPCDCHLQGSASAFCDAITGCHCFQGIYARQCDRLCPGWGF 840  
862 PSCQPCQNGHALDCDVTGEBCLSCDVTGTHNCERCLAGYGDPIIGSGDHCRPCPCPD 921  
841 PSCQPCQNGHALDCDVTGEBCLSCDVTGTHNCERCLAGYGDPIIGSGDHCRPCPCPD 900  
922 GDSGRQFARSCYQDPVTLQACVCDPGVIGSRCDCCASGFGNPSDFGSGCQPCQCHN 981  
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961 IDTTDPEACDKTGRKCLYHTEGDHCLQCOYGYGDALRQDCRKCVCNLYLTGTVKEHCN 1020  
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1021 GSDCHCDKATGQCSCLPNVIGONCDRCAPNTWOLASGTGCGPCNCAHSGPSCNBEFTG 1080  
1102 QCCQMPFGGRTCSBQELFWGDDPVECRACDPCDPRGIETPCQDOSTQCQCVGVEGVR 1161  
1081 QCCQMPFGGRTCSBQELFWGDDPVECRACDPCDPRGIETPCQDOSTQCQCVGVEGVR 1140  
1162 CDKTRGSGVPPDCTPCHQCPALMDAIIIGELTNTHKFLKAKALKISGVIGPYRETVD 1221  
1141 CDKTRGSGVPPDCTPCHQCPALMDAIIIGELTNTHKFLKAKALKISGVIGPYRETVD 1200  
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1201 SYEKVKVNETKDTLAOSPAAPLKNIGILFEAEKLTQVTEMAQVEVKTDTTASQSNST 1260  
1282 AGELGALQAEBSLDTVKELAEQLEFIKNSDIQALDSITIKYFOMSLAEKRVNASTTD 1341  
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1621 TNASQISIKLERNVBEELKKAQNSGEAEYIEKVYVSVKQNAADVKKTLDDGLDEKYYKV 1680  
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1681 ENLIAKTESADARAKAELLQNEAKTLLAQANSKLQLELDERKVEDNOKYLEDKAQEL 1740  
1762 VRLGEVRSLLKDISEKVAVYSTCL 1786  
1741 ARLEGEVRSLLKDISEKVAVYSTCL 1765

## RESULT 9

US-09-561-818A-16  
; Sequence 16, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarrko  
; APPLICANT: Tytgovason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-16

Query Match 93.2%; Score 9092; DB 4; Length 1765;  
Best Local Similarity 93.0%; Pred. No. 0;  
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

22 QBEFYSYGAAGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCVIVSHLOEDKPCFICDS 81  
1 QBEFYSYGAAGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCVIVSHLOEDKPCFICDS 60  
82 RDPYHETLAPDLSHLENNVTTTAPNELKIWQSENGVENVTIQLDEAFHFTHLIMTFK 141  
61 QDPYHETLAPDLSHLENNVTTTAPNELKIWQSENGVENVTIQLDEAFHFTHLIMTFK 120  
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121 TPRPAAMLIERSSDFGKTGWVYRYFAYDCESFPFGISTGPMKKVDDIICDSYSIDIEPST 180  
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181 EGVIFRALDPAPKIEDPSPRIQNLKITTNRKFKVHLTGLDNLDSRMEIREKYYA 240

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DB 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCMCRHNTKGLNCELCHDFHDLPW 300  
QY 322 RPAEGRNSACKKCNKCNHSSCHPDMVFLATGNVSGVCDNCHTNGRNCCECKPXY 381  
DB 301 RPAEGRNSACKKCNKCNHSSCHPDMVFLATGNVSGVCDNCHTNGRNCCECKPXY 360  
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DB 421 EGYFDLSADPPYCKKCANPLGTIPGPNPCDSETCYCKLVGTGRCDCQCLPOHWGLS 480  
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DB 481 NDLGCRPCDCLGGLNNSCSDSDQSCCLPHMIGRQCNVESGYFTLDPHYIYEAEE 540  
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DB 601 DHWEKAVITVQRPKIPASSRCNGTVPDDNQNVSLSPGSRVYVLPVPCFEGMNYTVR 660  
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DB 661 LEIPQYTAGSDVESPTFTDSLVLMPYCKSLDIFTVGSGDGEVNTNSAWETFORVCLLE 720  
QY 742 NSRWVKTPTMTDVCNRIIFISALIHQTLGACBDCPDQGSLSVSCDPPNGQCCOCPNVR 801  
DB 721 NSRWVKTPTMTDVCNRIIFISALIHQTLGACBDCPDQGSLSVSCDPPNGQCCOCPNVR 780  
QY 802 TCRNCAPEGTGFGPNCKPCDCHLQGSASAFCDATGQCHFCQGIYARCDCLPQWGF 861  
DB 781 TCRNCAPEGTGFGPNCKPCDCHLQGSASAFCDATGQCHFCQGIYARCDCLPQWGF 840  
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DB 841 PSQPCQCNHGLDCTVTGECISQDQYTHGNCERCLAGYDPIIGSDHCRPCPCPD 900  
QY 922 GPDGGRQFARSCYQDPVTLOLACVCDPQYIGSRCDCCASGFFGNPSPDFGSCQPCCHN 981  
DB 901 GPDGGRQFARSCYQDPVTLOLACVCDPQYIGSRCDCCASGFFGNPSPDFGSCQPCCHN 960  
QY 982 IDTTDPAACDKTGRCLKCLYHTGDCOLCOXYGVDALRQCRKVCNLYGTVKEHCN 1041  
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QY 1042 GSDCHCDKATGQCCCLPNVIGQNDRCAPNTWOLASGTGCGPCNCAHSGFSPSCNEFTG 1101  
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DB 1081 QCQCMFGGFTCECOELFNGDPDVCACDCCDPRGIEPTQDQSQGVGVEGGR 1140  
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DB 1141 CDKCTRGVGVFPDCTPCHQCFALWDALIIIGELNTRTHKFLKAKALKISGIVGYRETVD 1200  
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DB 1201 SVEKWEIKDILAQSPAAPLKNIGILFBAEKLTKDVTCKMAQVEVKLTDTASQSNST 1260  
QY 1282 AGELCALQABAEISDKTVKEALQLEFTKNSDIOGALDSITKYPQMSLEAKRVNASTTD 1341  
DB 1261 AKELDSLQTEASLNDTVTKELAEQLFKNSDIRGALDSITKYPQMSLEAKRVNASTTE 1320  
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DB 1321 PNSTVEQALTRDRVEDMLNRESFFKEQEQBARLLDELAKGLQSLDLSAAAMTCGTP 1380  
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DB 1381 PGADCSSESCEGPNCRTEDEGEKCGPGCGGLVTVVAHSAWQKAMDPRDVLALAEVEQL 1440  
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DB 1441 SKMYSBAKVADRAKQNAQDVLKTKWATKEKVDKSNEDLNLIKQIRNFLTEDSADLDSI 1500  
QY 1522 EAVANEVLKSGNASTPOOLQNLITEDIRREVETIJSQVEVILQQAADIAIARLLEBAKRA 1581  
DB 1501 EAVANEVLKSGNASTPOOLQNLITEDIRREVETIJSQVEVILQQAADIAIARLLEBAKRA 1560  
QY 1582 SKSATDVKTADVMYKEALEBAEKAQVAERAKIQAODEDIOGTQNLITSISETAASZETL 1641  
DB 1561 SKSATDVKTADVMYKEALEBAEKAQVAERAKIQAODEDIOGTQNLITSISETAASZETL 1620  
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DB 1681 BSLIAQKTESADARRKAEILQNEAKTLLAQANSKLOLLEDBERKYNEDNOKYLEDKAQEL 1740  
QY 1762 VRLGEVRSLLKDISEKAVYVSTCL 1786  
DB 1741 VRLGEVRSLLKDISEKAVYVSTCL 1765

## RESULT 10

US-08-144-121-4  
; Sequence 4, Application US/08144121  
; Patent No. 5610031  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagonman, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/144,121  
; FILING DATE: 27-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: (MGN-0780.0) MGP-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Domain



LOCATION: 1..250  
FEATURE: Domain  
NAME/KEY: 251..437  
LOCATION: 251..437  
FEATURE: Domain  
NAME/KEY: 438..807  
LOCATION: 438..807  
FEATURE: Domain  
NAME/KEY: 808..840  
LOCATION: 808..840  
FEATURE: Domain  
NAME/KEY: 841..1196  
LOCATION: 841..1196  
US-08-144-121-4

Query Match 58.4%; Score 5697.5; DB 1; Length 1196;  
Best Local Similarity 63.3%; Pred. No. 0;  
Matches 1117; Conservative 46; Mismatches 32; Indels 571; Gaps 2;

QY 22 QEPESYCAEGSCYPATGDLIIIGRAQKLSVTS..TCGLHKPEPYCIIVSHLOEDKKCRICD 80  
DB 1 QEPESYCAEGSCYPATGDLIIIGRAQKLSVTS..TCGLHKPEPYCIIVSHLOEDKKCRICD 60  
QY 81 SDPPHETLNPDSHLIENVTTFAPNRLKIWMQSENGVENVTIQDLAEAFHFTLIMTF 140  
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DB 121 KTFRAAMLIERSDFGKTGWYRYPAYDCRSSPFGISTGPMKKVDDIIICDSRYSDIEPS 180  
QY 201 TSEGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLDDSRMEIREKYYY 260  
DB 181 TSEGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLDDSRMEIREKYYY 240  
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DB 241 AYDMVVRGNCFCYGHASECAPVDGVNEEVEGMVHGHCMCRHNTKGLNCELMDFYHDL 300  
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DB 301 WPAEGRSNACKKNCNEHSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEQCKPF 360  
QY 381 YFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGLIAGCRCKLHVEGRCDCV 440  
DB 361 YFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGLIAGCRCKLHVEGRCDCV 420  
QY 441 XEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYCKRLVTGQRCQCLPQHWGL 500  
DB 421 XEGFYDLSAEDPYGCKSCACNPLGTIPGNPCDSETGYCYCKRLVTGQRCQCLPQHWGL 437  
QY 501 SNDLDCRCPDCLGALNNSCSDSGCCLPHMIGRCNEVESGYFTTLDHYIEAE 560  
DB 438 ----- 437  
QY 561 EANLGGVVVVERQYIQDRI PSWTGPGFVRVPEGAYLEFFDINIPYSMEYELIRYEPOL 620  
DB 438 ----- 437  
QY 621 PDHWEKAVITVQPGKIPASSRCGNTVPDDDNQVSLSPGSRVYVLPVPRVCEKGMVTV 680  
DB 438 ----- 437  
QY 681 RLELPQYTAGSDVESPYTFIDSLVMPYCKSLDFTVGGSGDGEVTSANETFORYRCL 740  
DB 438 ----- 437  
QY 741 ENSRSVVKTPMTDVCNIIIFSIALTHTQGLACECDPQGSLSVCDPQGGQCQCRPNVVG 800  
DB 438 ----- 437  
QY 801 RTCNRCAPGTGFGPNCKPCDCHLQGSASAFDAITGQCHCFQGIYARQCDRCLPGYWG 860

Db 438 ----- 437  
QY 861 FPSQPCQCNHGLDCDVTGECSCQDYTTGHCNRCERCLAGYVGPDIIGSGDHCPCP 920  
Db 438 ----- 437  
QY 921 DGPDSGRQFARSCYQDPVTLQACVDCPGYIGSRCDDCASGFFGNPSPDFGSGCQPCQCHH 980  
Db 438 ----- 437  
QY 981 NIDTTDPEACDKDUTGRCLKLYHTGHDHCLQCYGYGIDALRQDCRCKVCYNLGTVKEHC 1040  
Db 438 ----- 437  
QY 1041 NGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWOLASGTGCGPCNCAHSGPSCNFT 1100  
Db 451 NGSDCQCDKATGQCSCLPNVIGQNCRCAPNTWOLASGTGCGPCNCAHSGPSCNFT 510  
QY 1101 GQCCMPGFGGRCTSCQELFWGDPDVECRACDPCDPRGIETPCCDQSTQCCQCVGEVGP 1160  
Db 511 GQCCMPGFGGRCTSCQELFWGDPDVECRACDPCDPRGIETPCCDQSTQCCQCVGEVGP 570  
QY 1161 RCDKTRGSGVPPDCTPCHQCFALMDAIIIGELTNRTHFLEKAKALKISGIVGPYREV 1220  
Db 571 RCDKTRGSGVPPDCTPCHQCFALMDAIIIGELTNRTHFLEKAKALKISGIVGPYREV 630  
QY 1221 DSEKVKNEIKDILASPAAPLKNIGILFEAEKLTQDVTQMAQVEKLTDTASQNS 1280  
Db 631 DSEKVKNEIKDILASPAAPLKNIGILFEAEKLTQDVTQMAQVEKLTDTASQNS 690  
QY 1281 TAGELGALQABESLDTVKELAEQLEFIKNDSIOGALDSITKYFQMSLEAEKRVNAST 1340  
Db 691 TAGELGALQABESLDTVKELAEQLEFIKNDSIOGALDSITKYFQMSLEAEKRVNAST 750  
QY 1341 DPNSTVEQSALTRDVEDLMLRESPEKQEQEALDELAKLQSLDLSAAQVTCCT 1400  
Db 751 EPNSTVEQSALTRDVEDLMLRESPEKQEQEALDELAKLQSLDLSAAQVTCCT 810  
QY 1401 PPGADCSSECGGPNCRDTEGKCKGCGGGLVTVVAHSAQKAMDFFDVLALAEVQ 1460  
Db 811 PPGADCSSECGGPNCRDTEGKCKGCGGGLVTVVAHSAQKAMDFFDVLALAEVQ 870  
QY 1461 LSKWSEAKVRADAEKQADVLTKNATKEKVDKSNEDLNLIKQIRNFLTSDSADLS 1520  
Db 871 LSKWSEAKVRADAEKQADVLTKNATKEKVDKSNEDLNLIKQIRNFLTSDSADLS 930  
QY 1521 IEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQCSAADIARAEILLLEAKR 1580  
Db 931 IEAVANEVLKSGNASTPQQLQNLTEDIRERVETLSQVEVILQCSAADIARAEILLLEAKR 990  
QY 1581 ASKSATDVKVTADWVKEALEEAEKQAAEKAQADEDIQGTQNLITSISETAASEET 1640  
Db 991 ASKSATDVKVTADWVKEALEEAEKQAAEKAQADEDIQGTQNLITSISETAASEET 1050  
QY 1641 LTNASORISKLERNVSELKKAQNSGEAEYIEKVYYSVKQNAADVKTLDGELDEKYYK 1700  
Db 1051 LTNASORISKLERNVSELKKAQNSGEAEYIEKVYYSVKQNAADVKTLDGELDEKYYK 1110  
QY 1701 VESLIAQKTESADARAKKAEKLLQNEAKTLQAQNSKQLLEDLERKYENQKYLEKAOE 1760  
Db 1111 VENLIAKTESADARAKKAEKLLQNEAKTLQAQNSKQLLEDLERKYENQKYLEKAOE 1170  
QY 1761 LVPLEGEVRSLLKDISEKVAVYSTCL 1786  
Db 1171 LARLEGEVRSLLKDISEKVAVYSTCL 1196

RESULT 11  
US-08-735-893-4  
; Sequence 4, Application US/08735893  
; Patent No. 5914317  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.

APPLICANT: Wagon, David W.  
TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:

ADDRESSES: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: BOSTON

STATE: Massachusetts  
COUNTRY: United States

Zip: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735,893  
FILING DATE: 18-OCT-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/144,121  
FILING DATE: 27-OCT-1993

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1196 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide

FRAGMENT TYPE: internal  
FEATURE:

NAME/KEY: Domain  
LOCATION: 1..250

FEATURE:  
NAME/KEY: Domain

LOCATION: 251..437  
FEATURE:

NAME/KEY: Domain  
LOCATION: 438..807

FEATURE:  
NAME/KEY: Domain

LOCATION: 808..840  
FEATURE:

NAME/KEY: Domain  
LOCATION: 841..1196

US-08-735-893-4

Query Match 58.4%; Score 5697.5; DB 2; Length 1196;

Best Local Similarity 63.3%; Pred. No. 0;  
Matches 1117; Conservative 46; Mismatches 32; Indels 571; Gaps 2;

QY 22 QEPFSGYGAAGSCYPATGDLIIIGRAQKLSVTS-TGLHKPFPYCIIVSHLQEDKKCFICD 80

DB 1 QEPFSGYGAAGSCYPATGDLIIIGRAQKLSVTS-TGLHKPFPYCIIVSHLQEDKKCFICN 60

QY 81 SRDPYHETLNPDGHLIENVVTTAPNRLKIWQSENGVENVTIQLDLAEFHTHLIMTF 140

DB 61 SQDPYHETLNPDGHLIENVVTTAPNRLKIWQSENGVENVTIQLDLAEFHTHLIMTF 120

QY 141 KTRFPAAMLTERSDFGKTGWVRYFAYDCESSFGISTGPMKKVDDIICDSRYSDIEPS 200

DB 121 KTRFPAAMLTERSDFGKTGWVRYFAYDCEASFGISTGPMKKVDDIICDSRYSDIEPS 180

QY 201 TEGEVIFRALDPKIEDPYSPIQNLLKTNRIRKPVKHTLGDNLDSRMEIREKYY 260

DB 181 TEGEVIFRALDPKIEDPYSPIQNLLKTNRIRKPVKHTLGDNLDSRMEIREKYY 240

QY 261 AVYDMVVRGNCFCYGHASECAPVDGVNEEVGVMVGHGCMCRNHTKGLNCELQMDFYHDL 320

DB 241 AVYDMVVRGNCFCYGHASECAPVDGVNEEVGVMVGHGCMCRNHTKGLNCELQMDFYHDL 300

QY 321 WRPAEGNSNACKKNCNCHSSCHDFMAVFLATGNVSGVCDNCOHNTMGRNCECKP 380

DB 301 WRPAEGNSNACKKNCNCHSSCHDFMAVFLATGNVSGVCDNCOHNTMGRNCECKP 360

QY 381 YFQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVC 440

DB 361 YFQHPERDIRDPNLCBPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVC 420

QY 441 KEGFYDLSEAEDPYGCKSCACNPLGTTPGGNCPDSEYCYCKELVTGQRCDQLPQHWGL 500

DB 421 KEGFYDLSEAEDPYGCKSCACNPLGTTPGGNCPDSEYCYCKELVTGQRCDQLPQHWGL 480

QY 501 SNDLDGCRPCDCLGALNANCSSEDSGQSCCLPHMIGRQCNEVESGYFTTLDHYEAE 560

DB 481 SNDLDGCRPCDCLGALNANCSSEDSGQSCCLPHMIGRQCNEVESGYFTTLDHYEAE 540

QY 561 EANLGGVVVVERQYIQRIPSWTGFVVRVPEGAYLEFFIDNIPYSMEVEILIRYEPQL 620

DB 541 EANLGGVVVVERQYIQRIPSWTGFVVRVPEGAYLEFFIDNIPYSMEVEILIRYEPQL 600

QY 621 PDHWKAVITVQRPGKIPASSRCGNTVPDDNQVWSLSPGSRVYVLPVPYCFEKGMYTV 680

DB 601 PDHWKAVITVQRPGKIPASSRCGNTVPDDNQVWSLSPGSRVYVLPVPYCFEKGMYTV 660

QY 681 RLPLQYTAGSDVESPYTFIDSLVLMYCKSLDITFVSGSDGGEVTSANWTFQRYCL 740

DB 661 RLPLQYTAGSDVESPYTFIDSLVLMYCKSLDITFVSGSDGGEVTSANWTFQRYCL 720

QY 741 ENSRSVVKTPMTDVCNRIIFISALIHQTLGACECPQGSLSVCDPENGQCCQENNVG 800

DB 721 ENSRSVVKTPMTDVCNRIIFISALIHQTLGACECPQGSLSVCDPENGQCCQENNVG 780

QY 801 RTNRCAPGTFGFGPNGKPCDCHLOSSAFCDALTGQCHCFQGIYAKQCDRLCYWG 860

DB 781 RTNRCAPGTFGFGPNGKPCDCHLOSSAFCDALTGQCHCFQGIYAKQCDRLCYWG 840

QY 861 FPSQPCQCNHGLDCTVTGECLSQDYYTGHNCERCLAGYGDPIIGSGDHCRPCPCP 920

DB 841 FPSQPCQCNHGLDCTVTGECLSQDYYTGHNCERCLAGYGDPIIGSGDHCRPCPCP 900

QY 921 DGPDSGRQFARCYQDPVTIQLACVCDPVGISGRCDDCASGFFGNPSDFGSGCQPCQCH 980

DB 901 DGPDSGRQFARCYQDPVTIQLACVCDPVGISGRCDDCASGFFGNPSDFGSGCQPCQCH 960

QY 981 NIDTDPACDKDTGRCLKLYHTEGDHCLQCYGYGDALRODCRKCVCNLYGTVEHC 1040

DB 961 NIDTDPACDKDTGRCLKLYHTEGDHCLQCYGYGDALRODCRKCVCNLYGTVEHC 1020

QY 1041 NGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGCGPCNCAHSPGSCNEFT 1100

DB 1021 NGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTGCGPCNCAHSPGSCNEFT 1080

QY 1101 GQCCQMFPGGRITCECOELFWGDDPVECRACDPRGIEPTDOSTGOCVCEGVEGP 1160

DB 1081 GQCCQMFPGGRITCECOELFWGDDPVECRACDPRGIEPTDOSTGOCVCEGVEGP 1140

QY 1161 RCDKTRGYSGVFPDCTPCHQCFALMDAILIGELTNRTHKFLKAKALKISGVIGPVRET 1220

DB 1141 RCDKTRGYSGVFPDCTPCHQCFALMDAILIGELTNRTHKFLKAKALKISGVIGPVRET 1200

QY 1221 DSVKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQVTEKMAQVEVKLTDTASQNS 1280

DB 1201 DSVKKNVEIKDILAQSPAAEPLKNIGILFEEAEKLTQVTEKMAQVEVKLTDTASQNS 1260

QY 1281 TAGELGALQAEALDKTVKELAEQLEFIKNSDITQALDSITKYFQMSLEAEKRVNAST 1340

DB 1261 TAGELGALQAEALDKTVKELAEQLEFIKNSDITQALDSITKYFQMSLEAEKRVNAST 1320



Db	1265	GLRHEIGKTTERTUQLEAEALTAVODNFANHALSGLEDRGFPALNLTJLQLOHLEILKH	1324
Qy	1312	SDIQGALDSITKYFQMSLEAEKVNASTTDPNSTVEQSALTDRVEDLMERESPFKEQQ	1371
Db	1325	SNFLGAYDSIRHAHSQSTAEERANASTFAVSPVNSADTRRTTEVLGMAQKFNFRQH	1384
Qy	1372	EQOARILDELAKLQSLDLSAAQMTCTGPPGNADCESECGGNCRCTDGEKKCGPGCC	1431
Db	1385	LANQOALGRLSAHAHTLSLTGINELVCGAPGDAPCATSPCGAGCRDEDPQRCGLGCS	1444
Qy	1432	GLVTVAHSWQKAMDPRDVLASALAEVQLSKMSVSEAKVRADBEAKQADQVLLKTNATKE	1491
Db	1445	GAAPADLALGRARHQAELQALVEGGILSRVSETRQAEEAQAQAAALDKANASRG	1504
Qy	1492	KVDSNEDURNLIKQTRNFLETESALDSIEAVANEVLKSNASTPQOLQNTEDIRERY	1551
Db	1505	QVEQANQELRELINQWDFLSQSGADPDSIEMWATRVLDISIPASPEQORLASIAERV	1564
Qy	1552	ETLSQVEVILQQAADIARAELLEAKRASKATDVKVTADMVKEALEEAEKAQVAAEK	1611
Db	1565	RSIADVTILAHMGDVRAEQILLOAHRAARSRAEGERQKAEIVQAALAEQAQAQAG	1624
Qy	1612	AIKQADEIDGTONLITSIESETAASEETUNASQISIKLERNVELKRAKQNSGEARY	1671
Db	1625	AIRGAVVDTQTEQTLQVQOERMAGAEKSLNSAGERARQILDALLEALKKRAGNSLAAS	1684
Qy	1672	IEKVVSQKQADVVKTLQDELDEKVKKVESLIAQTEESADARRKAEILLQNEAKTLIA	1731
Db	1685	ABETAGSAQRAREAEKQLEQVQDQYQTVRAAERKAEGLVAAQARAEQLDERADLLQ	1744
Qy	1732	QANSKLQLEDERKEDNOKYLEDKAQELVRLEGEVRSLLKDISKVAIVSTC	1785
Db	1745	AAQDKLQRLQLEGTVEENERALEGKAAQLDGLEARNRSVLQAINLQVQIYNTC	1798
RESULT 13			
US-09-561-709B-11			
; Sequence 11, Application US/09561709B			
; Patent No. 6682911			
; GENERAL INFORMATION:			
; APPLICANT: Burgeson, Robert			
; APPLICANT: Champliand, Marie-France			
; APPLICANT: Olson, Pamela			
; APPLICANT: Koch, Manuel			
; APPLICANT: Brunken, William			
; TITLE OF INVENTION: LAMININS AND USES THEREOF			
; FILE REFERENCE: 10287-060001			
; CURRENT APPLICATION NUMBER: US/09/561,709B			
; CURRENT FILING DATE: 2000-05-01			
; PRIOR APPLICATION NUMBER: US 09/168,949			
; PRIOR FILING DATE: 1998-10-09			
; PRIOR APPLICATION NUMBER: US 60/061,609			
; PRIOR FILING DATE: 1997-10-10			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 11			
; LENGTH: 1798			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-561-709B-11			
Query Match 50.38; Score 4907; DB 4; Length 1798;			
Best Local Similarity 49.68; Pred. No. 2.7e-281;			
Matches 888; Conservative 308; Mismatches 573; Indels 20; Gaps 8;			
Qy	3	LLOVAFGLVLMWTRVCAQEPFSGCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPE	62
Db	23	LLSVLA-----ATLAQAPADVP-GCSRSCYCYPATADLLVGRADRLTASSTCGLNGRQ	74
Qy	63	PYCVISHLOEKKCFICDSRDPHYETLNPDSHLEIENVVTFAPNRLKWKWQSENGVNT	122
Db	75	PYCVISHLOEKKCFICDSRDRPFPARDNPHTRIQNVVTSFAPORRAAWQSQNGIPAVT	134

Qy	123	IQLDLBAEFTHLIMTKTFRPAANLIERSSDFGKTGWVRYVPAYDCESSFEGISTGPM	182
Db	135	IQLDLBAEFTHLIMTKTFRPAANLIERSSDFGKTGWVRYVPAYDCESSFEGISTGPM	194
Qy	183	KKVDIIICDSRYSIDIEPSTEGEVIIFRALDPAFKIEDPSPRIQNLKITLNRKFKVLKHT	242
Db	195	RHWDVVCSRYSEIEPSTEGEVIYRVLDPAIPIDPYPSSRIQNLKITLNRVNLTELHT	254
Qy	243	LGMNLLDSRMEIRKYYAVYDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGHQWCRH	302
Db	255	LGMNLLDSRMEIRKYYAVYDMVVRGNCFCYGHASECAPVDGVNBEVEGMVHGHQWCRH	314
Qy	303	NTKGLNCELQWDFYHDLWPAERNSNACKNCKNCHSSCHFDMAVFATGNGVSGGVC	362
Db	315	NTRGLNCEQODFYHDLWPAERNSNACKNCKNCHSSCHFDMAVFATGNGVSGGVC	374
Qy	363	DNCHNTWGRNCECKPFYQHPERDTRDNLCEPCTCDPAGSENGICDGYTDFSVGLI	422
Db	375	DGCHNTAYRHELCLRFYFVDPTKLDPAVCRSCDCDPMGSDQGRCDHDDPALGLV	434
Qy	423	AGQCRKLVHEGERCDYCKEGFYDLSEAEDPYGCKSCACNPLGTIPGGNCPDSTGYCYCK	482
Db	435	SGQCRKEHVVTCCQCRDGFGLSISDPGCRRCQCNARGTVPSTPCDNPNGSGCYCK	494
Qy	483	RLVTGQRCDQCLPOHWGLSNDLDCRCDCDLGGALNNSCSDSGQCSCLPHMIGROCN	542
Db	495	RLVTGQRCDQCLPOHWGLSNDLDCRCDCDLGGALNNSCSDSGQCSCLPHMIGROCN	554
Qy	543	VESGYFTTLDHYIYEAEEANLPGVWVVERQVIQDRIPSWTGPFGFVRVEGAYLEFID	602
Db	555	VQPGYFPFLDLHLLWEAENTR-QQVLDVVERLVTPTGTPSWTSGFVRVEGAYLEFID	613
Qy	603	NIPYSMEYELIRYEPOLPDHWEKAVITVORPGKIASSRCGNVTVPDDDDNQVVISLPSGR	662
Db	614	SVPNAMDYDLMLRLPEQVPEQWAEELIVORPGFVPAHSLCGLHVRDRDRIQOTLQPHAR	673
Qy	663	YVVLPRVCPKEKGMNVTYRLLEPOYTASGSDVESPYT---FIDSLVLMPEYKSLDIFTV	718
Db	674	YLIFENPVCLPEPGISYKHLKLV-TCGSAQPTPTSGPGLLDSLVLLPRVLVLENF--	730
Qy	719	GGSGDGEVTSNAWETFORYLENSRSVVKTPMTDVCRNIIFISALIHOTGLACECDPQ	778
Db	731	--SGDAAALERQATFERYQCHEBGLVPSKTSPEACAPLLISLTLIYNGALPCQCNPQ	788
Qy	779	GSLSVCDPNQGGQCCPNVVGRTCNFCAGTGTGFGNGCKPCDCHLQGSASAFCDAITG	838
Db	789	GSLSECNPHGGQCLCKPVGVRRCDDTCAPGYGFTGTCQACQCSFPGALSLCERSTG	848
Qy	839	QCHCFQGIYARQCDRCPLPGYWGFPSCQCNHGLDCDVTGECLESCDYTTGHNCR	899
Db	849	QCLCTGAFGLRCDACQCGQGWGFTSCRCPCVNGHDECNTHTGACLCGRDHTGHEHCRC	908
Qy	899	LAGYQSDPIIGSDHCRPCPCPDGSDGRQPARCYQDPVTLQACVCDPGYIGSRCDCC	958
Db	909	IAGFHGDPRLPYGAQCRPCPCPEGSGQRHFAFSCHQDEYSQQIVCHCRAGYTLGRCEAC	968
Qy	959	ASGFGNPSDFGSGCQPCQCHNIDTTPACADKDTGRCLKCLYHTEGDHCQLQCYGYG	1018
Db	969	APGQGFDSRFGRCQLCECSGNIDPMDPADCPHPQCLRLHHTGPHCAHSGKPGFPG	1028
Qy	1019	DALRQDCRKCVCNVLGTVKEHNGSD-CHDKATGQCSCLPNVIGQNCDCRCAPTWQLAS	1077
Db	1029	QAARQSCHRCTNLLGTNPQCPSPDQCHDCHDPSGQCPCLPNVQALAVDRCAPFWNLTS	1088
Qy	1078	GTGCGPCNCAHSGPSCNEFTGQCCMPCGFGGRTCECOLEFWGPDVCECRACDCDPR	1137
Db	1089	GHCQPCACLSPEBEGFTCNFTGQCHCLCGFGGRTCECOLEHWGPDGLQCHACDCDSR	1148
Qy	1138	GIETPQCDQSTGCQVCVEGVEGPRCDKTRGYSGVFPDCTPCHQCQFALWDIAIIGELTNR	1197
Db	1149	GIDTFCQHRFTGCTCRPGVSGVRCDCQARGFSGIFPACHPCFACFGDWRVWDQLAART	1208
Qy	1198	HKFEKAKALKISGVIQPYRETVDSEKKNVNEIKDIL-AQSPAAAEPLKNIGILFEAEKL	1256

Db 1209 QRLBORAELQOTGVLGAFESFWMQEKGIQVIGVARTNSAATAQLVATEELRRE 1268  
Qy 1257 TKDVTKMAQVEVKLTDTASQSNSTAGELGAQAEASLDKTVKELAEQLEFIKNSDIQ 1316  
Db 1269 IGEATEHLTQLEADLTDVDENFNANHALSGLERDLALNLTQLQDLHLDLLKHSNPLG 1328  
Qy 1317 ALDSITKTFQMSLEAKRVNASTTDPNSVTQCSALTDRVEDIMLERESPKEQOEQAR 1376  
Db 1329 AYDSIRHAHSQSAEARRANTSALAVPSPVNSASARHRTALDAQKEDFNSRKHMANQR 1388  
Qy 1377 LLDLGLAGLQSLDLSAAQMTCTGTPPGADCESECGGNCNTRDEGEKKCGGPGCGGLVT 1436  
Db 1389 ALGKLSAHTHLSLTDINELVCGAQLHHDRTSPCGGAGCRDEGQPRCCGLSCNGAAAT 1448  
Qy 1437 AHSAMQKMDPRDVLKSLAEVEQLSKVMSAKVRADAKQNAQDVLKTNATKEKVDKS 1496  
Db 1449 ADLALGRAPHTQAEQLRALAEGGSILSRVASTRQASEAQQAQALDKANASRGQVEQA 1508  
Qy 1497 NEDLNRLKJOFNFTFEDSADLDSAEVANEVLKSGNASTTPOQLNLTEDIRREVETLSQ 1556  
Db 1509 NOELQELLQSVKDFLNQSGAPDSIEMVATRVLELSIPASAEQIOLHLAGALAEVRSLAD 1568  
Qy 1557 VEVILQOASADTARAEILLLEBAKRASKATDVKVTADVMVKALBEAEKAQVAEAKIKQA 1616  
Db 1569 VDAILARTVGDVRRARQLQDARRARSWAEDBKQKAEVQAALEBAQRAQGIQAIRGA 1628  
Qy 1617 DEDIGTONLITSIESETAASEITLTNASORISKLENNVBEELKRAKAAQNSGEAEVIEKV 1676  
Db 1629 VADTRDTQTLQVQVERWAGAEALSSAGERARQDLLEALKLKRAQNSLAASABETA 1688  
Qy 1677 YSVKQADVDKTLDELDELKYEKVESLIAQKTESADARRAKELLQNEATLIAQANSK 1736  
Db 1689 GSAQRAQAEQLLRGLDQYQTKALAEAKAQGLAAQAEQLPDEARDLLQAAQDK 1748  
Qy 1737 LQLEDLEKVEDNOKYLEDKAEQVLRLEGEVRSLLKDISKAVVYSTC 1785  
Db 1749 LQRLQLEGTYBENERALESKAAQDLGLEARNRSVLQAINQVQIYNIC 1797

RESULT 14  
US-09-845-583A-8  
; Sequence 8, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 1798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-845-583A-8

Query Match 50.2%; Score 4902; DB 4; Length 1798;  
Best Local Similarity 49.6%; Pred No. 5,3e-281;  
Matches 887; Conservative 308; Mismatches 574; Indels 20; Gaps 8;  
Qy 3 LQVFAFVGLWGRVCAQEPFYGCAAGSCYPATGDLIGRAQKLSVSTGCLHKPE 62  
Db 23 LLSVLA-----ATLAQAPADVP--GCSRGSCYPATADLLVGRADRLTASSTGCLNGRQ 74  
Qy 63 PYCIYSHLOEDKKCFICSDRDPYHETLNPDSHLIENVTTPAPNLKTMQSEKVENVT 122

Db 75 PYCIYSHLOEDKKCFICSDRDPYHETLNPDSHLIENVTTPAPNLKTMQSEKVENVT 134  
Qy 123 IQLDLBAEFHFTLIMTFTKTPPAAMLTERRSDFGKTVGVVRYFAYDCSSSPFGISTGPM 182  
Db 135 IQLDLBAEFHFTLIMTFTKTPPAAMLTERRSDFGKTVGVVRYFAYDCSSSPFGISTGPM 194  
Qy 183 KKYDDIICDSRYSDIEPSTEGEVIYFALDPAFKIEDPSPRIQNLKIITNLRIKFKLHT 242  
Db 195 RHWDDVVCESRSEIEPSTEGEVIYFALDPAFKIEDPSPRIQNLKIITNLRIKFKLHT 254  
Qy 243 LGLNLLDSREIREKYYAYVDMVRGNCFCYGHASECAPDGVGVNEVEGMVGHCMCHR 302  
Db 255 LGLNLLDPREREIKYYAYVDMVRGNCFCYGHASECAPDGVGVNEVEGMVGHCMCHR 314  
Qy 303 NTKGLNCELMPFYHDLPMRPAEGRNSNACKKCNCHNESHSSCHFDMAVFLATGNVSGGVC 362  
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Qy 363 DNCQHTMGRNCEQKPFYFQHPERDIRPNI,CEPCTCDPAGSENGGICOGYTFDSVGLI 422  
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Qy 423 AGOCRCKLHVEGBCRDVCKEGFVLSAEDPYGCKSCACNPLGTIPGNCPCDSETGYCYCK 482  
Db 435 SGOCRCHEVVGTRCOQCRDGGFFGLSISDPGCRRCQCNARGTVPSTFCDPNSGSCYCK 494  
Qy 483 RLVTGQRCDQCLPQHNLGSLNDLDCRCPDCDLGGALNNSCEDSGQSCCLPHMIRQCNNE 542  
Db 495 RLVTGRCDCRCLPGHWGLSLDLLGCRPCDCDVGALDPQCDGEGTQCHCRQHMVGRCEQ 554  
Qy 543 VESGYFTTLDHYIAEAEANLPGVVVVERQYIQDRIPSWTGPVVRPEGAYLEFFID 602  
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Qy 603 NIPYSMEYILIRYEPQLPDHMEKAVITVQRPKIPASSRCNCTVDDDNQVNVLSFGSR 662  
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Qy 663 YVVLPRPVPEKGMNTVRLLELPQYTAGSDVESPYT----FIDSLVLMPYCKSLDIFTV 718  
Db 674 YLIFPNPVCLEPGISYKJHLKLV--TGSSAQPETPYSGPGLLIDSULLVPRVLVLEMF-- 730  
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Db 1751 EOEKYYARC 1759

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Job time : 23.5107 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 45.4374 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-10  
Perfect score: 9758  
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Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:\*
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  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	9758	100.0	1786	14	US-10-037-182-10
3	9429	96.6	1725	14	US-10-037-182-12
4	9144	93.7	1786	9	US-09-873-676-113
5	9144	93.7	1786	9	US-09-938-275-6
6	9144	93.7	1786	14	US-10-037-182-6
7	9092	93.2	1765	14	US-10-037-182-8
8	5690.5	58.3	1196	16	US-10-443-349-4
9	5087.5	52.1	1801	9	US-09-938-275-8
10	5066.5	51.9	1799	9	US-09-845-583-6
11	5031.5	51.6	1798	9	US-09-938-275-9
12	4902	50.2	1798	9	US-09-845-583-8
13	3742.5	38.4	1808	15	US-10-369-493-5986
14	3068.5	31.4	1101	12	US-10-287-971-18
15	2154	22.1	527	12	US-09-925-298-703

16	2154	22.1	527	14	US-10-102-806-703	Sequence 703, Appl
17	1751	17.9	3672	15	US-10-369-493-6146	Sequence 6146, Ap
18	1675	17.2	3712	12	US-10-037-417-48	Sequence 47, Appl
19	1675	17.2	3712	13	US-10-108-605-103	Sequence 103, Appl
20	1671	17.1	3712	12	US-10-037-417-51	Sequence 51, Appl
21	1661.5	17.0	1572	14	US-10-037-182-20	Sequence 20, Appl
22	1661.5	17.0	1605	14	US-10-037-182-18	Sequence 18, Appl
23	1651	16.9	1609	14	US-10-037-182-14	Sequence 14, Appl
24	1651	16.9	1609	14	US-10-299-058-12	Sequence 12, Appl
25	1647	16.9	1609	9	US-09-938-275-11	Sequence 11, Appl
26	1647	16.9	1609	15	US-10-372-683-36	Sequence 36, Appl
27	1645.5	16.9	1557	15	US-10-369-493-6816	Sequence 6816, Ap
28	1643	16.8	1576	14	US-10-037-182-16	Sequence 16, Appl
29	1634.5	16.8	1607	9	US-09-938-275-10	Sequence 10, Appl
30	1584	16.2	3635	9	US-09-845-583-2	Sequence 2, Appl
31	1584	16.2	3635	12	US-10-037-417-47	Sequence 47, Appl
32	1584	16.2	3635	14	US-10-037-182-4	Sequence 4, Appl
33	1577	16.1	3696	15	US-10-312-088-31	Sequence 31, Appl
34	1573.5	16.1	3075	9	US-09-938-275-5	Sequence 5, Appl
35	1572.5	16.1	2743	14	US-10-037-182-36	Sequence 36, Appl
36	1572.5	16.1	3695	12	US-10-312-352-22	Sequence 22, Appl
37	1572.5	16.1	3695	14	US-10-037-182-2	Sequence 2, Appl
38	1567.5	16.0	3690	12	US-10-112-944-347	Sequence 347, Appl
39	1560.5	16.0	1174	15	US-10-603-725-22	Sequence 22, Appl
40	1557.5	16.0	1186	15	US-10-603-725-18	Sequence 18, Appl
41	1555	15.9	3070	10	US-09-961-403-7	Sequence 7, Appl
42	1552.5	15.9	3705	15	US-10-312-088-30	Sequence 30, Appl
43	1551.5	15.9	1155	15	US-10-603-725-24	Sequence 24, Appl
44	1551.5	15.9	1167	15	US-10-603-725-20	Sequence 20, Appl
45	1550.5	15.9	1172	9	US-09-919-172-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-938-275-7  
; Sequence 7, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P02469  
; DATABASE ENTRY DATE: 1989-07-01  
US-09-938-275-7

Query Match	100.0%;	Score	9758;	DB	9;	Length	1786;
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Gaps	0;						
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## RESULT 2

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; Sequence 10, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-10

Query Match 100.0%; Score 9758; DB 14; Length 1786;  
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Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 RHNTKGLNCEL.CMDFYHDL.PMRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGG 360  
301 RHNTKGLNCEL.CMDFYHDL.PMRPAEGRNSNACKKNCNEHSSCHFDMAVFLATGNVSGG 360  
361 VCDNCOHNTWGRNCEQCKPPYFQHPEDIRDPNLCEBCTCDPAGSENGGICDGVTFDSVG 420  
361 VCDNCOHNTWGRNCEQCKPPYFQHPEDIRDPNLCEBCTCDPAGSENGGICDGVTFDSVG 420  
421 LIAQCCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480  
421 LIAQCCKLHVEGERCDVCKEGFYDLSAEDPYGCKSCACNPLGTIPGPNPCDSETGYCY 480  
481 CKRLVTGORCDOCL.POHWGLSNDLDGCEPCDCDGLGALNNSCSDSGCCSCLPHMIGROC 540  
481 CKRLVTGORCDOCL.POHWGLSNDLDGCEPCDCDGLGALNNSCSDSGCCSCLPHMIGROC 540  
541 NEVESGYFTTLDHYIYEAEBANLPGVWVVERQYIQDRIPSWTGPFGVVRPEGAYLEFF 600  
541 NEVESGYFTTLDHYIYEAEBANLPGVWVVERQYIQDRIPSWTGPFGVVRPEGAYLEFF 600  
601 IDNIPYSMEYELIRYEPOLPDHWEKAVITVORPKIPASSRCGNTVPDDNQVVSLSRG 660  
601 IDNIPYSMEYELIRYEPOLPDHWEKAVITVORPKIPASSRCGNTVPDDNQVVSLSRG 660  
661 SRYVVLPRPVCFEKGMNTVLELPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGG 720  
661 SRYVVLPRPVCFEKGMNTVLELPQYTAGSDVESPYTFIDSLVLMFYCKSLDIFTVGG 720  
721 SGDSEVTNSAWETFORPCLNSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780  
721 SGDSEVTNSAWETFORPCLNSRSVVKTPMTDVCNRIIFSISALIHQTGLACECDPQGS 780  
781 LSSVCDPNGGCOCQCPNPVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASFCDAITGQC 840  
781 LSSVCDPNGGCOCQCPNPVVGRTCNRCAPGTGFGPNGCKPCDCHLQGSASFCDAITGQC 840  
841 HCFQGIYARQCDRLCPGYWGFPPSCQPCQCNHGHALDCDVTGECLSQCDYTTGHNCRCLA 900  
841 HCFQGIYARQCDRLCPGYWGFPPSCQPCQCNHGHALDCDVTGECLSQCDYTTGHNCRCLA 900  
901 GYGDPIIGSGDHCEPCPCDGPDSGROFARSQYQDPVTLQACVDPGYIGSRCDCCAS 960  
901 GYGDPIIGSGDHCEPCPCDGPDSGROFARSQYQDPVTLQACVDPGYIGSRCDCCAS 960  
961 GFFGNPDSFGGSCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGHDHQLCQYGYGDA 1020  
961 GFFGNPDSFGGSCQPCQCHNIDITDPEACDKDTGRCLKCLYHTEGHDHQLCQYGYGDA 1020  
1021 LRQDCKRCVNYLGVTKVHEKNGSDCHDKATGQCSCLPNVIGONCDRCAPNTWOLASGTG 1080  
1021 LRQDCKRCVNYLGVTKVHEKNGSDCHDKATGQCSCLPNVIGONCDRCAPNTWOLASGTG 1080  
1081 CGPCNCAAHSGFSPSCNEFTQCCQMPGFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140  
1081 CGPCNCAAHSGFSPSCNEFTQCCQMPGFGGRTCEQELFWGDPDVECRACDCDPRGIE 1140  
1141 TPQCDQSTGQCVCEGVGPRCDKTRGYSGVFPDCTPCHOCFALWDAITGELNTRTHKF 1200  
1141 TPQCDQSTGQCVCEGVGPRCDKTRGYSGVFPDCTPCHOCFALWDAITGELNTRTHKF 1200  
1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILPEAEKLTQDV 1260

1201 LEKAKALKISGVIGPYRETVDSEKKNVEIKDILAQSPAAPLKNIGILPEAEKLTQDV 1260  
1261 TEKMAQVEVKLTDTASQSNSTAGELALQAEASLSDTKVLAELQLEFIKNSDIQGALDS 1320  
1261 TEKMAQVEVKLTDTASQSNSTAGELALQAEASLSDTKVLAELQLEFIKNSDIQGALDS 1320  
1321 ITKYFQMSLEAPKRVNASTTDPNPNSTVQSALTDRDRVEDMLERESPFFKEQOEQARLLDE 1380  
1321 ITKYFQMSLEAPKRVNASTTDPNPNSTVQSALTDRDRVEDMLERESPFFKEQOEQARLLDE 1380  
1381 LAGKLOSLDLSAAQOMTCGTPPGADCSSECGGPNCRDDEGKKCGGPGCGLVTVAHSA 1440  
1381 LAGKLOSLDLSAAQOMTCGTPPGADCSSECGGPNCRDDEGKKCGGPGCGLVTVAHSA 1440  
1441 WQKAMDFDRDVLASALAEVEQLSKMWSEAKVRADEAKQNAQDVLLKTNATKPKVDSKSNEDL 1500  
1441 WQKAMDFDRDVLASALAEVEQLSKMWSEAKVRADEAKQNAQDVLLKTNATKPKVDSKSNEDL 1500  
1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSNASTPOOLQNLTEDIERVETLSQVEVI 1560  
1501 RNLIKQIRNFLTSDSADLDSIEAVANEVLKSNASTPOOLQNLTEDIERVETLSQVEVI 1560  
1561 LQOSAADTARABELLEAEKASKSATDVKVTADVMVKEALEEAEKAQVAAEKAQADEDI 1620  
1561 LQOSAADTARABELLEAEKASKSATDVKVTADVMVKEALEEAEKAQVAAEKAQADEDI 1620  
1621 QGTQNLNLTISBETAASBETLTNASQRIKSLERNVEELKRAAQNSEAEYIEKVVYSVK 1680  
1621 QGTQNLNLTISBETAASBETLTNASQRIKSLERNVEELKRAAQNSEAEYIEKVVYSVK 1680  
1681 QNADDVKKTLDCGELDEKVKVESLTAQKTESADARRKAEILQNEAKTLLAQANSKLQLL 1740  
1681 QNADDVKKTLDCGELDEKVKVESLTAQKTESADARRKAEILQNEAKTLLAQANSKLQLL 1740  
1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786  
1741 EDLERKYEDNQKYLEDKAQELVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3

US-10-037-182-12  
; Sequence 12, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trvggvasor, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-12

Query Match 96.6%; Score 9429; DB 14; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 EPCVISHLOEDKKFCICDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 121  
DB 1 EPCVISHLOEDKKFCICDRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENY 60  
QY 122 TIQLDLAEAFHFTLHMTFKTPRPAAMLIERSSDFGKTWGVYRYFAYDCESFPFGISTGP 181

Db 61 T T C L D L E A F F H T H L I M T F K T R P A M L I E R S D S F G K T W V Y R Y A Y C E S F F G I S T G P 120  
Qy 182 M K K V D D I I C D S R Y S D I E P T E G E V I F R A L D P A F K I E D P Y S P R I Q N L K I T N L R I K F V K L H 241  
Db 121 M K K V D D I I C D S R Y S D I E P T E G E V I F R A L D P A F K I E D P Y S P R I Q N L K I T N L R I K F V K L H 180  
Qy 242 T L G D N L L D S R M E I R E K Y Y A V Y D M V R G N C F C Y G H A S E C A P V D G V N E E V E G M W H G C M C R 301  
Db 181 T L G D N L L D S R M E I R E K Y Y A V Y D M V R G N C F C Y G H A S E C A P V D G V N E E V E G M W H G C M C R 240  
Qy 302 H N T K G L N C L C M D F Y H D L P W R P A E G R N S N A C K K C N C N E H S S C H P D M A V F L A T G N V S G G V 361  
Db 241 H N T K G L N C L C M D F Y H D L P W R P A E G R N S N A C K K C N C N E H S S C H P D M A V F L A T G N V S G G V 300  
Qy 362 C N C Q H N T M G R N C E O C K P Y F G H P E R D I R D P N L C E P C T C D P A S S E N G G I C D G Y T D F S V G L 421  
Db 301 C N C Q H N T M G R N C E O C K P Y F G H P E R D I R D P N L C E P C T C D P A S S E N G G I C D G Y T D F S V G L 360  
Qy 422 I A Q C R C K L H V E G E R C D V C K E G F Y D L S A E D P Y G C K S C A C N P L G T I P G G N P C D S E T G Y C Y C 481  
Db 361 I A Q C R C K L H V E G E R C D V C K E G F Y D L S A E D P Y G C K S C A C N P L G T I P G G N P C D S E T G Y C Y C 420  
Qy 482 K R L V T Q R C D C Q L P Q H W G L S N D L D G R P C D C D L G A L A N N S C E D S G C S C L P H M I T G R C N 541  
Db 421 K R L V T Q R C D C Q L P Q H W G L S N D L D G R P C D C D L G A L A N N S C E D S G C S C L P H M I T G R C N 480  
Qy 542 E V E S G Y Y F T L D H Y I Y E A E E A N L G P G V V V V E R Q Y I Q D R I P S W T G F G F V R P E G A Y L E F F I 601  
Db 481 E V E S G Y Y F T L D H Y I Y E A E E A N L G P G V V V V E R Q Y I Q D R I P S W T G F G F V R P E G A Y L E F F I 540  
Qy 602 D N I P Y S M E Y E I L I R Y E P Q L P D H W E K A V I T V Q R P G K I P A S S R C G N T V P D D D Q V S L S P G S 661  
Db 541 D N I P Y S M E Y E I L I R Y E P Q L P D H W E K A V I T V Q R P G K I P A S S R C G N T V P D D D Q V S L S P G S 600  
Qy 662 R Y V L P R P V C F E K G M N Y V R L E L P O Y T A S G S D V E S P Y T F I D S L V L M P Y C K S L D I F T V G G S 721  
Db 601 R Y V L P R P V C F E K G M N Y V R L E L P O Y T A S G S D V E S P Y T F I D S L V L M P Y C K S L D I F T V G G S 660  
Qy 722 G G E V T N S A W E T F Q R V R C L E N S R S V V K T P M T D V C R N I I P S I S A L I H Q T G L A C E C D P Q G S L 781  
Db 661 G G E V T N S A W E T F Q R V R C L E N S R S V V K T P M T D V C R N I I P S I S A L I H Q T G L A C E C D P Q G S L 720  
Qy 782 S V C D P N G G C C R P N V G R T C N R C A P G T F G F G N G K P C D C H L G S A S A F C D A I T G Q C H 841  
Db 721 S V C D P N G G C C R P N V G R T C N R C A P G T F G F G N G K P C D C H L G S A S A F C D A I T G Q C H 780  
Qy 842 C F Q G I Y A R Q C D R C L P G Y W G F P S C Q P C Q C N G H A L D C D T V T G E C L S C Q D Y T T G H N C E R C I A G 901  
Db 781 C F Q G I Y A R Q C D R C L P G Y W G F P S C Q P C Q C N G H A L D C D T V T G E C L S C Q D Y T T G H N C E R C I A G 840  
Qy 902 Y Y G D P I I G S G D H C R P C P D P D S G R Q F A R S C Y Q D P V T L O L A C V D P G Y I G S R C D D C A S G 961  
Db 841 Y Y G D P I I G S G D H C R P C P D P D S G R Q F A R S C Y Q D P V T L O L A C V D P G Y I G S R C D D C A S G 900  
Qy 962 F F G N P S D F G S G Q P C O C C H N I D T T P E A C D K D T G R C L K C L Y H T E G D H Q L C O Y G Y G D A L 1021  
Db 901 F F G N P S D F G S G Q P C O C C H N I D T T P E A C D K D T G R C L K C L Y H T E G D H Q L C O Y G Y G D A L 960  
Qy 1022 R D C R K V C N Y L G T V K E H N G S D C H C D K A T G Q C S C L P N V I G N C D R C A P N T W L A S G T G C 1081  
Db 961 R D C R K V C N Y L G T V K E H N G S D C H C D K A T G Q C S C L P N V I G N C D R C A P N T W L A S G T G C 1020  
Qy 1082 G P C N C N A A H S F G P S C N E F T G Q C Q M P F G G R T C S E C Q E L F W G D P D V E C R A C D C D P R G I E T 1141  
Db 1021 G P C N C N A A H S F G P S C N E F T G Q C Q M P F G G R T C S E C Q E L F W G D P D V E C R A C D C D P R G I E T 1080  
Qy 1142 P Q C D Q S T G Q C V C V E G V E G P R C D K T R G Y S G V P D C T P C H Q C F A L M D A I I G E L T N R T H K F L 1201  
Db 1081 P Q C D Q S T G Q C V C V E G V E G P R C D K T R G Y S G V P D C T P C H Q C F A L M D A I I G E L T N R T H K F L 1140  
Qy 1202 E K A K A L K I S G V I G P Y R E T V D S V E K K V N E I K D I L A Q S P A A E P L K N I G I L F E A E K L T K D V T 1261

Db 1141 E K A K A L K I S G V I G P Y R E T V D S V E K K V N E I K D I L A Q S P A A E P L K N I G I L F E A E K L T K D V T 1200  
Qy 1262 E K A Q V E V K L T D T A S O S N S T A G E L G A L Q A E A S S L D K T V K E L A E O L F F I K N S D I Q G A L D S I 1321  
Db 1201 E K A Q V E V K L T D T A S O S N S T A G E L G A L Q A E A S S L D K T V K E L A E O L F F I K N S D I Q G A L D S I 1260  
Qy 1322 T K Y F Q M S L E A E K R V N A S T T D P N S T V E Q S A L T R D R V E D L M L E R E S P P F K E Q E Q E Q A R L L D E L 1381  
Db 1261 T K Y F Q M S L E A E K R V N A S T T D P N S T V E Q S A L T R D R V E D L M L E R E S P P F K E Q E Q E Q A R L L D E L 1320  
Qy 1382 A G K L Q S L D L S A A A Q M T C G T P P G A D C S E S C G G P N C T D E G E K K C G G P G C G G L V T V A H S A W 1441  
Db 1321 A G K L Q S L D L S A A A Q M T C G T P P G A D C S E S C G G P N C T D E G E K K C G G P G C G G L V T V A H S A W 1380  
Qy 1442 Q K A M D F R D R V L S A L A E V O L S K M V S E A K V R A D E A K A Q A O D V L L K T N A T K E K V D K S N E D L R 1501  
Db 1381 Q K A M D F R D R V L S A L A E V O L S K M V S E A K V R A D E A K A Q A O D V L L K T N A T K E K V D K S N E D L R 1440  
Qy 1502 N L I K Q I R N F L T E S A D L D S I E A V A N E V L S G N A S T P Q O L Q N L T E D I R E R V E T I S Q V E V I L 1561  
Db 1441 N L I K Q I R N F L T E S A D L D S I E A V A N E V L S G N A S T P Q O L Q N L T E D I R E R V E T I S Q V E V I L 1500  
Qy 1562 Q Q S A A D I A R A E L L E B A K R A S K A T D V K V T A D M V K E A L B E A E K A Q A A E K A I K Q A D E D I Q 1621  
Db 1501 Q Q S A A D I A R A E L L E B A K R A S K A T D V K V T A D M V K E A L B E A E K A Q A A E K A I K Q A D E D I Q 1560  
Qy 1622 G T Q N L L T S I E S E T A A S E E T L T N A S Q R I S K L E R N V E L K R A A Q N S G E A E Y I E K V Y S V K Q 1681  
Db 1561 G T Q N L L T S I E S E T A A S E E T L T N A S Q R I S K L E R N V E L K R A A Q N S G E A E Y I E K V Y S V K Q 1620  
Qy 1682 N A D D V K T L D G E L D E K Y K V E S L I A C K T E S A D A R K A E L L Q N E A K T L L A Q A N S K L Q L L E 1741  
Db 1621 N A D D V K T L D G E L D E K Y K V E S L I A C K T E S A D A R K A E L L Q N E A K T L L A Q A N S K L Q L L E 1680  
Qy 1742 D L E R K Y E D N Q K Y L E D K A Q E L V R L E G E V R S L L K D I S E K V A Y S T C L 1786  
Db 1681 D L E R K Y E D N Q K Y L E D K A Q E L V R L E G E V R S L L K D I S E K V A Y S T C L 1725

## RESULT 4

US-09-873-676-113  
; Sequence 113, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 113  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-873-676-113

Query Match 93.7%; Score 9144; DB 9; Length 1786;  
Best Local Similarity 92.7%; Pred. NO. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 M G L L Q P A F G V L A M G T R V C A Q E P E F S Y C A E G S C Y P A T G D L L I G R A Q K L S V T S T C G L H K 60  
Db 1 M G L L Q L L A F L A L C A R A R V A Q E P E F S Y C A E G S C Y P A T G D L L I G R A Q K L S V T S T C G L H K 60  
Qy 61 P E P Y C I V S H L Q E D K C F I C D S R D P Y H E T L N P D S H L I E N V V T T F A P N R L K I W Q S E N G V E N 120  
Db 61 P E P Y C I V S H L Q E D K C F I C N S Q D P Y H E T L N P D S H L I E N V V T T F A P N R L K I W Q S E N G V E N 120

121 VTIQDLBAEFHFLIMFTKTRPAAMLIRSSDFGKTGWYRYFAYDCSSPFGISTG 180  
121 VTIQDLBAEFHFLIMFTKTRPAAMLIRSSDFGKTGWYRYFAYDCSSPFGISTG 180  
181 PMKVVDDIICDSRYSDIIPSTGEVI FRALDPAFKIEDPYSPRIQNLKINLRIKFVKL 240  
181 PMKVVDDIICDSRYSDIIPSTGEVI FRALDPAFKIEDPYSPRIQNLKINLRIKFVKL 240  
241 HTLGNLLDSRMEIREKYYAYVDMVRGNCFYGHASECAPVDGVNBEVGMVGHCMC 300  
241 HTLGNLLDSRMEIREKYYAYVDMVRGNCFYGHASECAPVDGVNBEVGMVGHCMC 300  
301 RHNTYGLACELCWDYHDLPMRPAGRNSNACKCNKNEHSSCHDFMAVLATGNVSGG 360  
301 RHNTYGLACELCWDYHDLPMRPAGRNSNACKCNKNEHSSCHDFMAVLATGNVSGG 360  
361 VCDNCHNTMGNCRQCPFFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420  
361 VCDNCHNTMGNCRQCPFFYQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDFSVG 420  
421 LIAGCRCKLHVEGRCDVCKGFFDLNADPYGCKSCACNPLGTIRPGNCDSETGYCY 480  
421 LIAGCRCKLHVEGRCDVCKGFFDLNADPYGCKSCACNPLGTIRPGNCDSETGYCY 480  
481 CKRLVTGQPCDCLPOHWGLSNDLDGCRPCDCLGALNNSCEDSGCCLPHMIGRQC 540  
481 CKRLVTGQPCDCLPOHWGLSNDLDGCRPCDCLGALNNSCEDSGCCLPHMIGRQC 540  
541 NEVESGYTTLDHYIYEAEANLPGVGVVVERQIQRIPSWTGGFVRVPEGAYLEFF 600  
541 NEVESGYTTLDHYIYEAEANLPGVGVVVERQIQRIPSWTGGFVRVPEGAYLEFF 600  
601 IDNIPYSMEVILLIRVEPOLPHWEKAVITVORPGKIPASSRCGNVTDDNNOVVSLSFG 660  
601 IDNIPYSMEVILLIRVEPOLPHWEKAVITVORPGKIPASSRCGNVTDDNNOVVSLSFG 660  
661 SRYVLPVPCFEKGMNYTVRLLEPOYTASGSDVSPTFIDSLVMPYCKSLDIFTVGG 720  
661 SRYVLPVPCFEKGMNYTVRLLEPOYTASGSDVSPTFIDSLVMPYCKSLDIFTVGG 720  
721 SGGEVTSNAWTFORVRCLENSRSVVKTPMTDVCNRIIFSIHALHOTGLACEDPOGS 780  
721 SGGEVTSNAWTFORVRCLENSRSVVKTPMTDVCNRIIFSIHALHOTGLACEDPOGS 780  
781 LSSVCDPNGGQOCRENVVGRICNRCAPGTGFGPCKPCDCHLQGSASAFCDAITQC 840  
781 LSSVCDPNGGQOCRENVVGRICNRCAPGTGFGPCKPCDCHLQGSASAFCDAITQC 840  
841 HCFQGIYARQDRCLPGYWGFPSCQPCQCNHALDCDVTGELSCQDYTTGHCNRCCLA 900  
841 HCFQGIYARQDRCLPGYWGFPSCQPCQCNHALDCDVTGELSCQDYTTGHCNRCCLA 900  
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901 GYGDPIIGSDHCRPCPCPDGDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
961 GFGNPSDFGSGSQPCQCHNNDITDTPERACDXTGRCLKCLVHTGSDHCLQCYGYGDA 1020  
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1021 LRQDCRCKVCNLYGTVEHCNNSDCHDKATGQCCLPNVIGONCDRCAPNTWQLASGTG 1080  
1021 LRQDCRCKVCNLYGTVEHCNNSDCHDKATGQCCLPNVIGONCDRCAPNTWQLASGTG 1080  
1081 CGFCNNAHAFSGPSNFTGQCQMPGFGRTCEQBCLFWGDDPVECRACDPCPRGIE 1140  
1081 CGFCNNAHAFSGPSNFTGQCQMPGFGRTCEQBCLFWGDDPVECRACDPCPRGIE 1140  
1141 TPQCDOSTGQCVCEGVGPRCDKTRGYSGVFFDCTPCQCFALWDALIGBLTNRTHKF 1200  
1141 TPQCDOSTGQCVCEGVGPRCDKTRGYSGVFFDCTPCQCFALWDALIGBLTNRTHKF 1200

1201 LEKAKALKISGVIGPVRETVDSEKKNBEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260  
1201 LEKAKALKISGVIGPVRETVDSEKKNBEIKDILAQSPAAEPLKNIGILFEEAEKLTQDV 1260  
1261 TERQAQVEVKLTDTASQNSTAGELGALQAEASLDKTKVLAELQLEFTKNSDIQCALDS 1320  
1261 TERQAQVEVKLTDTASQNSTAGELGALQAEASLDKTKVLAELQLEFTKNSDIQCALDS 1320  
1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQOEQEARLLDE 1380  
1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLERESPFKEQOEQEARLLDE 1380  
1381 LAGKLSLDLSAAAOQTCGTPPGADCSESCGPGNCRCTDEGEKKCGGPGCGGLVTVVAHA 1440  
1381 LAGKLSLDLSAAAOQTCGTPPGADCSESCGPGNCRCTDEGEKKCGGPGCGGLVTVVAHA 1440  
1441 WQKAMFDRDYLALAEVQLSKVSEAKVRADEAKONAQDVLTKTNATKEKVDKSNEDL 1500  
1441 WQKAMFDRDYLALAEVQLSKVSEAKVRADEAKONAQDVLTKTNATKEKVDKSNEDL 1500  
1501 RNLIKOIRNELTSDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560  
1501 RNLIKOIRNELTSDSADLDSIEAVANVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560  
1561 LQSAADIAAEALLBEAKGASKSATDVKTADWVKEALBEAKAQVAEAKAIKQADEDI 1620  
1561 LQSAADIAAEALLBEAKGASKSATDVKTADWVKEALBEAKAQVAEAKAIKQADEDI 1620  
1621 QGTQNLITSSETAASEETLTNASORISKLEBNVEELKRAAONSGEABYIEKVYVSVK 1680  
1621 QGTQNLITSSETAASEETLTNASORISKLEBNVEELKRAAONSGEABYIEKVYVSVK 1680  
1681 QNADVVKTLDGBLDEKYEKVESLIAQKTESADARRKAEELLQNEAKTLIAQNSKLQLL 1740  
1681 QNADVVKTLDGBLDEKYEKVESLIAQKTESADARRKAEELLQNEAKTLIAQNSKLQLL 1740  
1741 EDLERKVEDNOKYLEKAEKAEVLRLGEVRSLLKDISKVAVYSTCL 1786  
1741 EDLERKVEDNOKYLEKAEKAEVLRLGEVRSLLKDISKVAVYSTCL 1786

RESULT 5  
US-09-938-275-6  
; Sequence 6, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.203  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P07942  
; DATABASE ENTRY DATE: 1988-08-01  
US-09-938-275-6

Query Match 93.7%; Score 9144; DB 9; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

1 MGLLQVFAFGVYALWGTVCVAQEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
1 MGLLQVFAFGVYALWGTVCVAQEPFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60  
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Db 61 PEPYCVSHLQEDKCFICNSQDPVHETLNPDSHLIENNVVTFAPNRLKIWWQSENGVEN 120  
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Db 121 VTIQDLLEAFHPTHLIMTKFRPAAMLIERSDFGKTGWYRFAVDCSSPGISTG 180  
QY 181 PMKVVDDIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPYSPRIQNLKIINLRIKFKVL 240  
Db 181 PMKVVDDIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPYSPRIQNLKIINLRIKFKVL 240  
QY 241 HTLGDNLLDSRWEIREKYYAYVDMVRGNCFCYGHASECAPVDGNEVEGWHGHCW 300  
Db 241 HTLGDNLLDSRWEIREKYYAYVDMVRGNCFCYGHASECAPVDGNEVEGWHGHCW 300  
QY 301 RENTKGLNCELWDFYHDLJPMRPAEGRNSNAKCKNCNEHSSCHFDMAVILATGNVSGG 360  
Db 301 RENTKGLNCELWDFYHDLJPMRPAEGRNSNAKCKNCNEHSSCHFDMAVILATGNVSGG 360  
QY 361 VCDNCOHNTWGRNCECKPFYQHBERDIRDNLCPECTCDPAGSENGGICDGYTDFSVG 420  
Db 361 VCDNCOHNTWGRNCECKPFYQHBERDIRDNLCPECTCDPAGSENGGICDGYTDFSVG 420  
QY 421 LIAGQCRCKLHVGEGRCDVCKEGFYDLSAEDPVGCKSCACNPLGTIPGNCPCDSETGYC 480  
Db 421 LIAGQCRCKLHVGEGRCDVCKEGFYDLSAEDPVGCKSCACNPLGTIPGNCPCDSETGYC 480  
QY 481 CKELVTRQRCQDLPOHWGLSNDLDCRCPDCLDGGALNNSCEDSGOCSCLPHMIGRQC 540  
Db 481 CKELVTRQRCQDLPOHWGLSNDLDCRCPDCLDGGALNNSCEDSGOCSCLPHMIGRQC 540  
QY 541 NEVESGYFTTLDHYLYEAEANLPGVVVVERQYIQRIPSWTGFVVRPEGAYLEFF 600  
Db 541 NEVESGYFTTLDHYLYEAEANLPGVVVVERQYIQRIPSWTGFVVRPEGAYLEFF 600  
QY 601 IDNIPYSMEYIILIRYEPOLPDHWEKAVITVQRPKIPASSRCNGTVPDDNQVVSLSFG 660  
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Db 661 SRYVLPVPCFKGMNYVRLPELPOYTASGDSVESPYTFIDSLVMPYCKSLDIFTVGG 720  
QY 721 SGGEVNTSAWETFORVRCLENSRSVVTPTMTDVCNRIIFSALHTQTLGACECDPQS 780  
Db 721 SGGEVNTSAWETFORVRCLENSRSVVTPTMTDVCNRIIFSALHTQTLGACECDPQS 780  
QY 781 LSSVCDPNGQCCQCRNVVVRTNRCAPGTFFGPNCGKPCDCHLOGSASAFCDALTGC 840  
Db 781 LSSVCDPNGQCCQCRNVVVRTNRCAPGTFFGPNCGKPCDCHLOGSASAFCDALTGC 840  
QY 841 HCFQGIYARQCDRLPGYWGFPSCQCCQNGHALDCDVTGECSCQDYTTGHCNRCCLA 900  
Db 841 HCFQGIYARQCDRLPGYWGFPSCQCCQNGHALDCDVTGECSCQDYTTGHCNRCCLA 900  
QY 901 GYTGDPPIIGSGDHCRCPCPDGPDGSRQFARSQYQDPVTQLACVCDPGYIGSRCDCCAS 960  
Db 901 GYTGDPPIIGSGDHCRCPCPDGPDGSRQFARSQYQDPVTQLACVCDPGYIGSRCDCCAS 960  
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Db 961 GFPGNPSDFGSCQPCOCHNIDTTPDPEACDKTGRCLKLYHTEGDHCOLCOYGYGDA 1020  
QY 1021 LRQDCRCVCNLYGTVKEHNGSGDCHCDKATGQCSCLPNVIGQNCDCRCAPTWQLASGTG 1080  
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Db 1081 CGPCNCAHAFSGSCNEFTGQCCQMPFGGRCTSCOEALFWGDPDVECRACDCDPRGTE 1140  
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHFX 1200

Db 1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSGVFPDCTPCHQCFCALWDALIGELTNRTHFX 1200  
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Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVEIKOILAQSPAAEPKNTGILIFESAELTKOV 1260  
QY 1261 TEMQAQVEVKLTDTASQSNSTAGELCALQAEASLDTVKELAEQLEFTKNSDIOCALDS 1320  
Db 1261 TEMQAQVEVKLTDTASQSNSTAGELCALQAEASLDTVKELAEQLEFTKNSDIOCALDS 1320  
QY 1321 ITKYFQWLSAEAEKRVNASTTDPNSTVQESALTRDRVEDLMLERESPFKQEQEQAELDE 1380  
Db 1321 ITKYFQWLSAEAEKRVNASTTDPNSTVQESALTRDRVEDLMLERESPFKQEQEQAELDE 1380  
QY 1381 LAGKLOSLDLSAAAQNTCGTPPGADCSSECCGPNCTDEGEKKCGGCGGLVTVVAHSA 1440  
Db 1381 LAGKLOSLDLSAAAQNTCGTPPGADCSSECCGPNCTDEGEKKCGGCGGLVTVVAHSA 1440  
QY 1441 WQKAMPDRDVLASALAEVQESLQWSEAKVRADEAKQADQVLLKTNATKEKVKDSNEDL 1500  
Db 1441 WQKAMPDRDVLASALAEVQESLQWSEAKVRADEAKQADQVLLKTNATKEKVKDSNEDL 1500  
QY 1501 RNLIKQIRNPLTBDSDADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560  
Db 1501 RNLIKQIRNPLTBDSDADLDSIEAVANEVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560  
QY 1561 LQSAADIAEAELLLBEAKRSASATDVKTADWKEALEEAEAKQAAEKAIKQADEDI 1620  
Db 1561 LQSAADIAEAELLLBEAKRSASATDVKTADWKEALEEAEAKQAAEKAIKQADEDI 1620  
QY 1621 QGTQNLTSIETSETAASEETLTNASORISKLENVVELKRAAQAQNSGEABYIEKVYTVK 1680  
Db 1621 QGTQNLTSIETSETAASEETLTNASORISKLENVVELKRAAQAQNSGEABYIEKVYTVK 1680  
QY 1681 QNADDVKTLDGELDEKVKVRESILAKTTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740  
Db 1681 QNADDVKTLDGELDEKVKVRESILAKTTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740  
QY 1741 EDLERKYEDNQKYLEDKAELVLEGEVRSLLKDISEKVAVYSTCL 1786  
Db 1741 EDLERKYEDNQKYLEDKAELVLEGEVRSLLKDISEKVAVYSTCL 1786  
  
RESULT 6  
US-10-037-182-6  
; Sequence 6, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggevason, Karl  
; APPLICANT: Dol, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-6  
  
Query Match 93.7%; Score 9144; DB 14; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
  
QY 1 MGLLOVAFGVIALWGTVCQAQEPFVSFGCAEGSCYPATGDLIGRAKLSVTSTCGLHK 60

Db 1 MGLLQLLAFLALCRARVRAQEPFESYGCAEGSCYPATGDLILIGRAQKLSVTSTCGLHK 60  
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Db 61 PEPYCIIVSHLOEDKKCFICNSQDPVHETLNPSHLIENAVTTPAPNBLKIKWQSENGVEN 120  
Qy 121 VTIOLEAEFHFTHLIMTFKTPFAAMLIRSSDFGKTGWGYFYFAYDESSPPGISTG 180  
Db 121 VTIOLEAEFHFTHLIMTFKTPFAAMLIRSSDFGKTGWGYFYFAYDESSPPGISTG 180  
Qy 181 PMKVVDDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPRIQNLKILNLRKIFVKL 240  
Db 181 PMKVVDDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPRIQNLKILNLRKIFVKL 240  
Qy 241 HTLGNLLDSRMEIREKYYIAYVDMVRNGFCYGHASECAPVDGVNBEVEGMVHGCMC 300  
Db 241 HTLGNLLDSRMEIREKYYIAYVDMVRNGFCYGHASECAPVDGVNBEVEGMVHGCMC 300  
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Qy 361 VCDNCOHNTMGRNCBQCKPFPQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVG 420  
Db 361 VCDNCOHNTMGRNCBQCKPFPQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVG 420  
Qy 421 LIAGCRCKLHVEGRDVCKEGFDLSAEDPYGCKSCACNPLGTIPGNCPCDSEYCY 480  
Db 421 LIAGCRCKLHVEGRDVCKEGFDLSAEDPYGCKSCACNPLGTIPGNCPCDSEYCY 480  
Qy 481 CRLVITGQCDCLPQHGLSLNDLGRPCDCLGGLNNSCSDSGCCLPHMIGRQC 540  
Db 481 CRLVITGQCDCLPQHGLSLNDLGRPCDCLGGLNNSCSDSGCCLPHMIGRQC 540  
Qy 541 NEVESGYFTTLDHYIYEAENLGPVVVERQYIDRIPSWTGPVVRPEGAYLEFF 600  
Db 541 NEVESGYFTTLDHYIYEAENLGPVVVERQYIDRIPSWTGPVVRPEGAYLEFF 600  
Qy 601 IDNIPSYMEYELIYEPOLPHWEKAVITVORPKIPASSRCGNVTDDNQVVSLSG 660  
Db 601 IDNIPSYMEYELIYEPOLPHWEKAVITVORPKIPASSRCGNVTDDNQVVSLSG 660  
Qy 661 SRYVLPVPCPEKGMNYTVRIELPQYTAGSDVESPTFIDSLVMPYCKSLDIFTVGG 720  
Db 661 SRYVLPVPCPEKGMNYTVRIELPQYTAGSDVESPTFIDSLVMPYCKSLDIFTVGG 720  
Qy 721 SGGEVNTSAWETPORYRCLENSRSVVKTPMTDVCNRIIFISALIHOTGLACEDPQGS 780  
Db 721 SGGEVNTSAWETPORYRCLENSRSVVKTPMTDVCNRIIFISALIHOTGLACEDPQGS 780  
Qy 781 LSSVCDPNGGQCCRPNVVGRFCNRCAPGTGFGNGCKPCDCHLQGSASAFCDAITGQC 840  
Db 781 LSSVCDPNGGQCCRPNVVGRFCNRCAPGTGFGNGCKPCDCHLQGSASAFCDAITGQC 840  
Qy 841 HCFQGIYARQCDRLPLGVWFPSCQPCQNGHALDCDVTGECUSCQDYTTGHNRCERCLA 900  
Db 841 HCFQGIYARQCDRLPLGVWFPSCQPCQNGHALDCDVTGECUSCQDYTTGHNRCERCLA 900  
Qy 901 GYGGPITGSDGHCPCPCDPSGRPFARSQYQDPVTLQACVCDPFGYIGSRCDCCAS 960  
Db 901 GYGGPITGSDGHCPCPCDPSGRPFARSQYQDPVTLQACVCDPFGYIGSRCDCCAS 960  
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Db 1081 CQPCNCNAAHSGPSCNEFTGQCQMPFGGRTCSQCQLFWGDPDVECRACDCCDPRGIE 1140

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Qy 1261 TEKQAEVVKLTDTASQSNSTAGELGALQAEASLDKTVKELAEOLFIKNSDIOGALDS 1320  
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Qy 1321 ITKYFQMSLEAEKRVNASTTDPNSIVQSAITFDVRVEDLMLRESPPFKQEQEAEKLDE 1380  
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSIVQSAITFDVRVEDLMLRESPPFKQEQEAEKLDE 1380  
Qy 1381 LAGKLSLDLSAAQMTCTPPGADCSSECEGPNCRITDEGEKCKGCGGPGCGGLTVVAHSA 1440  
Db 1381 LAGKLSLDLSAAQMTCTPPGADCSSECEGPNCRITDEGEKCKGCGGPGCGGLTVVAHSA 1440  
Qy 1441 WQKAMPDFRDVTSALAEVQLSKWSEAKVRADAEKQADVLLKTNATKVKVDKSNEDL 1500  
Db 1441 WQKAMPDFRDVTSALAEVQLSKWSEAKVRADAEKQADVLLKTNATKVKVDKSNEDL 1500  
Qy 1501 RNLIKQIRNPLFTSDADLDSIEAVANVLKSGNASTPQOLQNLTEDIRERVETLSQVEVI 1560  
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Db 1561 LQSAADIAPAEALLBEAKRASKSATDVKTADMKVKEALEAEKQAAEAKIKQADEDI 1620  
Qy 1621 OQTNLLTSTESSTAASEETLTNASORISKLRNVEELRKAQNSGEAEYIEKVYYSVK 1680  
Db 1621 OQTNLLTSTESSTAASEETLTNASORISKLRNVEELRKAQNSGEAEYIEKVYYSVK 1680  
Qy 1681 QNADVVKTLTGDELDEKIKKVESLIAQKTESADARRKAEELLQNEAKTLQAQNSKLQLL 1740  
Db 1681 QNADVVKTLTGDELDEKIKKVESLIAQKTESADARRKAEELLQNEAKTLQAQNSKLQLL 1740  
Qy 1741 EDLERKYEDNOKVLEDAQELVRLEGEVSLKQISEKVAVYSTCL 1786  
Db 1741 EDLERKYEDNOKVLEDAQELVRLEGEVSLKQISEKVAVYSTCL 1786

RESULT 7  
US-10-037-182-8  
; Sequence 8, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thybøll, Jøll  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-8  
Query Match 93.2%; Score 9092; DB 14; Length 1765;  
Best Local Similarity 93.0%; Pred. No. 0;  
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;



QY 22 QBPFSYSGAEGSCYPATGDLIIIGRAQKLSVTSTGLHKBPPYCIYVSHLQBDKCKFCIDS 81  
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QY 82 RDPYHETLNPDSHLL:ENVVTTTAPNRLKTIWQSENGVENVTIQLDLBAEFHFTLHMTFK 141  
DB 61 QDPYHETLNPDSHLL:ENVVTTTAPNRLKTIWQSENGVENVTIQLDLBAEFHFTLHMTFK 120  
QY 142 TFRPAAMLTERSDFGKTGWVRYFAYDCESFFPGISTGPMKVKDDIIICDSRYSDIEBPT 201  
DB 121 TFRPAAMLTERSDFGKTGWVRYFAYDCESFFPGISTGPMKVKDDIIICDSRYSDIEBPT 180  
QY 202 EGEVIFRALDPAPFKIEDPYSPIQNLKTIURIKFVKLHTLGDNLDSRMEIRKYYIA 261  
DB 181 EGEVIFRALDPAPFKIEDPYSPIQNLKTIURIKFVKLHTLGDNLDSRMEIRKYYIA 240  
QY 262 VYDMVVRGNCFCYGHASECAPVDGVNEVEGVHGHCMCRHNTKGLNCELCHLWDFVHDLPW 321  
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DB 301 RPAEGRNSNACKKCNKNEHSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEOCKPFPY 360  
QY 382 FOHPERDIEDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 441  
DB 361 YCHPERDIEDPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLHVEGERCDVCK 420  
QY 442 EGFYDLASABDPYCKSCACNPLGTIPGPNCPDSETCYCYKELVGTQRCDCQCLPQHWGLS 501  
DB 421 EGFYDLASABDPYCKSCACNPLGTIPGPNCPDSETCYCYKELVGTQRCDCQCLPQHWGLS 480  
QY 502 NDLGCRPCDCLGGLNNSCEDSGQCSCLPHMIGROCNVESGYFTTLDHYLYEAE 561  
DB 481 NDLGCRPCDCLGGLNNSCEDSGQCSCLPHMIGROCNVESGYFTTLDHYLYEAE 540  
QY 562 ANLPGVWVVERQYIQRIPSTMTGPFVVPVPGAVLEFFIDNIPYSMEYELILIRYEPQLP 621  
DB 541 ANLPGVWVVERQYIQRIPSTMTGPFVVPVPGAVLEFFIDNIPYSMEYELILIRYEPQLP 600  
QY 622 DHWEKAVITVQRPKGTIPASRCGNTVDDNQNVSLSPGSRVYVLPVPCPEKGNVTVR 681  
DB 601 DHWEKAVITVQRPKGTIPASRCGNTVDDNQNVSLSPGSRVYVLPVPCPEKGNVTVR 660  
QY 682 LELPQYTAGSDVESPYTIDSLVMPYCKSLDIFTVGGSGDGVNTNSAWETFORVRCLE 741  
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QY 742 NSRSVVKTPMTDVCNRIIFSIHALIHTQGLACECDPQGSLSVCDPNGSCQCRPNVYGR 801  
DB 721 NSRSVVKTPMTDVCNRIIFSIHALIHTQGLACECDPQGSLSVCDPNGSCQCRPNVYGR 780  
QY 802 TCNRCAPGTGFGPNCKPCDCHLOGSASAFCDALTQCHCFQGIYAROCDCRLPGYWG 861  
DB 781 TCNRCAPGTGFGPNCKPCDCHLOGSASAFCDALTQCHCFQGIYAROCDCRLPGYWG 840  
QY 862 PSQPCQCNHGLDCTVTGECCLSCODYTTGHNCRCLAGYGDPIIGSGDCHRCPCPCPD 921  
DB 841 PSQPCQCNHGLDCTVTGECCLSCODYTTGHNCRCLAGYGDPIIGSGDCHRCPCPCPD 900  
QY 922 GPDSGQFARSCYQDPVTLQACVDPGYIGSRCDDCASGFGNPSDFGSGCQPCQCHN 981  
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QY 982 IDTTDPEACDKDGRCLKCLYHTEGHDHCOLCOYGGYGDALRQDCRCVCNVLGTVKEHCN 1041  
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DB 1021 GSDCHDKATGQSCSLPNVIGQNCDCRCPNTWOLASGTGCGPCNCAHSPFCSCNEFTG 1080

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QY 1162 CDKCTRGYSGVFPDCTPCHQCFCALMDALIGELTNRTHKELEKAKALKISGVIGPYRETV 1221  
DB 1141 CDKCTRGYSGVFPDCTPCHQCFCALMDALIGELTNRTHKELEKAKALKISGVIGPYRETV 1200  
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DB 1201 SVKKNVNEIKDILAQSPAAPLKNIGILFEEBAKLTKVTEKMAQVEVLKTDITASQNST 1260  
QY 1282 AGELGALQAEAEALDQTKVELAEQLEFIKNSDIQDGLDITTKYFQMSLEAEKVNASTTD 1341  
DB 1261 AKELDSLQTEAEALDQTKVELAEQLEFIKNSDIQDGLDITTKYFQMSLEAEKVNASTTD 1320  
QY 1342 PNSTVQSALTRDRVEDLMLERESPKEQOEBOARLLDELAKLQSLDLSAAQMTCCGP 1401  
DB 1321 PNSTVQSALTRDRVEDLMLERESPKEQOEBOARLLDELAKLQSLDLSAAQMTCCGP 1380  
QY 1402 PGADCSSECGGNCRTDEGEKCGGPGCGGLVTVVAHSAWQKAMDPRDVLALAEVEQL 1461  
DB 1381 PGADCSSECGGNCRTDEGEKCGGPGCGGLVTVVAHSAWQKAMDPRDVLALAEVEQL 1440  
QY 1462 SKVSEAKVRAADAKQNAQDVLKTNATKVDKSNEDLRLIKQIRNFUTEDSALDSI 1521  
DB 1441 SKVSEAKVRAADAKQNAQDVLKTNATKVDKSNEDLRLIKQIRNFUTEDSALDSI 1500  
QY 1522 EAVANEVLKSGNASTPOQLQNTLTERVETLSQVEVILQOSAAIDIAEAELLEBAKRA 1581  
DB 1501 EAVANEVLKSGNASTPOQLQNTLTERVETLSQVEVILQOSAAIDIAEAELLEBAKRA 1560  
QY 1582 SKSATDVKVTADVMVKEALEBAEAKAIAKQADEIOGTQNLTSIETETAASEETL 1641  
DB 1561 SKSATDVKVTADVMVKEALEBAEAKAIAKQADEIOGTQNLTSIETETAASEETL 1620  
QY 1642 TNASQISKLERNVVELKRAQNSGEAEYIEKVYVSVKQADDDVKKTLDDGELDEKVKV 1701  
DB 1621 TNASQISKLERNVVELKRAQNSGEAEYIEKVYVSVKQADDDVKKTLDDGELDEKVKV 1680  
QY 1702 ESLIAQKTESADARKAELLQNEAKTLAQANSKLQLELDERKYEDNQKYLEDKAQEL 1761  
DB 1681 ESLIAQKTESADARKAELLQNEAKTLAQANSKLQLELDERKYEDNQKYLEDKAQEL 1740  
QY 1762 VRLEGEVRSLLKDISEKVAIVYSTCL 1786  
DB 1741 ARLEGEVRSLLKDISEKVAIVYSTCL 1765

## RESULT 8

US-10-443-349-4  
; Sequence 4, Application US/10443349  
; Publication No. US20040023856A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagman, David W.  
; TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE  
; FILE REFERENCE: 10287/021003  
; CURRENT APPLICATION NUMBER: US/10/443,349  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/161,872  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 08/735,893  
; PRIOR FILING DATE: 1996-10-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(250)

OTHER INFORMATION: Human B1 chain	
FEATURE:	
NAME/KEY: DOMAIN	
LOCATION: (251)...(437)	
OTHER INFORMATION: Human B1 chain	
FEATURE:	
NAME/KEY: DOMAIN	
LOCATION: (438)...(807)	
OTHER INFORMATION: Human B1 chain	
FEATURE:	
NAME/KEY: DOMAIN	
LOCATION: (808)...(840)	
OTHER INFORMATION: Human B1 chain	
FEATURE:	
NAME/KEY: DOMAIN	
LOCATION: (841)...(1196)	
OTHER INFORMATION: Human B1 chain	
US-10-443-349-4	
Query Match 58.3%; Score 5690.5; DB 16; Length 1196;	
Best Local Similarity 63.2%; Pred. No. 6.7e-314;	
Matches 1116; Conservative 46; Mismatches 33; Indels 571; Gaps 2;	
QY	22 QPERSYGAEGSCYPATGCDLLIGRAQKLSVTS-TCGLHKPEPYCIIVSHLOEDKKCFICD 80
DB	1 QPERSYGAEGSCYPATGCDLLIGRAQKLSVTSITTCGLHKPEPYCIIVSHLOEDKKCFICN 60
QY	81 SRDPYHETLNPSHLIENVVITFAPNRLKIWQSENGVENVTIQLDLAEAEFFHFLIMTF 140
DB	61 SDPYHETLNPSHLIENVVITFAPNRLKIWQSENGVENVTIQLDLAEAEFFHFLIMTF 120
QY	141 KTFRAAMLIERSDFGKTGWYRYPAYDCSSFGISTGPMKKVDDIICDSRSDIEPS 200
DB	121 KTFRAAMLIERSDFGKTGWYRYFAYDCEASFFGISTGPMKKVDDIICDSRSDIEPS 180
QY	201 TEGEVI FALDPAFKIEDPYSPRIQNLKIITNLRKFKVLTGDNLLDSRMEIREKYYY 260
DB	181 TEGEVI FALDPAFKIEDPYSPRIQNLKIITNLRKFKVLTGDNLLDSRMEIREKYYY 240
QY	261 AYDMVVRGNCFCYGHASCAPVDGNEVEGVHGHCMCRHNTKGLNCELMDFYHDL 320
DB	241 AYDMVVRGNCFCYGHASCAPVDGNEVEGVHGHCMCRHNTKGLNCELMDFYHDL 300
QY	321 WPAEGRNSACKKNCNEHSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEQCKPF 380
DB	301 WPAEGRNSACKKNCNEHSSCHFDMAVFLATGNVSGVCDNCOHNTMGRNCEQCKPF 360
QY	381 YFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGLIAGQCRCKLHVEGERCDVC 440
DB	361 YFQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVGLIAGQCRCKLHVEGERCDVC 420
QY	441 KEGFYDLNADPYGCKSCACNPLGTIPGNPCDSEYCYCKRLVTGRCQCLPQHWGL 500
DB	421 KEGFYDLNADPYGCKSCACNPLGTIPGNPCDSEYCYCKRLVTGRCQCLPQHWGL 437
QY	501 SNDLDCRCPDCDLGALNCSGSDSGCCLPHMIGRCNEVESGYVFTTLDHYIEAE 560
DB	438 ----- 437
QY	561 EANLPGVWVVERQVIOIRIPSWTGGFVRVPEGAYLEFFIDNIPYSMEYBILIRYBQL 620
DB	438 ----- 437
QY	621 PDHWEKAVITVQPGKIPASSRCGNTVPDDNQVVSLSFGSRVYVLPFVPCFEKGMNTV 680
DB	438 ----- 437
QY	681 RLELPQYTAGSDVSPYTFIDSLVMPYCKSLDIFTVGGSDGGEVWNSAWETFORVCL 740
DB	438 ----- 437
QY	741 ENSRSVVKTPMTDVCNRNIIFSALIHOTGLACECDPOGSLSSVCDPNGGQCKRPVVG 800

DB	438 ----- 437
QY	801 RTCNRCAPGTFGPGNGKPCDCHLOGSASAPCDALTGQCHCFQGIYARQCDCLPGYWG 860
DB	438 ----- 437
QY	861 FPSQPCQCNHALDCDVTGTECLSCQDYTTGHCERCCLAGYYGDPFIIGSDHCRPCPCP 920
DB	438 ----- 437
QY	921 DGPDSGRQPARSCYQDPVTLQACVCDPGYIGSRCDDCASGPFNGPDSFGGSCQPCQCHH 980
DB	438 ----- 437
QY	981 NIDTTPDCAKDTGRCLKLVHTGEGHCOLCOYGYGDDALRQDRCRKCVCNYLGTVKEHC 1040
DB	438 ----- CVCNVLGTVQEH 450
QY	1041 NGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGCGPCNCNAAHSFGPSCNEFT 1100
DB	451 NGSDCHCDKATGQCSCLPNVIGQNCRCAPNTWQLASGTGCGPCNCNAAHSFGPSCNEFT 510
QY	1101 GQCCQMPGFGGRTCSQBELFWGDDPVECRACDPRGIETPCQDQSTGQCCVCEGVEGP 1160
DB	511 GQCCQMPGFGGRTCSQBELFWGDDPVECRACDPRGIETPCQDQSTGQCCVCEGVEGP 570
QY	1161 RCDKTRGVSGVPPDCTPCHQCFALMDAIIIGELTNRTHFLKAKALKISGIVGPIRET 1220
DB	571 RCDKTRGVSGVPPDCTPCHQCFALMDVIIAELTNRTHFLKAKALKISGIVGPIRET 630
QY	1221 DSYEKKVNETKDI LAOSPAAEPLKNTGILFEAEKLTQDTEKMAQVEYKLTDTASQNS 1280
DB	631 DSYEKKVNETKDI LAOSPAAEPLKNTGILFEAEKLTQDTEKMAQVEYKLTDTASQNS 690
QY	1281 TAGELGALQAEBSLDTVKELAEQLEFIKNSDIQGALDSITKYFQMSLEAEKRVNASTT 1340
DB	691 TAGELGALQAEBSLDTVKELAEQLEFIKNSDIQGALDSITKYFQMSLEAEKRVNASTT 750
QY	1341 DPNSTVEOSALTRDVEDLMLERESPFKEQOEQARLLDELAKLOSLSAAAQMTCT 1400
DB	751 EPNSTVEQSAALMTRDVEDVWVERESQFKEQOEQARLLDELAKLOSLSAAAQMTCT 810
QY	1401 PPADCSSEBEGCGPNCRDTDEGKCGGPGCGGLVTVVAHSAWQKAMDFDRDLVSALAEVQ 1460
DB	811 PPADCSSEBEGCGPNCRDTDEGKCGGPGCGGLVTVVAHSAWQKAMDLDDQVLSALAEVQ 870
QY	1461 LSKWVSEAKVRDEAKQNAQDVLKTNATKVKDKNEDLRNLIKQIRPLTDSADLDS 1520
DB	871 LSKWVSEAKVRDEAKQNAQDVLKTNATKVKDKNEDLRNLIKQIRPLTDSADLDS 930
QY	1521 IEAVANEVLKSGNASTPQOLNLTEDIRBETVLSQVEVTLQOSAADIARAELLLBEAKR 1580
DB	931 IEAVANEVLKSGNASTPQOLNLTEDIRBETVLSQVEVTLQOSAADIARAELLLBEAKR 990
QY	1581 ASKATDVKVTADMVKEALEAEKAAQVAAEKAIKQADEDIQGTQNLTLTSEETAASEET 1640
DB	991 ASKATDVKVTADMVKEALEAEKAAQVAAEKAIKQADEDIQGTQNLTLTSEETAASEET 1050
QY	1641 LTNASORISKLERNVELKKAQNSGEAEYTEKVYVSVKQNAADDVKTLTDLGDLDEKYYK 1700
DB	1051 LFNASORISKLERNVELKKAQNSGEAEYTEKVYVSVKQNAADDVKTLTDLGDLDEKYYK 1110
QY	1701 VESLIACKTEESADARRKAEKLLQNEAKTLQAQNSKQLLEDLERKYEDNQKYLEKQAE 1760
DB	1111 VENLIAKTEESADARRKAEKLLQNEAKTLQAQNSKQLLEDLERKYEDNQKYLEKQAE 1170
QY	1761 LVPLEGEVRSLLKDISEKVAVYSTCL 1786
DB	1171 LARLEGEVRSLLKDISEKVAVYSTCL 1196





RESULT 11

US-09-938-275-9  
; Sequence 9, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1798  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P55268  
; DATABASE ENTRY DATE: 1996-10-01  
US-09-938-275-9

Query Match 51.6%; Score 5031.5; DB 9; Length 1798;  
Best Local Similarity 50.4%; Pred. No. 2.6e-276;  
Matches 903; Conservative 313; Mismatches 556; Indels 19; Gaps 9;

QY	1	MGLQVFAFGVLMWTRVCAQEPESVCAEGSCYPATGDLILGKRAOKLSVTSGLHK	60
DB	20	LGILL-----LSVLA--ATLAQAPADVP-CGSRGSCYPATGDLVLRADRLTASCTGLNG	72
QY	61	PPYICVSHLQDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIWMQSENGVEN	120
DB	73	PQYICVSHLQDKKCFICDSRDPFARNDSHRIQNVTSFAPQRRAAWQSENGIPA	132
QY	121	VTIQDLEAEFHTLINTKFRPAALIESSDFGKTMGVYRFAVDCSSPFGISTG	180
DB	133	VTIQDLEAEFHTLINTKFRPAALIESSDFGKTMGVYRFAVDCSSPFGISTG	192
QY	181	PNKKVDIICDSRYSIEPSTGEVIFRALDPAFKIEDPYSRIQNLKITNLRIFVKL	240
DB	193	PPRHWDVVCSEYSIEPSTGEVIVRVLDPALIPDPYSRIQNLKITNLRVNLRL	252
QY	241	HTLGNLLDSRMEIRKYYAVYDMVVRGNCFCYHASECAPVDGNEVEGWHGCMC	300
DB	253	HTLGNLLDPRREIRKYYALYELVVRGNCFCYHASECAPAPAPAHAGMVGACIC	312
QY	301	RHNTKGLNCELWDFYHDLWPAPAGERNACKCNKNEHSSCHFDMVFLATGNVSGG	360
DB	313	KENTRGLNCEQQODFYRDLWPAPAGCHSHARKCECHGTHSCHDFMAYVLASGNVSG	372
QY	361	VCDNCOHNTWGRNCEQCKPFYQHPERDIRDNLCEPCTCDPAGSENGICDGYTDFSVG	420
DB	373	VCDGCOHNTAGRHCELCRPFYRDPFKDLRDPAPVCRSCDCDPMGSDGGRCDSDHDDPALG	432
QY	421	LIAGQCRCKLHVEGERCDVCKGFDLSAEDPYGKSCACNPLGITPGNPNCDSTGYCY	480
DB	433	LVSQCRCKEHVGTTCQQCRDGFGLSISDRIGCRCCNARGIVPGTTPCDPNSGSCY	492
QY	481	CKELVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGLANNSSSEDSGQCSCLPHMIGRC	540
DB	493	CKELVTGGRCDRLCPHWGLSHDILLGCRPCDCLVGGALDPQCDGEGTGQCHCRQHMVGRRC	552
QY	541	NEVESGYFTTLDHYIYEAENLGGVVVVERQYIQDRIPSWTGPGFVRVPEGAYLEFF	600
DB	553	EQVQPGYFPFPLDHLIWEAEDTR-GQVLDVVERLVTPGTPTSGTSGFVRLEGGOTLEFL	611
QY	601	IDNIPYSMEYELIRYEPOLPDHWEKAVITVQRPKIPASSRCGNTPVDDDNQVVSLSFG	660
DB	612	VASVPKAMDYDILLRLERPEQWAELELIVQRPGPVPAHSLCGLHVLVPKDRIQGTLOPH	671

QY	661	SRVVLPRPVCPEKGMNVTVRLELPOYTASGSDVESPYT-----FIDSLVMPYCKSLDIF	716
DB	672	ARYLIFFNPVCLPEPGISYKHLKLYR-TGGSQAQPTPYSGPGLLIDSLVLLPRVLVLEMF	730
QY	717	TVGSGSDGEVTSNAWTFORYRCLENSRSVVTMTDVCNRIIFSISALIHOTGLACECD	776
DB	731	-----SGDAAALERQATPERYQCHEEGLVPSKTSSEACAPILISLTIYNGALPCQCN	786
QY	777	POGSLSSVCDPNGGQCQCRPNVVRFCNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAI	836
DB	787	POGSLSSVCDPNGGQCQCRPNVVRFCNRCAPGTFGFGPNCGKPCDCHLQGSASAFCDAI	846
QY	837	TGCHCFQGIYARQCRCLPGVWGFPSQPCQCNHALDCDVTGBCLSQDYYTTHGNC	896
DB	847	SGQCLRTGAFGLRCRCQCGQMGFPSCPCVCGNHADECNTHTGACLRCDHDTGHEHC	906
QY	897	RCLAGYVGDPLIGSDHCRPCPCPDGSRGPFARSCYQDPVTLQALACVCDPQYIGSRCD	956
DB	907	RCLAGYVGDPLIGSDHCRPCPCPDGSRGPFARSCYQDPVTLQALACVCDPQYIGSRCD	966
QY	957	DCASGFFGNPSDFGSGCQPCQCHHNTDTPDACDKDTCGRCLKCLYHTGHDHQLCYGY	1016
DB	967	ACAPGHGDPDRPGRCQLCECSGNIDPMDPDACDPHTGQCLRLHHTGPHCAHCKPGF	1026
QY	1017	YGALRQDCCKVCNVLTGVEHCNGSD-CHCDKATGQCSCLENVIGONCDRCAPNTWL	1075
DB	1027	HGAAQSCCHRCNLTGNTNPOCPSPDQCHDPSGQCFCLPNVQSPSCDCAPNFWNL	1086
QY	1076	ASGTGCGPCNCNAHSGFSGNEFTQCCQCMFPGGRTCTSECQELFWGPDVCECRACD	1135
DB	1087	TSHGCGPCACHPSRARGPTCNEFTQCHCRAGFGGRTCTSECQELFWGPDVCECRACD	1146
QY	1136	PRGIEPQCDQSTGQCVGVEGPGCDKCTGYSVGFDPCTPCHOCFALWDAIICELTN	1195
DB	1147	SRGIDTPQCHRFTHGSCRCRPGVSGRCDQCARFGSGIFPACHPCHACFGDWRVVDLAA	1206
QY	1196	RTKHFLEKAKALISGVIGPYRETVDVSKVKNVNEIKDIL-AQSPAAEPLKNGILFEEAB	1254
DB	1207	RTQLEBQRAQELQQTGVLGAFESSFWMQBEKLGIVQIVGARNTSAASTAQLVEATEELR	1266
QY	1255	KLTKDVTKEQAQVEVKLTDTASOSNSTAGELGALQAEASLDKTVKELAEQEFKNSDI	1314
DB	1267	REIGEAETHLTLEADLTVDQDENFANHALSGLENDRLALNLTLLQLOHLLKHSNF	1326
QY	1315	QGLDLSITKYFQMSBAEKRVNASTTDPNSTVQSALTDRDVEDLMRESPPFKEQEEQ	1374
DB	1327	LGAYDSIRHAHSQSAEAREPANT-SALAVSPVNSASARHTEALMDAQEDFNSKHMAN	1386
QY	1375	ARLLDELAKLQSLDLSAAQMTCTGTPPGADCSSECGGPNCTDEGEKKCGGPGGGLV	1434
DB	1387	QALGKLSAHTHTLSLTDINELVCGAPGAPCATSPCGGAGCDEDEQPCRCGLSNGAA	1446
QY	1435	TVAHSAQKAMDPRDVLASAEVOLSKMVSEAKVRADEAKQADVLLKTNATKEVD	1494
DB	1447	ATADLALGRARHTQAELOALAEGLSILSRVATRCQASEAQQAALDKANASRGQVE	1506
QY	1495	KSNEDLNLKIQIRNFLTSDSADLSIEAVANVLKSGNASTPQQLONTEDTIRERVETL	1554
DB	1507	QANQELQIOLSVKDFLNQEGADPDSIEMVATRVLSIPASAEQIHLGAGAIAERVSL	1566
QY	1555	SOVEVILQQSAADIAAEILLLEAKSKATDVKTADMVKEALEAEAKQVAAEAKAIK	1614
DB	1567	ADVDAIILARIVGVRRAEQQLQARRARSWAEDEKOKAETVQALAEQAQAGIAIR	1626
QY	1615	QADEDIQCTQNLTSIESEETAETLTNASQIRISKLERNVBELKKAQNSGEAEVIEK	1674
DB	1627	GAVADTRDTETQTLVQVQERWAGAEALSSAGERARQLDALLEALKLRAGNSLAATAEE	1686
QY	1675	VYYSVKONADVKTLTDLGELDEKVKVESLIQKTESADARSKAEKLEONEKTLAQAN	1734
DB	1687	TAGSAQRAQAEALQRLGPDQYQTVKALAERKAQGVLAQAQARAEQRLDEARDLLQAAQ	1746
QY	1735	SKLQLEDLERKYEDNOKYLEDKAEQLVRLGEVRSLLKDISEKVAVYSTC	1785

Db 1747 DKLQRIQLEGTVEENERALESAQAQDGLGEARMRSVLQAINLQVQIYNTC 1799

RESULT 12

US-09-845-583-8

; Sequence 8, Application US/098445583

; Patent No. US20020142954A1

GENERAL INFORMATION:

; APPLICANT: Burgeson, Robert

; APPLICANT: Brunken, William Joseph

; APPLICANT: Champlaud, Marie-France

; APPLICANT: Hunter, Dale

; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF

; FILE REFERENCE: 10287-056001

; CURRENT APPLICATION NUMBER: US/09/845,583

; CURRENT FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: US 60/200,863

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 1798

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-845-583-8

Query Match 50.2%; Score 4902; DB 9; Length 1798;

Best Local Similarity 49.6%; Pred. No. 5.6e-269;

Matches 887; Conservative 308; Mismatches 574; Indels 20; Gaps 8;

Qy	3	LLQVFATGVLALMGTRVCQAQPEFSYCGAEGSCYPATGDLILIGRAQKLSVTSCTGLHKPE	62
Db	23	LLSVLA-----ATLAQAPADVP-GGSRGSCYPATADLLVGRADRLTASSTCGLNGRQ	74
Qy	63	PYCIIVSHLQEDKKCFICDSRDPYTHETLNPDSHLIENVVTTAPNRLKIWQSGENVVT	122
Db	75	PYCIIVSHLQDEKKCFCLDSRPFPGARDNPHFTHRIQNVVTSFAPORRAAWQSQNGIPAVT	134
Qy	123	IQLDLAEAFHETHLIMTKTFRPAAMLTERSDDFGKWTGVVRYFAYDCSESPFGISTGPM	182
Db	135	IQLDLAEAFHETHLIMTKTFRPAAMLVERSGADFGRTWHVTRYFSYHCGADFPVPLAPP	194
Qy	183	KKVDDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPSPRIQNLKLTINLRKFVKLHT	242
Db	195	RHWDDVVCESYSEIEPSTEGEVIVRLDPAIPIPDYSSRIQNLKLTINLRVNLTRLHT	254
Qy	243	LGDNLILDSRMEIREKYIYAVDMVVRGNCFCYGHASECAPVDGVNVEEYGVHGHCMCRH	302
Db	255	LGDNLILDPREIREKYIYALVELVVRGNCFCYGHASECAPAGAPAHAEWVHGACI CKH	314
Qy	303	NTKGLNCELMDPFYHDLPRWPAEGRNSNACKKNCNEHSSSCHFDPMVFLATGNVSGVC	362
Db	315	NTRGLNCEQCQDFYEDLPWRPAEDGSHACRDKDRHGHTHSCHPDMVVLGSGNVSGVC	374
Qy	363	DNCQNTWGRNCEQCKPYFOHPERDIIIDPNLCE3CTCDPAGSENGGICDGYTDFSVGLI	422
Db	375	DGCQNTAWRHCELCRPFYFYRDTFKDLRDPVCRSCDCDPMGSDQGGRCDSHDDPALGLV	434
Qy	423	AGQCRKLVSEGERCDVCKEGPYDLSAEDPYCKSKACNPLGTIPGNGPCDSETCGYCK	482
Db	435	SGQCRKCHVVTRCQCRDGRFFGLISIDPSCRCRCQCNARGTVFSGTFCDENSSGCYCK	494
Qy	483	RLVTRQRCDCQLPQHWGLSNDLDGRCPCDCDILGGALANNSCSDSGQCSCLPHMIQRCNE	542
Db	495	RLVTRGGRDCRCLPFGHWGLSLDLGLCRPCDCDVGVALDPQCDEGTQCHCRQHMVGRRCQ	554
Qy	543	VESGYFFTHLHYIYEAEEANLPGVVVVERQYIQDRIPSWTGPVVRVPEGAYLEFFID	602
Db	555	VQPGYFRPFLDLHWEAENR-GQVLDDVVERLVTGPETPSWTGSGFVRLQEQITLFLVA	613
Qy	603	NIPYSMEYELLIRYBPQLPDHWEKAVITVQRPEKIPASSRCGNTVPDDDNQVVSLSPSGR	662

Qy	1737	LQLLEDLERKYEDNQKYLEDKAQELVRLEGEVRSILKDXISEKVAVSTC	1785
Dd	1749	LQPLOELEGTYEENERALESKAQDCLGLEARMSVLQAINLQVQIYNTC	1797

RESULT 13

```

US-10-369-493-5986
/ Sequence 5986, Application US/10369493
/ Publication No. US2003023675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 5986
/ LENGTH: 1808
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-5986

```

Query Match 38.4%; Score 3742.5; DB 15; Length 1808;  
Best Local Similarity 39.5%; Pred. No. 3e-203;  
Matches 746; Conservative 315; Mismatches 635; Indels 193; Gaps 39;

1	QY	1	MCIIQVFAFGVIALMGTRVCAQEP--BFSYCABGSCYPATGDLIIIGRAQKLVSTVTCGL	58
8	DB	8	LGLL-----LSLLVVFIEAQHPLQONEDCDQRSCTYITGNLLIGRKSQKATSCGS	60
59	QY	59	HKPEPYCIVSHLQEDKKCFICDSRDPYHETLNPD--SHLIENVVTFAPNRLKIWMQSEN	116
61	DB	61	QGRQRCFIVSHLEQTKCFYCDSTEWKQPREPYRLSHRIENVVTEVMDKKNRWQSEN	120
117	QY	117	GVENVTIOLDIEAEHFHLLMTFKTPRPAAMLIERSDFGKTWGVYVPAYDCSSFPQ	176
121	DB	121	GAQNVSISFDEAEHFHLLMTFKSPRPAAMLIERSADFGKTWQVRYFAYDCDSSFPQ	180
177	QY	177	ISTGPMKKVDIIDCSRYSDIEPSTEGEVIFRALDPFAKIEDPYSPIQNLLKITNLRK	236
181	DB	181	IPEGPPKKHTDVICTQYSDVAPSTGSGEIVKVPSHIVTENPYADEISTLLKITNLRN	240
237	QY	237	FVKLHTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASCAPVD--GVNEEVE--	291
241	DB	241	FTKLHTLGDGDLVTRPEIDEKYYIAYIEIVVRSCSCIYHASKCIIDPHVSPNTWERA	300
292	QY	292	GMVGHCMCRNRTKGLNCELCMDFYHDLPRWPAEGRNSACKNCNEHSSCHFDMAVF	351
301	DB	301	DIVHGRCEMENTEGLANCEKCAFYNLPRWPAIGDEKNECRQCNRUALRCHFDRAVY	360
352	QY	352	LATGN-----VSGGVCNCOHNTMGRCNCECKCFYFQHBERDIRDN	393
361	DB	361	ESSGNTSSFSKSPFSKSPGFGVSGGVCDCHMTQGNKECKCFYFVDRPRRTIDDPH	420
394	QY	394	LCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRKLHVEGERCDYCKEGBFYDLSAEDPY	453
421	DB	421	VCLPECCDKAGSQNKGICEGEDAERGLVAGKCYCKTNVDGNCRCDRCKNGYWNLTETNVD	480
454	QY	454	GCKSCACNPLGTIPGNPCPDSCTGYCYKELVTGQRCDCLPOHWGLSNDLDGCRPCDD	513
481	DB	481	GVACTCNLLGTY--NNEGCDKTYGMCTCKRLVTGENCDQCLPHYGLSHVDOGKACDD	539
514	QY	514	LGGALNNSCSDSQSCCLPHMIGRQCNVEGYYFTTLDHYTAEAEANLGFVVYVER	573
540	DB	540	IGGSYDNTCEITIGOCKRCRFGFSRRCEIADSSFYCADITHVYEAVALTRGEVKYRE	599

QY	574	QYQIDRIPSWTGPFRVBPAGALYLBFFIDN--IPYSMEYELIRYE-POLPDHWEKAVIT	630
DB	600	WPSQPEQTFTEGCEFAQAVGTIITV--NPIVEVSQKYNVIIRHDGARDPVGHENIOIT	656
QY	631	VORPEKIPASSRCGNVTYDDDNQVTVLSFGSRIYVLPAPVCEPKGMNTVLEL-----	684
DB	657	VVRP-EARGDSCSDAPPSDDFIARIYIPGSIYIIVQPAICLEAGVQYELSIQNEKRG	715
QY	685	--PQYTAGSDVESPYTFIDSLVLMYPCKSLDIFTVGGSGDGEVNTNSAWETFORYRC--L	740
DB	716	SHPOERAAAN-----ILIDSILLAPPTSELHI FQGSARAEGHLETE-----YNYVQCRHL	764
QY	741	ENSSVVKPTMTDYCRNIPISISALLHQTLACEDPOGSLSSVCDPNDGGOCQCRPNVVG	800
DB	765	ALSLSLFQORNEVCERYCPIAALUNKTSJSCNDATGVSIGICNVGGOCCECKPNVVG	824
QY	801	FTONCARPTGFGPFGCKPCDCHLQGSASAFCDAITQCHCFQ-GIYARQCDRLCPYW	859
DB	825	RRCQCAIGTYGFGPSCKKCDADVSLGNDCKQSGQCVCREBKGIYGRQCNQCPQGF	884
QY	860	GFPSOCPQCNHALDCDVTGECISCDYTHNCESCLAGYGDPIIGSGDHCRCPC	919
DB	895	GFECRTQCNDRHANICDQSSGNACTIECDLTTHYCDRCQDGYGDFPLGVIKFCPCPC	944
QY	920	PDGPDGRQFARSQY---QDPVTLQACVCDPGYIGSRCDDCAGFFGNPSDFGSCQPC	976
DB	945	PGPSTGYQHADTYCLYRNSGNNTQDIVCNCKSGYQGERGCECAQNHMGSPREVGGTCERC	1004
QY	977	QCHNITDTPPEACDKDTGRCILKLYHTBEGDHCOLQGYGYGDALRODCRKCVCNYLGT	1036
DB	1005	DONGNIDWAMEGSCDAATBECILKCLHTEGAQCEHCVDGYGDAKLYTCQRVCVNELG	1063
QY	1037	KEHNGSDCHCDKATQCSCLPNVIGQNCDCRCPNTWOLASGTGCGPCNCA-----	1091
DB	1064	---NSTKGACDRAVSGQCPCHNITIGMQDQCAENHFNLASGACEACGDSNGVNLNHE	1119
QY	1092	FGP--SNCNFTGQCQMPGFGRTGCEGELFWGDPDVE--CRACDCDPRGIETPOCDOS	1147
DB	1120	GVPHLCNIPDQGCQCKPGRGRKCDQCEDLYWGDPTTPDCSCHRCECNPTGSKSLQCH	1179
QY	1148	TQCVCVGEVGBRCDKTRGSGVGPDPCTPCHQCFAWDALIGELNTRTHKELEKAKAL	1207
DB	1180	NGTECQAGSGGALCNECARGYTGOWPYCNPGCEGFHOWDINIMQLOKHVALIDTANNI	1239
QY	1208	KISGVIQFYRETVDSEKVKVNIKIDILAQSPAABPLKNIGILFBEAKLTKDVT-----	1261
DB	1240	EDTGASAYDADPEKMEETLKETK-----KALSDANISKEDIEEMSKLALLKKQV	1290
QY	1262	---EKVAQVEVKLTDTASQSNSTAGELCALQABASLDKTVLAEALQBFINKSDIOGA	1317
DB	1291	IAGREKUGALETISNITQAVDPAQKLEHLQKEVDKVTKATIELEDPKASKIHEADVLGA	1350
QY	1318	LDSITKYFQMSLEAKRVNASTTDPNSTVEOSALTDRVEDMLERESPKEQOEQARL	1377
DB	1351	FNI PRESASKSLDAQRRITDAA-IGKLAANAQAL---RASELLEKNKNDPEKQYVENE	1406
QY	1378	LDE---LAGKLSLDLSAAQNTGTPPGADCSSCECGPNCRDTBGEKKCGCGP---C	1430
DB	1407	LNEAETLLGLESV-LPKLNEQVCG-----ASSAPC-----DALCGPGSGCGFC	1449
QY	1431	GGLVTVAHSQWAKMDFDRDVLASALAEYQLSKMWSEAKVRADEAKQNAQ-----	1483
DB	1450	GG-----QSCME-----GAVSKANQAKSPATEADTLDEKQEAEBVLISVREDVL	1494
QY	1484	LKTWATKEKVDKSN-----DLRNLIKOIRNPLTSDSADLDSIEAVANEVL	1529
DB	1495	TETTKAKAKAYEVAKNTAQRANSRAELDKTAGEIGFPLTAQSSPQIIRNLAEVL	1554
QY	1530	KSGNASTPOOLQNLTEDIRERVETLSQVEVILQOOSAADIARAEULLLEAKRASKSATDVK	1589
DB	1555	GKEISLTPDQITDLTKIKESLAKINIDELINETRGKSIITANLKRASRYANKEALLQ	1614



1590	VTADMVKEALEAEAKQVAAEKAQKQADDEDIQOTQNLLTSIESETAASSETLTNASQRTS	1649
QY		
1615	KAMEEIREALQIADQAYNNVTSYLEBIDTVMQVQARELIDKARNSTEAVEGKAQAANTTIA	1674
DB		
1650	KLENNVEELKRKAQNSGEAEYEKVVYSVKQNAQDVKKTLDGEL-----DEKYKVES	1703
QY		
1675	ELEGVMSGVK-----VEYLQ-----ISESAKVALTVDAALAAANTNAEQGNKQIQT	1720
DB		
1704	-----LIAQKTEBSADARRKAEELIQNEAKTLLAQANSKLQLEDLERKYEDNQKYLE	1756
QY		
1721	DLERATELLEKMEGVNAPQORAEKLRRERAAKLLYQAQRHNDIDINLSK--DSTEMRLDD	1778
DB		
1757	KAQELVRLGEVRSLLKDISEKVAVYSTC	1785
QY		
1779	YETILADLNSRLSERVTRDIEHKTFDHATC	1807
DB		

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RESULT 14
US-10-287-971-18
; Sequence 18, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: CuroseqList version 0.1

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[illegible]

NUMBER OF SEQ ID NOS: 846  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 703  
LENGTH: 527  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (243)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (257)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
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NAME/KEY: SITE  
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NAME/KEY: SITE  
LOCATION: (511)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (519)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Search completed: May 18, 2004, 15:42:38  
Job time : 54.4374 secs

Db 471 -----XENPEXNFLEFXKQLSG-GNLVQVPRASSEFREDV 508  
Qy 1687 KKTLDGEL 1694  
Db 509 GRXLSGKL 516

Query Match 22.1%; Score 2154; DB 12; Length 527;  
Best Local Similarity 79.7%; Pred. No. 6.7e-114;  
Matches 437; Conservative 33; Mismatches 42; Indels 36; Gaps 3;

Qy 1151 CVCVEGVEGPRCDKTRGYSGVFPDTPCHQCFALMDVIAELTNRTHKFLKAKALKIS 1210  
Db 1 CVCVEGVEGPRCDKTRGYSGVFPDTPCHQCFALMDVIAELTNRTHKFLKAKALKIS 60  
Qy 1211 GVIGPYRETVDSEKVKNEIKDILASPAEPLKNGILFEAEKLTVDTEKMAQVEVK 1270  
Db 61 GVIGPYRETVDSEKVKNEIKDILASPAEPLKNGILFEAEKLTVDTEKMAQVEVK 120  
Qy 1271 LPTASQSNSTAGELGALQAEASLDKTVKELAEQLEFIKNSDIQCALDSITKYPQMSLE 1330  
Db 121 LSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYPQMSLE 180  
Qy 1331 AEKRVNASTDPSNTEQSGALTRDVEDLWLERESPFEKQCEQAEQLDELAKQLQSLDL 1390  
Db 181 AEKRVNASTDPSNTEQSGALTRDVEDLWLERESPFEKQCEQAEQLDELAKQLQSLDL 240  
Qy 1391 SAAQNTCTGTPPGADCSSECGGNPCRTDEGKCKGCGPGCGGLTVVAHSAWKAMDFFDR 1450  
Db 241 SAAQNTCTGTPPGADCSSECGGNPCRTDEGKCKGCGPGCGGLTVVAHSAWKAMDFFDR 300  
Qy 1451 VLSALAEVQLSKWSEAKVRADEAKQADVLKTNATKEKVDKSNEDLRNLIKQIRNF 1510  
Db 301 VLSALAEVQLSKWSEAKVRADEAKQADVLKTNATKEKVDKSNEDLRNLIKQIRNF 360  
Qy 1511 LTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEIRERVETLSQVEVILQCSAADIA 1570  
Db 361 LTEDSADLDSIEAVANEVLKSGNASTPQQLQNLTEIRERVETLSQVEVILQCSAADIA 420  
Qy 1571 AEILLBEAKRASKATDVKTADMTKEALBEAEKQVAAEKAKQADEDIQGTQNLTSI 1630  
Db 421 AEILLBEAKRASKATDVKTADMTKEALBEAEKQVAAEKAKQADEDI----- 470  
Qy 1631 ESETAASEETLTWASQRISKLEBNVE- ---ELKRAAQNSEAEYIEKVYVSKQNADDV 1686

Result No.	Score	Query #		Length	DB	ID	Description
		Match	%				
1	9140	93.7	1786	6	US-10-796-280-770		Sequence 770, App
2	5630.5	58.3	1196	6	US-10-841-133-4		Sequence 4, Appli
3	5039.5	51.6	1798	6	US-10-796-307-899		Sequence 899, App
4	5039.5	51.6	1798	6	US-10-796-307-900		Sequence 900, App
5	3610	37.0	1670	1	PCF-USG02-39555A-917		Sequence 917, App
6	1675	17.2	3712	6	US-10-108-605A-103		Sequence 103, App
7	1645	16.9	1573	6	US-10-796-280-1353		Sequence 1353, Ap
8	1645	16.9	1573	6	US-10-796-280-1354		Sequence 1354, Ap
9	1576.5	16.2	3690	6	US-10-796-280-1384		Sequence 1384, Ap
10	1576.5	16.2	3690	7	US-60-568-219-509		Sequence 509, App
11	1569	16.1	3885	1	PCF-USG02-39555A-2483		Sequence 2483, App
12	1567.5	16.1	3690	1	PCF-USG02-22858A-347		Sequence 347, App
13	1567.5	16.1	3717	6	US-10-821-234-1076		Sequence 1076, Ap
14	1555	15.9	2107	6	US-10-796-280-1108		Sequence 1108, Ap
15	1552	15.9	2207	6	US-10-796-307-671		Sequence 671, App
16	1555	15.9	2107	7	US-60-568-219-409		Sequence 409, App
17	1555	15.9	2480	6	US-10-796-280-1106		Sequence 1106, Ap
18	1555	15.9	2480	6	US-10-796-307-669		Sequence 669, App
19	1555	15.9	2480	7	US-60-568-219-407		Sequence 407, App
20	1555	15.9	3116	6	US-10-796-280-1107		Sequence 1107, Ap
21	1555	15.9	3116	6	US-10-796-307-670		Sequence 670, App
22	1555	15.9	3116	7	US-60-568-219-408		Sequence 408, App
23	1511.5	15.5	3714	6	US-10-796-280-1383		Sequence 1383, Ap
24	1511.5	15.5	3714	7	US-60-568-219-503		Sequence 508, App
25	1475	15.1	1165	6	US-10-841-139-2		Sequence 2, Appli
26	1468.5	15.0	1147	6	US-10-841-139-3		Sequence 3, Appli

QY 421 LIAGQCRCKLHVBERCDVCKGFGYDLNADSDPYGCKSCACNPLGTIPGNPCDSETGYCY 480  
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QY 481 CKRLVTGQRCDOCLPQHWGLSNDLDCRCDCLGGLNNSCSDSGQCSCLPHMIGRQC 540  
DB 481 CKRLVTGQRCDOCLPQHWGLSNDLDCRCDCLGGLNNSCSDSGQCSCLPHMIGRQC 540  
QY 541 NEVESGYFTTLDHYLYEAEANLGGVWVVERQYIDRIPSWTGPFGVVRPEGAYLEFF 600  
DB 541 NEVESGYFTTLDHYLYEAEANLGGVWVVERQYIDRIPSWTGPFGVVRPEGAYLEFF 600  
QY 601 IDNIPYSMEYELIRYEPOLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSFG 660  
DB 601 IDNIPYSMEYELIRYEPOLPDHWEKAVITVORPGKIPASSRCNGTVPDDNQVVSLSFG 660  
QY 661 SRYVLPVRCPEKGMNVTUULEPQYTAGSDVRESPTFTDSLVMPCYKSLDIFTVGG 720  
DB 661 SRYVLPVRCPEKGMNVTUULEPQYTAGSDVRESPTFTDSLVMPCYKSLDIFTVGG 720  
QY 721 SGGVYTNAGWETFORRYCLNRSRVVTKPMTDVCNRIIFSALITHOTGLACECDPOGS 780  
DB 721 SGGVYTNAGWETFORRYCLNRSRVVTKPMTDVCNRIIFSALITHOTGLACECDPOGS 780  
QY 781 LSSVCDPNGGQCCRCRPNVVRTCNRCAPGTGFGNGKPCDCHLQGSASAFCDAITQC 840  
DB 781 LSSVCDPNGGQCCRCRPNVVRTCNRCAPGTGFGNGKPCDCHLQGSASAFCDAITQC 840  
QY 841 HCFQGIYAROCCLGPGWGFSCQCCQNGHALDCDTVTGCLSCODYTTGHCNRCCLA 900  
DB 841 HCFQGIYAROCCLGPGWGFSCQCCQNGHALDCDTVTGCLSCODYTTGHCNRCCLA 900  
QY 901 GYVGDPIIGSGDRCPGCPDPSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960  
DB 901 GYVGDPIIGSGDRCPGCPDPSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960  
QY 961 GFTGNSDFGSCQPCQCHNITDTPBEACDKDTGRCCLVHTGDCOLQCYGYGDA 1020  
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DB 1561 LQSAADIAPAEALLIEAEKRAKASATDVKTADMKVEALEEAEKAOVAAEKAIKQADEDI 1620  
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DB 1621 QGTQNLITSIESETAASEETLTNASORISKLERNEVELKRKAAQNSGEAEYIEKVYVSX 1680  
QY 1681 QNADVVKTLDGSLDEKIKYKVESLIIQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740  
DB 1681 QNADVVKTLDGSLDEKIKYKVESLIIQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740  
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DB 1741 EDLERKYEDNQKYLEDKAQELVRLGEVRSLLXDISQKVAVYSTCL 1786

RESULT 2  
US-10-841-139-4  
; Sequence 4, Application US/10841139  
; GENERAL INFORMATION:  
; APPLICANT: Burgess, Robert E.  
; APPLICANT: Wegman, David W.  
; TITLE OF INVENTION: ELK CHAIN OF LAMININ AND METHODS OF USE  
; FILE REFERENCE: 10287/021003  
; CURRENT APPLICATION NUMBER: US/10/841,139  
; CURRENT FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US/10/443,349  
; PRIOR FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/161,872  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 08/735,893  
; PRIOR FILING DATE: 1996-10-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(250)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (438)...(807)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (808)...(840)  
; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (841)...(1196)  
; OTHER INFORMATION: Human B1 chain  
US-10-841-139-4

Query Match 58.3%; Score 5690.5; DB 6; Length 1196;  
Best Local Similarity 63.2%; Pred. No. 2.5e-235;  
Matches 1116; Conservative 46; Mismatches 33; Indels 571; Gaps 2;

QY 22 QEPFYSYGCAGSCVYPATGDLIGRAOKLSVTS-TCGLHKPEPICYVSHLQEDKKCFICD 80  
DB 1 QEPFYSYGCAGSCVYPATGDLIGRAOKLSVTS-TCGLHKPEPICYVSHLQEDKKCFICN 60

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.4366 Seconds

(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-10

Perfect score: 9758

Sequence: 1 MGLQVFAFGVLALWGTRVC.....EVRSLKDISEKVAIVSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9758	100.0	1786	1 MMHUB1	laminin beta-1 cha
2	9144	93.7	1786	1 MMHUB1	laminin beta-1 cha
3	5087.5	52.1	1801	1 MMRTS	laminin beta-2 cha
4	5033.5	51.6	1798	2 S53869	laminin beta-2 cha
5	4970.5	49.9	1797	2 A55677	laminin beta-2 cha
6	3958.5	39.5	1790	1 MMFPB1	laminin beta-1 cha
7	3742.5	38.4	1808	2 T15099	hypothetical prote
8	1751	17.9	3672	2 T23433	hypothetical prote
9	1751	17.9	3704	2 T37316	probable laminin a
10	1704	17.5	1639	1 MMFPB2	laminin gamma-1 ch
11	1675	17.2	3712	2 S18253	laminin alpha-1 ch
12	1647	16.9	1609	1 MMHUB2	laminin gamma-1 ch
13	1645.5	16.9	1557	2 T28811	hypothetical prote
14	1634.5	16.8	1607	1 MMHUB2	laminin gamma-1 ch
15	1584	16.2	3635	2 T10053	laminin alpha 5 ch
16	1575	16.1	303	2 B45067	laminin B1 chain
17	1573.5	16.1	3075	2 S14458	laminin alpha-1 ch
18	1541.5	15.8	1170	2 A53612	laminin B1k chain
19	1524	15.6	3106	1 S53868	laminin alpha-2 ch
20	1520.5	15.6	1168	2 I56985	laminin alpha-1 ch
21	1510	15.5	3084	1 MMHUB2	laminin alpha-1 ch
22	1305.5	13.4	2823	2 T23064	hypothetical prote
23	1305.5	13.4	2823	2 P87908	protein T22A3.8 li
24	1305.5	13.4	3102	2 T43291	laminin alpha cha
25	978.5	10.0	616	2 I38231	S-laminin - human
26	858.5	8.8	1193	2 A44018	laminin B2t chain
27	850.5	8.7	1192	2 S69000	laminin gamma 2 ch
28	685	7.0	606	2 A54665	netrin-1 precursor
29	682.5	7.0	1620	2 T27283	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

MMHUB1  
laminin beta-1 chain precursor mouse  
N:Alternate names: laminin chain  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Feb-1996 #sequence, revision 30-Jun-1991, #text change 10-Dec-1999  
C:Accession: A26413; S02679; S05326; S14877; A02871; S02036; S15543  
R:Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.  
Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987  
A:Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein.  
A:Reference number: A26413; MUID:87147212; PMID:3493487  
A:Accession: A26413  
A:Molecule type: mRNA  
A:Residues: 1-1786 <SAS>  
A:Cross-references: EMBL:M15525; NID:G198700  
A:Note: translation in Genbank has additional 48 residues at the amino end  
R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 257, 453-461, 1988  
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02679  
A:Molecule type: protein  
A:Residues: 28-42/932-946 <FUG>  
R:Hartl, L.; Oberbaumer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A:Title: The N terminus of laminin A chain is homologous to the B chains.  
A:Reference number: S00624; MUID:88225080; PMID:3267223  
A:Accession: S05326  
A:Molecule type: protein  
A:Residues: 457-466/854-868/932-946 <HAR>  
R:Mann, K.; Deutzmann, R.; Timpl, R.  
Eur. J. Biochem. 178, 71-80, 1988  
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th  
A:Reference number: S08895; MUID:89078415; PMID:2462498  
A:Accession: S14877  
A:Molecule type: protein  
A:Residues: 590-620 <MAN>  
R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.  
EMBO J. 3, 2355-2362, 1984  
A:Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a  
A:Reference number: A02870; MUID:85051302; PMID:6209134  
A:Accession: A02871  
A:Molecule type: mRNA  
A:Residues: 1292-1530, MEMP, 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>  
A:Cross-references: EMBL:X05212; NID:G52861; PIDN:CAA28839.1; PID:9809042  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te:  
A:Reference number: S01790; MUID:89030693; PMID:3191157  
A:Accession: S02036  
A:Molecule type: protein  
A:Residues: 1561-1587 <DEU>

MEG56 protein - ra  
hypothetical prote  
heparan sulfate pr  
perlecan precursor  
laminin-related pr  
netrin-2 precursor  
hypothetical prote  
laminin alpha-4 ch  
laminin alpha-2 ch  
notch3 protein - Af  
notch3 protein - h  
laminin B1 chain v  
notch protein - fr  
protein unc-52 [im  
hypothetical prote  
notch homolog - se

30 680 7.0 1574 2 T13954  
31 661.5 6.8 1111 2 T26972  
32 656 6.7 3707 2 S18252  
33 647.5 6.6 4391 2 A38096  
34 617 6.3 612 2 JH0799  
35 608.5 6.2 581 2 B54665  
36 561 5.7 400 2 T46383  
37 560.5 5.7 1816 1 S68960  
38 555.5 5.7 1751 1 MMHUMH  
39 531 5.4 2524 2 A35844  
40 527 5.4 2321 2 S78549  
41 520.5 5.3 188 2 A45067  
42 511.5 5.2 2703 1 A24420  
43 510 5.2 2295 2 C88369  
44 510 5.2 3375 2 T19821  
45 508.5 5.2 2531 2 T31070

R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
EMBO J. 4, 309-316, 1985  
A:Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
A:Reference number: S13543; MUID:85257455; PMID:3848400  
A:Accession: S13543  
A:Molecule type: protein  
A:Residues: 1700-1748, 'N', 1750-1759 <PAU>  
C:Genetics:  
A:Gene: Lamb-1  
A:Map position: 12  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-21/Domain: signal sequence; status predicted <SIG>  
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>  
F:22-270/Domain: VI <DOM5>  
F:271-540/Domain: V <DOM5>  
F:271-332/Domain: laminin-type EGF-like homology <LE01>  
F:335-395/Domain: laminin-type EGF-like homology <LE02>  
F:398-455/Domain: laminin-type EGF-like homology <LE03>  
F:458-507/Domain: laminin-type EGF-like homology <LE04>  
F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:541-772/Domain: IV <DOM4>  
F:773-1182/Domain: III <DOM3>  
F:773-818/Domain: laminin-type EGF-like homology <LE06>  
F:821-864/Domain: laminin-type EGF-like homology <LE07>  
F:867-914/Domain: laminin-type EGF-like homology <LE08>  
F:917-973/Domain: laminin-type EGF-like homology <LE09>  
F:976-1025/Domain: laminin-type EGF-like homology <LE10>  
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>  
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>  
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>  
F:1183-1397/Domain: II <DOM2>  
F:1183-1397/Region: heptad repeats  
F:1398-1430/Domain: alpha <ALP>  
F:1431-1786/Region: heptad repeats  
F:1431-1786/Domain: I <DOM1>  
F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:20-35/Disulfide bonds: #status predicted  
F:120-356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra  
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 9758; DB 1; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLQVFAFGVLAALWGTRVCAQBEFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

DB 1 MGLQVFAFGVLAALWGTRVCAQBEFSGYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

QY 61 PEPYCIVSHLOEDKCKFCDSRDPVHETLNPDSHLIENVTTPAPNRLKIWMQSENGVEN 120

DB 61 PEPYCIVSHLOEDKCKFCDSRDPVHETLNPDSHLIENVTTPAPNRLKIWMQSENGVEN 120

QY 121 VTIQDLAEAFHFLHINTFTFPAAMLIRSSDFOKTWGTRYFAYDCESFPGISGTG 180

DB 121 VTIQDLAEAFHFLHINTFTFPAAMLIRSSDFOKTWGTRYFAYDCESFPGISGTG 180

QY 181 PMKVVDDIICDSRYSDIEPSTGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKL 240

DB 181 PMKVVDDIICDSRYSDIEPSTGEVIFRALDPAPFKIEDPSPRIQNLKITNLRIKFVKL 240

QY 241 HTLGNLLDSMEIREKYIYAVDMVVRGNCFCVGHASECAPVDGVNEEVGVHGHCMC 300

DB 241 HTLGNLLDSMEIREKYIYAVDMVVRGNCFCVGHASECAPVDGVNEEVGVHGHCMC 300

QY 301 RHNTKGLNCELMPFYHDLPMRPAEGRNSNACKKCNHSSCHDFMAVFLATGNVSG 360

DB 301 RHNTKGLNCELMPFYHDLPMRPAEGRNSNACKKCNHSSCHDFMAVFLATGNVSG 360

QY 361 VCDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCBPTCTDPAGSENGGICDGYTDFSVG 420

DB 361 VCDNCOHNTMGRNCEQCKPFYFQHPERDIRDPNLCBPTCTDPAGSENGGICDGYTDFSVG 420

QY 421 LIAGQCRCKLHVEGERCDVCKEGFYDLASARDPYGCKSCACNPLGTIPGGNCPDSEYCY 480

DB 421 LIAGQCRCKLHVEGERCDVCKEGFYDLASARDPYGCKSCACNPLGTIPGGNCPDSEYCY 480

QY 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQSCSLPHMIGROC 540

DB 481 CKRLVTGQRCDQCLPQHWGLSNDLDGCRPCDCLGGALNNSCSEDSGQSCSLPHMIGROC 540

QY 541 NEVESGYFTLTDHYIYEAEANLPGVWVVERQYIQDRIPSWTGTGFRVVRPEGAYLEFF 600

DB 541 NEVESGYFTLTDHYIYEAEANLPGVWVVERQYIQDRIPSWTGTGFRVVRPEGAYLEFF 600

QY 601 IDNTPYSMEYILIRYEPQIPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVLSLSPG 660

DB 601 IDNTPYSMEYILIRYEPQIPDHWEKAVITVORPGKIPASSRCGNTVPDDDNQVLSLSPG 660

QY 661 SRYVVLPRPVCFEKGMNTYVRLLELPQYTAGSDVSESPYTFIDSLVLMPYCKSLDITFVG 720

DB 661 SRYVVLPRPVCFEKGMNTYVRLLELPQYTAGSDVSESPYTFIDSLVLMPYCKSLDITFVG 720

QY 721 SGDEVTNSAWETPQYRCLNERSVVKTPMTDVCNIIIFSIHALIHOTGLACECDPOGS 780

DB 721 SGDEVTNSAWETPQYRCLNERSVVKTPMTDVCNIIIFSIHALIHOTGLACECDPOGS 780

QY 781 LSSVCDPNNGGOCQCRPNVWGTNCRCAPTGFGPNCKPCDCHLOGSASAFCDAITGOC 840

DB 781 LSSVCDPNNGGOCQCRPNVWGTNCRCAPTGFGPNCKPCDCHLOGSASAFCDAITGOC 840

QY 841 HCFGIVARQCDRCLPGYWGFPSCQPCQNGHALDCDVTGECCLSCQDYTTGHNCERCLA 900

DB 841 HCFGIVARQCDRCLPGYWGFPSCQPCQNGHALDCDVTGECCLSCQDYTTGHNCERCLA 900

QY 901 GYGDPIIGSGDHCRCPCPDGSDGQPARSCYQDPVTLQACVCDPGYVIGSRCDCCAS 960

DB 901 GYGDPIIGSGDHCRCPCPDGSDGQPARSCYQDPVTLQACVCDPGYVIGSRCDCCAS 960

QY 961 GFGNPSDFGSCQPCQCHNIIITDPEACDKDTGRKCLVHTTEGHCQLQCYGYGDA 1020

DB 961 GFGNPSDFGSCQPCQCHNIIITDPEACDKDTGRKCLVHTTEGHCQLQCYGYGDA 1020

QY 1021 LRQCRKVCNVLGTVKEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTG 1080

DB 1021 LRQCRKVCNVLGTVKEHCNGSDCHCDKATGQSCCLPNVIGQNCRCAPNTWQLASGTG 1080

QY 1081 CGPCNCAHSGFSCNFTTQCCQCMFPGGRTCSQCQLFWGDDPVECRACDPPRGIE 1140

DB 1081 CGPCNCAHSGFSCNFTTQCCQCMFPGGRTCSQCQLFWGDDPVECRACDPPRGIE 1140

QY 1141 TPQCDQSTGQCVGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDALIGELTNRTHKF 1200

DB 1141 TPQCDQSTGQCVGVEGPRCDKCTRGYSVGFPPDCTPCHQCFALWDALIGELTNRTHKF 1200

QY 1201 LEKAKALKISGVIGPRETVDSVEKKVNEIKOILAQSPAEPKKNIGILFEAEKLTQDV 1260

DB 1201 LEKAKALKISGVIGPRETVDSVEKKVNEIKOILAQSPAEPKKNIGILFEAEKLTQDV 1260

QY 1261 TERMAQVEVKLTDTASQNSSTAGELGALQAEASLDKTVKELAEQLEFKNSDIQGLDS 1320

DB 1261 TERMAQVEVKLTDTASQNSSTAGELGALQAEASLDKTVKELAEQLEFKNSDIQGLDS 1320

QY 1321 ITKYFQMSLEAEKVENASTDNTSTVQSALITRDRVEDIMLRESPPFKEQEQEARLDE 1380

DB 1321 ITKYFQMSLEAEKVENASTDNTSTVQSALITRDRVEDIMLRESPPFKEQEQEARLDE 1380

QY 1381 LAGKLSGLDLSAAAQMTCTGTPGADCSSECCGPNCRITDEGEKKCGGPGCGGLVTVAHSA 1440

DB 1381 LAGKLSGLDLSAAAQMTCTGTPGADCSSECCGPNCRITDEGEKKCGGPGCGGLVTVAHSA 1440

QY 1441 WOKAMPDRDVLALAEVQLSKWYSEAKVRADAKONQDVILKTNATKEKVKDSNEDL 1500

Db 1441 WQAMDFDRVLSALAEVEQLSKVSEAKVRADAEAKQNAQVLLKTNATKEKVDKSNEDL 1500

Qy 1501 RNLIQIENFTEQSDADSDSEAVANEVLSKGNASTPQOLNLTEDIRERVETISQVEVI 1560

Db 1501 RNLIQIENFTEQSDADSDSEAVANEVLSKGNASTPQOLNLTEDIRERVETISQVEVI 1560

Qy 1561 LQQAADIAARAEELLEAEKRAKSKATDVKVVTADVMKEALEBAEKAQVAAEKAIKQADEDI 1620

Db 1561 LQQAADIAARAEELLEAEKRAKSKATDVKVVTADVMKEALEBAEKAQVAAEKAIKQADEDI 1620

Qy 1621 QGTQNLISISSETAASSETLTNASORISKLEFNVVEELKRAAONSGEAEVIEKVVYSVK 1680

Db 1621 QGTQNLISISSETAASSETLTNASORISKLEFNVVEELKRAAONSGEAEVIEKVVYSVK 1680

Qy 1681 QNADVDKTKDGLDEKVKYVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740

Db 1681 QNADVDKTKDGLDEKVKYVESLIAQKTEESADARRKAEELLQNEAKTLLAQANSKLQLL 1740

Qy 1741 EDLERKYEDNQYLEDKAEQELVRLGEVRSLLKDISEKVAVYSTCL 1786

Db 1741 EDLERKYEDNQYLEDKAEQELVRLGEVRSLLKDISEKVAVYSTCL 1786

RESULT 2

MOHUB1

laminin beta-1 chain precursor (human)

N:Alternate names: laminin chain B1

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text\_change 19-Jan-2001

A:Accession: S13547; A28483; A26994; S23566

R:Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.

J. Biol. Chem. 265, 15611-15616, 1990

A:Title: Structure of the human laminin B1 chain gene.

A:Reference number: S13547; PMID:1975589

A:Accession: S13547

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1786 <VUO>

A:Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

A:Note: the nucleotide sequence was submitted to GenBank, February 1991

R:Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sara

J. Biol. Chem. 262, 10454-10462, 1987

A:Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2

A:Reference number: A28483; PMID:87280097; PMID:3611077

A:Accession: A28483

A:Molecule type: mRNA

A:Residues: 1-1786 <PK>

A:Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

R:Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.

Am. J. Hum. Genet. 41, 605-615, 1987

A:Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localization

A:Reference number: A26994; PMID:88021029; PMID:3661559

A:Accession: A26994

A:Molecule type: mRNA

A:Residues: 1278-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>

A:Cross-references: EMBL:M20206; NID:G186914; PIDN:AAA59487.1; PID:G186915

R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkariainen, T.; Tryggvason, K.

In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P

A:Title: Genes for the human laminin B1 and B2 chains.

A:Reference number: S23566

A:Accession: S23566

A:Molecule type: DNA

A:Residues: 762-1786 <VU2>

A:Note: mRNA was also sequenced

C:Genetics:

A:Gene: GDB:LAMB1

A:Cross-references: GDB:119357; OMIM:150240

A:Map position: 7q31.1-7q31.3

A:Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 52

64/3; 1513/1; 1562/2; 1629/3; 1688/3; 1742/1

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F:22-270/Domain: VI <DOM6>

F:271-548/Domain: V <DOM5>

F:271-332/Domain: laminin-type EGF-like homology <LE01>

F:335-395/Domain: laminin-type EGF-like homology <LE02>

F:398-455/Domain: laminin-type EGF-like homology <LE03>

F:458-507/Domain: laminin-type EGF-like homology <LE04>

F:463-468/Region: cell adhesion #status predicted

F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:549-774/Domain: IV <DOM4>

F:662-668/Region: cell adhesion #status predicted

F:773-818/Domain: laminin-type EGF-like homology <LE06>

F:775-1178/Domain: III <DOM3>

F:821-864/Domain: laminin-type EGF-like homology <LE07>

F:857-914/Domain: laminin-type EGF-like homology <LE08>

F:917-973/Domain: laminin-type EGF-like homology <LE09>

F:923-927/Region: cell adhesion #status predicted

F:950-954/Region: cell adhesion #status predicted

F:976-1025/Domain: laminin-type EGF-like homology <LE10>

F:1028-1081/Domain: laminin-type EGF-like homology <LE11>

F:1084-1129/Domain: laminin-type EGF-like homology <LE12>

F:1132-1176/Domain: laminin-type EGF-like homology <LE13>

F:1179-1397/Domain: II <DOM2>

F:1179-1397/Region: heptad repeats

F:1398-1430/Domain: alpha <ALP>

F:1431-1786/Domain: I <DOM1>

F:1431-1786/Region: heptad repeats

F:30-35/Disulfide bonds: #status predicted

F:120-356, 519, 677, 965, 1041, 1195, 1279, 1336, 1343, 1487, 1542, 1643/Binding site: carbohydrate

F:1179, 1182, 1785/Disulfide bonds: interchain #status predicted

Query Match 93.7%; Score 9144; DB 1; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGLLQVAFGVLALWGTTRYCAQEPFESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQVAFGVLALWGTTRYCAQEPFESYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Qy 61 PEPYCVSHLQEDKCFICSDRPYHETLNPSHLIENVTTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCVSHLQEDKCFICNSQDPYHETLNPSHLIENVTTFAPNRLKIWQSENGVEN 120

Qy 121 VTIQLEAEFHFTHLIMTFKTPRAAMLIERSDDFGKTGWVRYPAYDCSSFPGISG 180

Db 121 VTIQLEAEFHFTHLIMTFKTPRAAMLIERSDDFGKTGWVRYPAYDCSSFPGISG 180

Qy 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPIQNLKITNLRKFVKL 240

Db 181 PMKKVDDIIICDSRYSDIEPSTEGEVI FRALDPAFKIEDPYSPIQNLKITNLRKFVKL 240

Qy 241 HTIGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGMVGHGCMC 300

Db 241 HTIGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGVNEEVGMVGHGCMC 300

Qy 301 RHNTKGLNCLCNDMFYHDLFWRPAEGRNSNACKKCNNEHSSCHDFDMAVFLATGNVSGG 360

Db 301 RHNTKGLNCLCNDMFYHDLFWRPAEGRNSNACKKCNNEHSSCHDFDMAVFLATGNVSGG 360

Qy 361 VCDNCQHTWGRNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDPFVG 420

Db 361 VCDNCQHTWGRNCEOCKEYFQHPERDIRDNLCEPCTCDPAGSENGGICDGYTDPFVG 420

Qy 421 LIAGQCRCKLHVSEGERCDVCKEGFYDLASADPVGCKSCACNPLGTIPGGNFCDSSETGYCY 480

Db 421 LIAGQCRCKLHVSEGERCDVCKEGFYDLASADPVGCKSCACNPLGTIPGGNFCDSSETGYCY 480

Qy 481 CKRLVTGQRCDQCLPOHWGLSNLDGCRPCDDDLGGALNNSCSDSGQSCSLPHMIGROC 540

Db 481 CKRLVTGQRCDQCLPOHWGLSNLDGCRPCDDDLGGALNNSCSDSGQSCSLPHMIGROC 540



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QY 541 NVEGSGYFTTLDHYIYEAEEANLGGVWVVERQVHQIDRIPSWTQPGFVRVPEGAYLEFF 600
Db 541 NVEGSGYFTTLDHYIYEAEEANLGGVWVVERQVHQIDRIPSWTQPGFVRVPEGAYLEFF 600
QY 601 INIPIYSMEYELIRYEPOLPHWEKAVITVQRPCKIPASSRCNGNTVPDDNQVVSLSPG 660
Db 601 INIPIYSMEYELIRYEPOLPHWEKAVITVQRPCKIPASSRCNGNTVPDDNQVVSLSPG 660
QY 661 SRYVLPVPRVCEKGNMYTVRLLEPOYTASGSDVESPTFDLSLMPYCKSLDIFTVGG 720
Db 661 SRYVLPVPRVCEKGNMYTVRLLEPOYTASGSDVESPTFDLSLMPYCKSLDIFTVGG 720
QY 721 SGGGEVTSASWETFORRYRCLNSRSVVKTPMTDVCNRIIFSALIHOTGLACEDCPGGS 780
Db 721 SGGGVVTSASWETFORRYRCLNSRSVVKTPMTDVCNRIIFSALIHOTGLACEDCPGGS 780
QY 781 LSSVCDPNNGGQCCQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITQC 840
Db 781 LSSVCDPNNGGQCCQCRPNVVGRTCNRCAPGTGFGPNCKPCDCHLQGSASAFCDAITQC 840
QY 841 HCFQGIYARQCRCPLPGYVGFSCQPCQCHALDCDVTGCLSCQDYTTGHCNRCCL 900
Db 841 HCFQGIYARQCRCPLPGYVGFSCQPCQCHALDCDVTGCLSCQDYTTGHCNRCCL 900
QY 901 GYVGDPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960
Db 901 GYVGDPIIGSDHCRPCPCDGPDSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCAS 960
QY 961 GFGNPSDFGGSCQPCQCHNIDTTPDEACDMDTGRCLKCLYHTGDRCOLQOYGYGDA 1020
Db 961 GFGNPSDFGGSCQPCQCHNIDTTPDEACDMDTGRCLKCLYHTGDRCOLQOYGYGDA 1020
QY 1021 LRQDCKVCNVLGTVEHCNSDCCQCKATQCCCLPLNVIGQNCDCRCAPTNQLASGTG 1080
Db 1021 LRQDCKVCNVLGTVEHCNSDCCQCKATQCCCLPLNVIGQNCDCRCAPTNQLASGTG 1080
QY 1081 CGPCNNAHSGFSCNFTGQCQMPGFGRTCECQBLFGWDPDVECRACDCDPRGIE 1140
Db 1081 CGPCNNAHSGFSCNFTGQCQMPGFGRTCECQBLFGWDPDVECRACDCDPRGIE 1140
QY 1141 TPQCDOSTGOCVCEGVEGPRCDKCTRGVSGVFPDCTPCQCFALWDALIGLNTNRTHKF 1200
Db 1141 TPQCDOSTGOCVCEGVEGPRCDKCTRGVSGVFPDCTPCQCFALWDALIGLNTNRTHKF 1200
QY 1201 LEXAKALKISGVIPYRETVDVSEKKNBIKQILAQSPAEPFKMIGILFEBAEKLTKDV 1260
Db 1201 LEXAKALKISGVIPYRETVDVSEKKNBIKQILAQSPAEPFKMIGILFEBAEKLTKDV 1260
QY 1261 TEKMAQVEVKLDTASQNSSTAGELCALQAEESLDKTVKELAEOLFTKNSDIOGALDS 1320
Db 1261 TEKMAQVEVKLDTASQNSSTAGELCALQAEESLDKTVKELAEOLFTKNSDIOGALDS 1320
QY 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLPREGSPFKQEQEQLLDE 1380
Db 1321 ITKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRVEDLMLPREGSPFKQEQEQLLDE 1380
QY 1381 LAKLQSLDLSAAQMTCTPPCADSECECGPNCTDEGKCKGCGGGLVTVHSA 1440
Db 1381 LAKLQSLDLSAAQMTCTPPCADSECECGPNCTDEGKCKGCGGGLVTVHSA 1440
QY 1441 WQKAMDFDRDLGALAEVEQLSKWSEAKVRADAEAKQADVLTKTATKEKVDKSNEDL 1500
Db 1441 WQKAMDFDRDLGALAEVEQLSKWSEAKVRADAEAKQADVLTKTATKEKVDKSNEDL 1500
QY 1501 RNLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQOLQNTEDIRREVETLSQVEVI 1560
Db 1501 RNLIKQIRNFLTDSADLDSIEAVANEVLKSGNASTPQOLQNTEDIRREVETLSQVEVI 1560
QY 1561 LQOSADIAEAELLLEAKKASATDKVYTDWVKEALEEAEKAQVAEKAQKQADEDI 1620
Db 1561 LQOSADIAEAELLLEAKKASATDKVYTDWVKEALEEAEKAQVAEKAQKQADEDI 1620
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QY 1621 QGTQNLTLTSTESSTAASEETLTNASORISKLRNVEELKRAAQNSEAEYIEKVYSVK 1680
Db 1621 QGTQNLTLTSTESSTAASEETLTNASORISKLRNVEELKRAAQNSEAEYIEKVYSVK 1680
QY 1681 QNADDDVKTLTDLGELDEKYKKVESLIAQKTESADARRKAEELLONEAKTLLAQANSKLQLL 1740
Db 1681 QNADDDVKTLTDLGELDEKYKKVESLIAQKTESADARRKAEELLONEAKTLLAQANSKLQLL 1740
QY 1741 EDLERKYEDNOKYLEDKAOBLVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 EDLERKYEDNOKYLEDKAOBLVRLEGEVRSLLKDISEKVAVYSTCL 1786
QY 1741 KDLERKYEDNOKYLEDKAOBLVRLEGEVRSLLKDISEKVAVYSTCL 1786
Db 1741 KDLERKYEDNOKYLEDKAOBLVRLEGEVRSLLKDISEKVAVYSTCL 1786

RESULT 3
MMRTS
laminin beta-2 chain precursor - rat
N/Alternate names: laminin chain B3; S-laminin
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C/Accession: S03539
R/Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nucleotide 338, 229-234, 1989
A/Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur
A/Reference number: S03539; MUID:89159410; PMID:2922051
A/Accession: S03539
A/Molecule type: mRNA
A/Residues: 1-1801 <HUN>
A/Cross-references: EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G57251
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function: interact with cells and with other basement membrane proteins to promote
A/Description: laminin beta-1 chain; laminin-type EGF-like homology
C/Superfamily: laminin membrane; calcium binding; cell binding; coiled coil; extracellular
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F/36-285/Domain: VI <DOM6>
F/286-555/Domain: V <DOM5>
F/286-347/Domain: laminin-type EGF-like homology <LE01>
F/350-410/Domain: laminin-type EGF-like homology <LE02>
F/413-470/Domain: laminin-type EGF-like homology <LE03>
F/473-522/Domain: laminin-type EGF-like homology <LE04>
F/525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F/556-784/Domain: IV <DOM4>
F/786-831/Domain: laminin-type EGF-like homology <LE06>
F/788-1196/Domain: III <DOM3>
F/834-877/Domain: laminin-type EGF-like homology <LE07>
F/880-927/Domain: laminin-type EGF-like homology <LE08>
F/930-986/Domain: laminin-type EGF-like homology <LE09>
F/989-1038/Domain: laminin-type EGF-like homology <LE10>
F/1041-1095/Domain: laminin-type EGF-like homology <LE11>
F/1098-1143/Domain: laminin-type EGF-like homology <LE12>
F/1146-1190/Domain: laminin-type EGF-like homology <LE13>
F/1197-1412/Domain: II <DOM2>
F/1197-1412/Region: heptad repeats
F/1413-1445/Domain: alpha <ALP>
F/1446-1801/Region: heptad repeats
F/1446-1801/Domain: I <DOM1>
F/45-50/Disulfide bonds: #status predicted
F/251, 371, 1088, 1252, 1311, 1351, 1502/Binding site: carbohydrate (Asn) (covalent) #status p
F/1193, 1196, 1800/Disulfide bonds: interchain #status predicted
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Query Match 52.1%; Score 5087.5; DB 1; Length 1801;
Best Local Similarity 51.2%; Pred. No. 2.8e-188;
Matches 920; Conservative 303; Mismatches 544; Indels 29; Gaps 11;

QY 1 MGLLQVAFGLVWTRVCAQEPFSY-GCAEGSCYPATGDLIGRAQKLSVTSTCGLH 59
Db 23 LGLL-----LSVLA-----ATLAQVPSLDVPGSRGSCYPATGDLVGRADRLTASSTCGLH 74
QY 60 KPEYICVSHLQEDKCFICSDRPYHETLNPSHLINVTTFAPNRLKIWQSENGVE 119
Db 75 SPQPYCIVSHLQEDKCFICSDRPYHETLNPSHLINVTTFAPNRLKIWQSENGVP 134
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QY 120 NVTIQLDLEAFHFFTHLIMTKTPRPAAMLIERSDFGKTVGWVYRYPAYVCESSPFGIST 179  
DB 135 MVTIQLDLEAFHFFTHLIMTKTPRPAAMLIERSADFGRTWRVYRYSYDCGADFPGL 194  
QY 180 GPMKKVDIICDSYSDIEBSTEVEIFRALDPFAFKIEDPVSRIQNLKLTINRIKFKV 239  
DB 195 APPRRWDVVCESYRISEIPESTEVEIYRVLPDPAIPDPYSSRIQNLKLTINRVNLT 254  
QY 240 LHTLGDNLLDSRMBIREIKYIYAVYVMVYVGNCFYGHASECAPVDGVNEBEVGMVGHCM 299  
DB 255 LHTLGDNLLDPREIREIKYIYALVELVIRGNCFYGHASCAPAPGAPAHAEVGMVHGACI 314  
QY 300 CRHNTKGLNCELNDWFYHDLPRWPAEGRNSNACKCNHSHSSCHDFMAVELATGNVSG 359  
DB 315 CXHNRGLNCEQCQDFYODLPHWPAEAGHTHACRKCNCNGHSHSCHDFMAVILASGNVSG 374  
QY 360 GVCNCOHNTWGRNCEOCKPFYFQHPBRDIRDPNLCBPFCTCDPAGSNGGICDGYTDFSV 419  
DB 375 GVCDCQHTAGRHCELCRPFYRDPDKMDRPAACRCDPDMGSDGCRCDSHDDPVL 434  
QY 420 GLIAGCRCKLVHGERCDVCKEGFYDLSABDPYCKSCACNPLGTTPGNGPCDSETGYC 479  
DB 435 GLVSGQCRKEHVVTGTCQCRDGFGLGSANPRGCRQCNSRGTVPGGTPCDSSSGTC 494  
QY 480 YCKELVTGORCQCLPQHWGLSNDLDGCRPCDCLGGALANSCSEDSGQCSCLPFHMIGRQ 539  
DB 495 FCKELVTGDCDRCLPQHWGLSHLLGCRPCDCLVGGALDPQCDDEATGQCFRPHMIGRR 554  
QY 540 CNEVESGYFTTLHYIYEAEEANLPGVWVVERQYIQDRIPSWTGPFGFVRPEGAYLEF 599  
DB 555 CEQVQPGYFRPFLDHLTWAEAGAH-GQVLEVERLVNRETPTSGTGVFRLREGQVEF 613  
QY 600 FIDNIPYMEVEILIRBEPOLPHEWAKAVIYVQPPGKIPASSRCGNVTVPDDNQVSLSP 659  
DB 614 LVTSLPRANDLILLRWEQVPEQWAELELVQPPGVPVSAHSPGCHVLPDRDRIQNLHP 673  
QY 660 GSRVYVLPVPFCFKGMNVTYRLBEPQVTAGSVDSESYT-----FIDSLVLMYPCKSLDI 715  
DB 674 NTRVLVFRPVCLEPGLSYKLKLTG-TGGRAPETPYSGSGILIDSLVLQPHVLMLEM 732  
QY 716 FTVGSGDGEVNTSNWETFORVYRCLNSRSYVTKPTMDVCFNIIFSIHALIHTGLACEC 775  
DB 733 F-----SGDDAALERTTFERYRCHIEGLMPSKTPLEACVPLISASSLYVNGALPCQC 788  
QY 776 DPQSLSSVCDPNNGQCCQCRNVYVGRTCNRCAPGTGFGNGKPCDCHLQGSASAFCD 835  
DB 789 DPQSLSECNPHGQCRCKPGVVGRRCDACATGYGFGPAGCQACQCSPDGALSALCEG 848  
QY 836 ITGQCHCFQGIYARQCDRLCYHNGFSPSCQCNCHALDCDVTYGECLSCQDYTTGHCN 895  
DB 849 TSGQCLRTGAFGLRCDHCQCGQWGFNCRPCVNCNGRAECDANTGACLCRDYTGGEHC 908  
QY 896 ERCLAGYGDPIIGSGDHCRCPCPCPDGSDGRQFARSYQDPVTLQALACVCDPFIYIGSRC 955  
DB 909 ERCTAGFHGDPRLPVGGQCRPCPCPEPGFSQRHPATSCHRDGYSQIVCHCRAGYTLGRC 968  
QY 956 DDCASGFTGNFSDPGSGSQPCQCHNIDTTPPEACDKDTGELCKLXYHTEGDHCQLCYG 1015  
DB 969 EACAPGHGFDPSKPGRCQLCECSGNTDPTDPGACDPHTQOCRLHHTGPHGCHGCKPG 1028  
QY 1016 YVGDALRODCRKCVCNVLGVTKHNGSD-CHCDKATGQCSCLPNVIGQNCDCRCAPNTWQ 1074  
DB 1029 PHGQAARSCHRCTNLLGTDPQRCPSIDLCHCDPSTGQCPCLPHVQGLSCDRCAPNFN 1088  
QY 1075 LASGTGCGPCNCAHSPGSCNFTGQCQCMFPGGRTGSECELFWGDPDVECRACDC 1134  
DB 1089 FTSGRGQCFACHPFSRARGPTCNFTGQCHCHAGFGGRTGSECELHWGDPGLQCRACDC 1148  
QY 1135 DPRGLETQCDQSTGQCVGVGVGPRCDKTRGVSGVFPDCTECHOCFALWDIAIGELT 1194  
DB 1149 DPRGIDKFCQHRSTGHCSCRFVGVGVRCDCQCARFGSGVFPACHCHACFGDWRVQDLA 1208  
QY 1195 NRTHKFLKAKALKISGVIGPYRETVDSEVKKVNEIKDLA--QSPAAPLEPLKNIGILFEE 1252

DB 1209 ATRRLQMAQLOQTGVIGAFESFLNLOKLGWQVIAVARTSAATAK----LVEA 1264  
QY 1253 AEKLTADV---TERMAQVEVKLTDTDSQSNSTAGELGALQAEASLDTKTVKELAEQLFI 1309  
DB 1265 TEGLRHEIGTKTTERLTQLEAELTDVODENFANHALSGLERDGLNALNLTLRLQDLHL 1324  
QY 1310 KNSDTQCALDSTTKYFQMSLEAEKRVNASTTDPNSTVEQSALTDRDVEDLMLRESPFKE 1369  
DB 1325 KHSNFLGAYDSIRHAHSQSTAEERANASTTFAIPSPVNSADTRRRAEVLMAQRENNR 1384  
QY 1370 QOEEOARLIDELAGLQSLDLSAAQMTCTGPPGACDSESECGGNCRTDEGEKCKGPG 1429  
DB 1385 QHLNQALGRLSLTHHTLSLTGVNELVCGAPDAPCATSPCGGACRDEDDGPRCGGLG 1444  
QY 1430 CGGLVTVAHSAWKMDRDRVLSALAEVEQLSKMWSEAKVRADAEAKQNAQDVLTKTNT 1489  
DB 1445 CSGAATADLALGRARHTQAELORALVEGGGLSVSETRQAEAEQAQQAALDKANAS 1504  
QY 1490 KSKVKSNEIDLNLKQIRNFLETSDADLSIEAVANVLKSGNASTPQQQLNLTEDIRE 1549  
DB 1505 RCQVEQANQELRELLQNVKDFLSQSGADPDSIEMVATRVLDISIPASPEQIQLASEIAE 1564  
QY 1550 RVETLSQVEVILQOASADIARAELLEBAKRAKSKATDVKTADVMVKEALBEAEKAQVAA 1609  
DB 1565 RVSLADVDLTILAHMTGVDVRRAEQLQDAORARSAGEERQKAETVQAALEBAQQAQAA 1624  
QY 1610 EKAIQOADDIQTGNLTSTIESETAASEETLTASORISKLRNVEELKKAQNSGEA 1669  
DB 1625 QSAIRGAVVDYTKNTTQTLQOVQERNAGTEQSLNSASERQHLHALLKLRAGNSLAA 1684  
QY 1670 EYIEKVYSVKQNDVKKTLDELDEKIKVKSIESLIAKTESADARKKAEELQNEAKTL 1729  
DB 1685 STAEETAGSAQSRAREAEKQLREQVGQDYQTVFALAERKAEGVLAQAQARAEQLRDEARGL 1744  
QY 1730 LAQANSKLLEDLEKVEDNOKYLEDKAQELVLEGEVRSLLKDISEKVAVYSTC 1785  
DB 1745 LQAQDKLQRLQELGTEENRELEVAQDLGLEARNVSRVLQAINLOVQIYNTC 1800

RESULT 4  
S53869  
laminin beta-2 chain precursor (version 2) - human  
N/Alternate names: s-laminin  
C/Species: Homo sapiens (man)  
C/Date: 27-Oct-1995 #sequence\_revision 23-Feb-1996 #text\_change 24-Sep-1998  
C/Accession: S53869  
R/Rivanaainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Tryggv  
Matrix Biol. 14, 489-497, 1994  
A/Ritle: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss  
A/Reference number: S53869  
A/Accession: S53869  
A/Molecule type: mRNA  
A/Residues: 1-1798 <11v>  
C/Genetics:  
A/Gene: GDB:LAMB2  
A/Cross-references: GDB:132363; OMIM:150325  
A/Map position: 3p21.3-3p21.2  
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C/Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F/1-32/Domain: signal sequence #status predicted <SIG>  
F/33-1798/Product: laminin beta-2 chain #status predicted <MAT>  
F/283-344/Domain: laminin-type EGF-like homology <LE01>  
F/347-407/Domain: laminin-type EGF-like homology <LE02>  
F/410-467/Domain: laminin-type EGF-like homology <LE03>  
F/470-519/Domain: laminin-type EGF-like homology <LE04>  
F/522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F/783-874/Domain: laminin-type EGF-like homology <LE06>  
F/877-924/Domain: laminin-type EGF-like homology <LE07>  
F/927-983/Domain: laminin-type EGF-like homology <LE08>  
F/986-1035/Domain: laminin-type EGF-like homology <LE10>  
F/1038-1092/Domain: laminin-type EGF-like homology <LE11>

F.1095-1140/Domain: laminin-type EGF-like homology <LE12>  
F.1143-1187/Domain: laminin-type EGF-like homology <LE13>

Query Match		51.6%	Score 5033.5	DB 2	Length 1798
Best Local Similarity		50.4%	Pred. No. 3.3e-186		
Matches 903		Conservative 313	Mismatches 556	Indels 19	Gaps 9
QY	1	MGLLVFAFGVLA	WTRVCAQEP	EFYSGCAGSGSCYPATG	LLIGRAQKLSVTSCGLHK 60
Db	20	LGLL-----LSVLA--	ATLAQAPADVP	-GCSRGSCYPATG	LLVGRADRLTASCTGLNG 72
QY	61	PEYCTIVSHLODKKCF	CDSDPDYHETLNPDSHLI	ENVTTFAPNRLKI	WQSENGVEN 120
Db	73	POPYCTIVSHLODKKCF	CDSDRPFASDNPDSHRI	QNVVTSFAPQRAA	WQSENGIPA 132
QY	121	VTIQDLLEAEFFH	THLIMTKFRAALMI	ERSDFGKTGWYRYFAYD	CESSPFGISTG 180
Db	133	VTIQDLLEAEFFH	THLIMTKFRAALMI	ERSADFGTWHYRYSF	DCGADPGVPLA 192
QY	181	PMKVDDIICD	SYSDIEPSTSEGEVIF	RALDPAFKIEDPYSP	RIQNLKINLRIKFKVL 240
Db	193	PPRHWDVVCES	RYSEIEPSTSEGEVIR	YVLDPAIPDPYSSRI	QNLKINLRIKFKVL 252
QY	241	HTLGNLDSRWEIR	EKKYAYVDMVVRGNC	FCYGHASECAPDVG	NEEVMGHGCMC 300
Db	253	HTLGNLDSRWEIR	EKKYAYVDMVVRGNC	FCYGHASECAPD	PAHAEGWVGACIC 312
QY	301	RHNTGLNCEL	CMDFYHDLWPAEGR	NSNACKCNKNEHSS	CHFDMAVFLATGNVSGG 360
Db	313	KHNTGLNCE	QCQDFYRDLWPAEGR	NSNACKCNKNEHSS	CHFDMAVFLATGNVSGG 372
QY	361	VDNCCHNTNRC	CECKFPYQHPERD	IRDNLCPECTCDP	AGSENGICDGYTDFSVG 420
Db	373	VDNCCHNTNRC	CECKFPYQHPERD	IRDNLCPECTCDP	AGSENGICDGYTDFSVG 432
QY	421	LIAGQCRKLV	HEGRCDCVKGFGY	DLSAEDPYGCKSCA	CNPLGTIPGPNCDSTGYCY 480
Db	433	LVSGQCRKEH	VVGTACQCRDQGF	GLSISDLRCRCQ	CNARGTVPGSTPCDPSNGCY 492
QY	481	CKRLVTGQRC	QDCLPOHNGLSNDL	DCRCDCDLOGALNS	SEDSGCSCPLPMIGRQC 540
Db	493	CKRLVTGQRC	QDCLPOHNGLSNDL	DCRCDCDLOGALNS	SEDSGCSCPLPMIGRQC 552
QY	541	NEVESGYFT	LDHYIYEAEANL	PGVVVERQYIQRIP	PSMTGPFVVRPEGAYLEFF 600
Db	553	EQVQPGYFR	FDLHLWEADTR	-GOVLDVVERLYTP	GTPTSGFVRLQEGQTLLEFL 611
QY	601	IDNIPYMEY	ELIRYEPQLPDHWEK	AVITVORPGKIPAS	RCGNVTVPDDDNQVLSLSPG 660
Db	612	VASVPKAMDY	DLRLLEPQVPEQW	AELELIVORPGVPS	LCHLVPKDDRIQSTLOPH 671
QY	661	SRVVLPRVC	FEKGMNVTVRLLEP	YVLTASGSDVESPYT	---FIDSLVLMFYCKSLDIF 716
Db	672	ARYLIIFNP	VLPEPGLSYKHLK	LVTR-TGSAQPE	TPYSGPGLLIDSLVLLPRVLVLEMF 730
QY	717	TVGGSGDGE	VNTSAWETFOR	RYRCLENSRVVVT	PMTPMTDVCNRIIFISALIHOTGLACBCD 776
Db	731	-----SGD	AAALBRQATFERY	QCHEEGLVPSKT	SPSEACAPLLISLTLYNGALPCQCN 786
QY	777	PQGLSVSD	CNPGQCCRNVTG	RCNRCAPGTFG	PGNGKPCDCHLQGSASAFCDAI 836
Db	787	PQGLSVSD	CNPGQCCRNVTG	RCNRCAPGTFG	PGNGKPCDCHLQGSASAFCDAI 846
QY	837	TGCHCFQGI	YARQCRCLP	SYGWFPSQPCQ	CNGHALDCTVTGBCLSQDYTTGHNCE 896
Db	847	SGQCLCHT	GAFLRCRDCR	QCGQGFPS	CRPCVCNCHADECNHTGACLCGRDHTGGEHC 906
QY	897	RLAGYGGDI	IGSDHCRCP	CDGDSGRQ	RSQRCYDPTVLQACVCDPGYISGRC 956
Db	907	RTAGFGDP	RLPYGGQRC	PCPCPEGPG	SGRHHFATSCHQDEYSQQIVCHCRAGYGLRCE 966
QY	957	DCASGFG	FNPSDFGSG	QPCQCHNID	ITDTPACDXTGRCLKCLYHTEGDHCOLQCYQY 1016

967	ACAPGHFG	DFSRPGR	QCQCESG	NIDPMDP	DACDPHTG	QCQLRCLLHHT	EGPHCAKCPG	1026		
Db										
QY	1017	YGDLRQDC	RKVCYNYL	GTVKEH	CNGSD-CH	CDKATG	QCSCLPNV	IGQNCDCRCAPNTWOL 1075		
Db	1027	HGAARQS	CHRCTCN	LLGTPNQ	CPSPDQ	CHDCHD	CPSPGQ	CPCLPNVQGPS	CDRCAPFWNL 1086	
QY	1076	ASTGCGPC	NCNAH	SFGPSC	NEFTG	COCOCM	PFGRT	CSECELF	FWGDPDVECRACD	1135
Db	1087	TSGHGQ	PCPACH	PSRARG	PTCNEFT	QCCHCR	AGFGRT	CSECELF	FWGDPG	1146
QY	1136	PRGIET	PQDQST	GCQCV	GVGEG	PRCDK	CTRGYS	VFPDCT	PCCHQCFALMDAI	1195
Db	1147	SRGIDT	POCHRF	FTGH	CSRC	PGV	VRCDQ	CAFAFS	GIFPACHPC	1206
QY	1196	RTHKFL	EKA	KALIS	GVIP	RETVD	SVKNE	KDIL-AQ	SPAAEPLKNIGIL	1254
Db	1207	RTORLE	QRQAEL	QOQT	VLGAF	ESSFW	HQEKIG	IVQGVIG	ARNTSAASTAQL	1266
QY	1255	KLTKDVT	EMAQ	QVEVKL	TDITAS	OSNST	AGELQA	EAESLD	KTVKELAEQLEFI	1314
Db	1267	REIGATE	HLTQ	LEADL	TDVOD	ENFN	HALSGL	ERDLAL	NLTQLQDHL	1326
QY	1315	QGALD	ITIKY	FQMS	BAEK	VNA	STTDP	MSVQS	ALTDRVEDLML	1374
Db	1327	LGAYDS	IRHA	QS	AEARR	ANTS	SALAV	SPVSN	SASARHRTALMDA	1386
QY	1375	ARLLDEL	AGKLQ	SLD	LSAA	QMT	CGTP	PGAD	CSECECGGPNCR	1434
Db	1387	QRALGK	USANTH	SLT	LDNEL	VC	GPAP	PCATSP	CGGAGC	1446
QY	1435	TVASHA	QKAMD	FRD	VL	SALAE	VEQLSK	WSEAK	VRABEAK	1494
Db	1447	ATADL	ALGRAR	HTQ	AE	QALAE	GGSTLS	SRVAT	REQA	1506
QY	1495	KSNE	DLNLK	IQ	RN	FL	TEDS	ADLDSI	EA	1554
Db	1507	QANQEL	Q	EL	Q	SVK	DFLN	QEGAD	PD	1566
QY	1555	SQVE	IL	Q	Q	SAAD	IA	RAEL	LE	1614
Db	1567	ADVD	AILART	VG	DV	RAEQ	LLQD	ARBAR	SWAE	1626
QY	1615	QABED	IOGT	QNL	LT	ST	ET	SE	TA	1674
Db	1627	GAVAD	TRD	T	ET	LYQ	VOER	MAGAR	AL	1686
QY	1675	VVSVK	Q	NA	DDV	KRT	LDG	EL	DE	1734
Db	1687	TAGS	AQ	RA	Q	AE	Q	ELL	RG	1746
QY	1735	SKLQ	LED	ER	KY	ED	NK	YLED	KA	1785
Db	1747	DKLQ	R	LE	GT	ET	Y	E	N	1797

RESULT 5

A:Species: Homo sapiens (man)  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 17-Mar-1999  
C:Accession: A55677  
R:Wewer, U.M.; Gerecke, D.R.; Durkin, M.B.; Kurtz, K.S.; Mattei, M.G.; Champlaud, M.F.;  
Genomics 24, 243-252, 1994  
A:Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca.  
A:Reference number: A55677; MUID:95213013; PMID:7698745  
A:Accession: A55677  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1797 <MEW>  
A:Cross-references: GB:X79683  
C:Genetics:  
A:Gene: GDB:LAMB2  
A:Cross-references: GDB:132363; OMIM:150325

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.4366 Seconds  
(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-6  
Perfect score: 9754  
Sequence: 1 MGILLQLAFSLFCARVR.....EVRLLKDISQKAVYSTCL 1786

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9754	100.0	1786	1 MMHUB1	laminin beta-1 cha
2	9144	93.7	1786	1 MMHUB1	laminin beta-1 cha
3	5088.5	52.2	1801	1 MWRP2	laminin beta-2 cha
4	5054.5	51.8	1798	2 S53869	laminin beta-2 cha
5	4888	50.1	1797	2 A55677	laminin beta-2 cha
6	3846	39.4	1790	1 MMHUB1	laminin beta-1 cha
7	3772.5	38.7	1808	2 T15099	hypothetical prote
8	1758.5	18.0	1639	1 MMHUB1	laminin gamma-1 ch
9	1729.5	17.7	3672	2 T23433	hypothetical prote
10	1485.5	15.2	1786	2 T23433	probable laminin a
11	1396.5	14.4	1557	2 T28811	hypothetical prote
12	1676.5	17.2	1609	1 MMHUB1	laminin gamma-1 ch
13	1658	17.0	1607	1 MMHUB1	laminin gamma-1 ch
14	1645.5	16.9	3712	2 S18253	laminin alpha-1 ch
15	1605	16.5	3635	2 T10053	laminin alpha 5 ch
16	1583	16.2	303	2 B45067	laminin B1 chain -
17	1543.5	15.8	1170	2 A53612	laminin B1 chain
18	1539	15.8	3106	1 S53868	laminin alpha-2 ch
19	1529.5	15.7	3075	2 S14458	laminin alpha-1 ch
20	1510	15.5	3084	1 MMHUB1	laminin alpha-1 ch
21	1485.5	15.2	1168	2 T56985	kalinin B1 - mouse
22	1307.5	13.4	2823	2 T23064	hypothetical prote
23	1307.5	13.4	2823	2 F87908	protein T22A3.8 (i
24	1307.5	13.4	3102	2 T43291	laminin alpha cha
25	1001.5	10.3	616	2 T38231	S-laminin - human
26	871	8.9	1193	2 A44018	laminin B2t chain
27	862.5	8.8	1192	2 S69000	laminin gamma 2 ch
28	692	7.1	606	2 A54665	netrin-1 precursor
29	679	7.0	1620	2 T27283	hypothetical prote

30	669.5	6.9	1574	2 T13954	MEGF6 protein - ra
31	666	6.8	3707	2 S18252	heparan sulfate pr
32	663.5	6.8	1111	2 T26972	hypothetical prote
33	657	6.7	4391	2 A38096	perlecan precursor
34	608	6.2	581	2 B54665	netrin-2 precursor
35	580.5	6.0	1816	1 S68960	laminin alpha-4 ch
36	579	5.9	612	2 JH0799	laminin-related pr
37	577.5	5.9	1751	1 MMHUB1	laminin alpha-2 ch
38	568	5.8	400	2 T46383	hypothetical prote
39	527	5.4	2555	2 A40043	notch protein homo
40	526	5.4	2295	2 C88369	protein unc-52 (im
41	526	5.4	3375	2 T19821	hypothetical prote
42	523	5.4	1160	2 F88369	protein unc-52 (im
43	511	5.2	198	2 A45067	laminin B1 chain v
44	509	5.2	2524	2 A35844	notch protein - Af
45	506.5	5.2	2703	1 A24420	notch protein - fr

ALIGNMENTS

RESULT 1  
MMHUB1  
laminin beta-1 chain precursor - human  
N:Alternate names: laminin chain B1  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text\_change 19-Jan-2001  
C:Accession: S13547; A28483; A26994; S23566  
R:Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.  
J-Biol-Chem. 265, 15611-15616, 1990  
A>Title: Structure of the human laminin B1 chain gene.  
A:Reference number: S13547; MUID:90368768; PMID:1975589  
A:Accession: S13547  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1786 <VUO>  
A:Cross-references: GB:M61951; GB:J02778; NID:gl86911; PIDN:AAAS9486.1; PID:gl86913  
A>Note: The nucleotide sequence was submitted to GenBank, February 1991  
R:Pikkariainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sars  
J-Biol-Chem. 262, 10454-10462, 1987  
A>Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2  
A:Reference number: A28483; MUID:87280097; PMID:3611077  
A:Accession: A28483  
A:Molecule type: mRNA  
A:Residues: 1-1786 <PIK>  
A:Cross-references: GB:M61951; GB:J02778; NID:gl86911; PIDN:AAAS9486.1; PID:gl86913  
R:Jay, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.  
Am J Hum Genet. 41, 605-615, 1987  
A>Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localizat  
A:Reference number: A26994; MUID:88021029; PMID:3661559  
A:Accession: A26994  
A:Molecule type: mRNA  
A:Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>  
A:Cross-references: EMBL:M20206; NID:gl86914; PIDN:AAAS9487.1; PID:gl86915  
R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkariainen, T.; Tryggvason, K.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P  
A>Title: Genes for the human laminin B1 and B2 chains.  
A:Reference number: S23566  
A:Accession: S23566  
A:Molecule type: DNA  
A:Residues: 762-1786 <VU2>  
A>Note: mRNA was also sequenced  
C:Genetics:  
A:Gene: GDB:LAMB1  
A:Cross-references: GDB:119357; OMIM:150240  
A:Map position: 7q31.1-7q31.3  
A:Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 457/1; 494/3; 52  
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type BGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-21/Domain: signal sequence #status predicted <SIG>		
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>		
F:22-270/Domain: VI <DOM5>		
F:271-548/Domain: V <DOM5>		
F:271-332/Domain: laminin-type EGF-like homology <LE01>		
F:335-395/Domain: laminin-type EGF-like homology <LE02>		
F:398-455/Domain: laminin-type EGF-like homology <LE03>		
F:458-507/Domain: laminin-type EGF-like homology <LE04>		
F:468-468/Region: cell adhesion #status predicted		
F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>		
F:549-774/Domain: IV <DOM4>		
F:662-668/Region: cell adhesion #status predicted		
F:773-818/Domain: laminin-type EGF-like homology <LE06>		
F:775-1178/Domain: III <DOM3>		
F:821-864/Domain: laminin-type EGF-like homology <LE07>		
F:867-914/Domain: laminin-type EGF-like homology <LE08>		
F:917-973/Domain: laminin-type EGF-like homology <LE09>		
F:923-927/Region: cell adhesion #status predicted		
F:950-954/Region: cell adhesion #status predicted		
F:976-1025/Domain: laminin-type EGF-like homology <LE10>		
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>		
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>		
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>		
F:1179-1397/Domain: II <DOM2>		
F:1179-1397/Region: heptad repeats		
F:1398-1430/Domain: alpha <ALP>		
F:1431-1786/Domain: I <DOM1>		
F:1431-1786/Region: heptad repeats		
F:30-35/Disulfide bonds: #status predicted		
F:120,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate		
F:1179,1182,1785/Disulfide bonds: interchain #status predicted		
Query Match	100.0%; Score 9754; DB 1; Length 1786;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1786; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGLIQLAFSLALCARVRAQAEPEFSGYGAEGSCYPATGDLIGRAQKLSVTSTGLHK	60
Db	1 MGLIQLAFSLALCARVRAQAEPEFSGYGAEGSCYPATGDLIGRAQKLSVTSTGLHK	60
Qy	61 PEPYCVIYSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTPAPNLKIWMQSENGVEN	120
Db	61 PEPYCVIYSHLQEDKKCFICNSQDPYHETLNPDSHLIENVTTPAPNLKIWMQSENGVEN	120
Qy	121 VTIOQLDEAPHFHLMFTKTPAPAMLIERSDFPKTWGVYRYPAYDCEASFPGISTG	180
Db	121 VTIOQLDEAPHFHLMFTKTPAPAMLIERSDFPKTWGVYRYPAYDCEASFPGISTG	180
Qy	181 PMKVVDDIICDSRYSDIEPSTEGEVIIPALDPAPFKIEDPSPRIQNLKITNLRIKPVKL	240
Db	181 PMKVVDDIICDSRYSDIEPSTEGEVIIPALDPAPFKIEDPSPRIQNLKITNLRIKPVKL	240
Qy	241 HTLGNLLDSRMEIREKYIYAYDMVYRGNCFCYGHASECAPVDGFNEEVEGMVHGHC	300
Db	241 HTLGNLLDSRMEIREKYIYAYDMVYRGNCFCYGHASECAPVDGFNEEVEGMVHGHC	300
Qy	301 RHNTKGLNCELMDYHDLPHRPAEGNSNACKKNCNEHSISCHFDMAVYLATGNVSGG	360
Db	301 RHNTKGLNCELMDYHDLPHRPAEGNSNACKKNCNEHSISCHFDMAVYLATGNVSGG	360
Qy	361 VCDCCQNTMGRNCEQCKPFYIYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTG	420
Db	361 VCDCCQNTMGRNCEQCKPFYIYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDSTG	420
Qy	421 LIAQCRCRLNVEGEHCDVCKEGYDLSSEDPFCCKSCACNPLGTIPGGNFCDSYTGHCY	480
Db	421 LIAQCRCRLNVEGEHCDVCKEGYDLSSEDPFCCKSCACNPLGTIPGGNFCDSYTGHCY	480
Qy	481 CKRLVTGQHCQCLPEHWNGLSNDLDCRCPDCLGGALNNSCPAESQCCSCRPHEMIGRQC	540
Db	481 CKRLVTGQHCQCLPEHWNGLSNDLDCRCPDCLGGALNNSCPAESQCCSCRPHEMIGRQC	540
Qy	541 NEVEPGYFFATLDHYLYEABEANLPGVSVIVERQYIQRIQISWGTAGFVRVPEGAYLEFF	600

Db	541 NEVEPGYFFATLDHYLYEABEANLPGVSVIVERQYIQRIQISWGTAGFVRVPEGAYLEFF	600
Qy	601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPPTSSRCNGNTIPDDNQVVSLSGP	660
Db	601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPPTSSRCNGNTIPDDNQVVSLSGP	660
Qy	661 SHYVYLPRPVCFERKGTNTVLELPQYTSDDSDVESPYTLDSLVLMPEYCKSLDIFTVGG	720
Db	661 SHYVYLPRPVCFERKGTNTVLELPQYTSDDSDVESPYTLDSLVLMPEYCKSLDIFTVGG	720
Qy	721 SGDGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACEDCPQGS	780
Db	721 SGDGVVTNSAWETFORYRCLENSRSVVKTPMTDVCNRIIFSISALLHQTGLACEDCPQGS	780
Qy	781 LSSVCDPNGGQCCQCPNVVGTTCNRCAPTGTFPGSPGCKPCCECHLQGSVNAFCNPVTQC	840
Db	781 LSSVCDPNGGQCCQCPNVVGTTCNRCAPTGTFPGSPGCKPCCECHLQGSVNAFCNPVTQC	840
Qy	841 HCFQGVYARQCDRCLPGHGWGFPSPQPCQCNHADDCCPVTGECNLCQDVTMGNHCERCLA	900
Db	841 HCFQGVYARQCDRCLPGHGWGFPSPQPCQCNHADDCCPVTGECNLCQDVTMGNHCERCLA	900
Qy	901 GYIGDPIIGSGDHCRPCPCPDGSPGSGRQFARSCYQDPVTLQACVCPGYIGSRCDPCAS	960
Db	901 GYIGDPIIGSGDHCRPCPCPDGSPGSGRQFARSCYQDPVTLQACVCPGYIGSRCDPCAS	960
Qy	961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKLYHTEGHEHCOFCRGGYVGA	1020
Db	961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKLYHTEGHEHCOFCRGGYVGA	1020
Qy	1021 LRQDCRKVCNLYLGTVQEHCHNGSCQCDKATGQCLCLPNVIGQNCDCRCPNTWQASGTG	1080
Db	1021 LRQDCRKVCNLYLGTVQEHCHNGSCQCDKATGQCLCLPNVIGQNCDCRCPNTWQASGTG	1080
Qy	1081 CDPNCNAAHFGSCNEFTGQCCQCPGFGGRTCSQCLFWGDPDPVECRACDCDPRGIE	1140
Db	1081 CDPNCNAAHFGSCNEFTGQCCQCPGFGGRTCSQCLFWGDPDPVECRACDCDPRGIE	1140
Qy	1141 TPQCDQSTGQCVCEGVGEGPRCDKTRGYSVGFDPCTPHQCQFALMDVIAELNTRTHRF	1200
Db	1141 TPQCDQSTGQCVCEGVGEGPRCDKTRGYSVGFDPCTPHQCQFALMDVIAELNTRTHRF	1200
Qy	1201 LEKAKALKISGVIQPYRETVDSEKVSSEIKDIIAQSPAAPLKNIGLFEAEKLIKDV	1260
Db	1201 LEKAKALKISGVIQPYRETVDSEKVSSEIKDIIAQSPAAPLKNIGLFEAEKLIKDV	1260
Qy	1261 TEMMAQVEVKLSDDTTQSQNSTAKELDSLQTEAEASLDNTVKELAQLEFIKNSDIRGALDS	1320
Db	1261 TEMMAQVEVKLSDDTTQSQNSTAKELDSLQTEAEASLDNTVKELAQLEFIKNSDIRGALDS	1320
Qy	1321 ITKYFQMSLEAEERVNASITTEPNSTVQESALMRDVEDVMMERESQFKEKQSEARLLDE	1380
Db	1321 ITKYFQMSLEAEERVNASITTEPNSTVQESALMRDVEDVMMERESQFKEKQSEARLLDE	1380
Qy	1381 LAGKQLSLDLASAAEMTCGTPPGASCSETGCGPNCRITDEGERKCGGPGCGGLVTVAHNA	1440
Db	1381 LAGKQLSLDLASAAEMTCGTPPGASCSETGCGPNCRITDEGERKCGGPGCGGLVTVAHNA	1440
Qy	1441 WQKAMDLQDVLALAEVEQLSKMVSSEAKLRADAEKQSAEDILLKTNAKEMDKSNEEL	1500
Db	1441 WQKAMDLQDVLALAEVEQLSKMVSSEAKLRADAEKQSAEDILLKTNAKEMDKSNEEL	1500
Qy	1501 RNLIQIKNFLTQDSADLDSIEAVANEVLKVMEMPSTPQOLQNLTEDIRERVESLSQVEVI	1560
Db	1501 RNLIQIKNFLTQDSADLDSIEAVANEVLKVMEMPSTPQOLQNLTEDIRERVESLSQVEVI	1560
Qy	1561 LQHSAADTARABMLLEAKRASKATDVVKVTADVMKEALEAEAKQVAAEKAIKQADBDI	1620
Db	1561 LQHSAADTARABMLLEAKRASKATDVVKVTADVMKEALEAEAKQVAAEKAIKQADBDI	1620
Qy	1621 QGTQNLITSISEETAASEETLFNASORISELERNVEELKRAAQNQSGAEYIEKVVTVK	1680

Db 1621 OQTQNTLLTSEBTAASEETLFNQSRISELRNVEELKRAQNSGEAEYIEKYVYTVK 1680

Qy 1681 QSAEDVKKTLDELDEKYYKVENLAKTTEESADARRAEMLQNEAKTLLAQANSKLQLL 1740

Db 1681 QSAEDVKKTLDELDEKYYKVENLAKTTEESADARRAEMLQNEAKTLLAQANSKLQLL 1740

Qy 1741 KOLERYEDNQRYLEDKAOELARLGEVRSLLKDISQKAVVYSTCL 1786

Db 1741 KOLERYEDNQRYLEDKAOELARLGEVRSLLKDISQKAVVYSTCL 1786

RESULT 2

MMMSB1

laminin beta-1 chain precursor - mouse

N:Alternate names: laminin chain B1

C:Species: Mus musculus (house mouse)

C:Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C:Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543

R:Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.

Proc.Natl. Acad. Sci. U.S.A. 84, 935-939, 1987

A:Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein

A:Reference number: A26413; MUID:87147212; PMID:3493487

A:Accession: A26413

A:Molecule type: mRNA

A:Residues: 1-1786 <SAS>

A:Cross-references: EMBL:M15525; NID:G198700

A:Note: translation in GenBank has additional 48 residues at the amino end

R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Stochem. J. 252, 453-461, 1988

A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A:Reference number: S02678; MUID:88326259; PMID:2458101

A:Accession: S02679

A:Molecule type: protein

A:Residues: 28-42;932-946 <FUJ>

R:Haril, J.; Oberbauer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A:Title: The N terminus of laminin A chain is homologous to the B chains.

A:Reference number: S00624; MUID:88225080; PMID:3267223

A:Accession: S05326

A:Molecule type: protein

A:Residues: 457-466;854-868;932-946 <HAR>

R:Mann, K.; Deutzmann, R.; Timpl, R.

Eur. J. Biochem. 178, 71-80, 1988

A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th

A:Reference number: S08895; MUID:89078415; PMID:2462498

A:Accession: S14877

A:Molecule type: protein

A:Residues: 590-620 <MAN>

R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A:Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A:Reference number: A02870; MUID:85051302; PMID:6209134

A:Accession: A02871

A:Molecule type: mRNA

A:Residues: 1292-1530, 'MEMP', 1535-1591, 'C', 1693-1748, 'N', 1750-1786 <BAR>

A:Cross-references: EMBL:X05212; NID:G52861; FIDN:CAA28839.1; PID:9809042

R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A:Reference number: S01790; MUID:89030693; PMID:3181157

A:Accession: S02036

A:Molecule type: protein

A:Residues: 1561-1597 <DEU>

R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A:Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A:Reference number: S13543; MUID:85257455; PMID:3848400

A:Accession: S13543

A:Molecule type: protein

A:Residues: 1700-1748, 'N', 1750-1759 <PAU>

C:Genetics:

A:Gene: Lamb-1

A:Map position: 12

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F:22-270/Domain: VI <DOM6>

F:271-540/Domain: V <DOM5>

F:271-332/Domain: laminin-type EGF-like homology <LE01>

F:335-395/Domain: laminin-type EGF-like homology <LE02>

F:398-455/Domain: laminin-type EGF-like homology <LE03>

F:458-507/Domain: laminin-type EGF-like homology <LE04>

F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:541-772/Domain: IV <DOM4>

F:773-1182/Domain: III <DOM3>

F:773-818/Domain: laminin-type EGF-like homology <LE06>

F:821-864/Domain: laminin-type EGF-like homology <LE07>

F:867-914/Domain: laminin-type EGF-like homology <LE08>

F:917-973/Domain: laminin-type EGF-like homology <LE09>

F:976-1025/Domain: laminin-type EGF-like homology <LE10>

F:1028-1084/Domain: laminin-type EGF-like homology <LE11>

F:1084-1129/Domain: laminin-type EGF-like homology <LE12>

F:1132-1176/Domain: laminin-type EGF-like homology <LE13>

F:1183-1397/Domain: II <DOM2>

F:1183-1397/Region: heptad repeats

F:1398-1430/Domain: alpha <ALP>

F:1431-1786/Region: heptad repeats

F:1431-1786/Domain: I <DOM1>

F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F:30-35/Disulfide bonds: #status predicted

F:120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydra

F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 93.7%; Score 9144; DB 1; Length 1786;

Best Local Similarity 92.7%; Pred. NO. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGLQLLAFSLALCRARVRAQEPESYCAEGSCYPATGDLIIIGRAQKLSVTSTGLHX 60

Db 1 MGLQLVAFGLVLMGTRVCAQEPESYCAEGSCYPATGDLIIIGRAQKLSVTSTGLHX 60

Qy 61 PEPYCVSHLQEDKCKFCINSDPYHETLNPDSHLLIENVTTFAPNRLKIWQSENGVEN 120

Db 61 PEPYCVSHLQEDKCKFCINSDPYHETLNPDSHLLIENVTTFAPNRLKIWQSENGVEN 120

Qy 121 VTIQDLLEAFHFTHLIMTFKTERPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISG 180

Db 121 VTIQDLLEAFHFTHLIMTFKTERPAAMLIERSDFGKTGWVYRYFAYDCEASFPGISG 180

Qy 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKITNRIKFKVL 240

Db 181 PMKKVDDIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLKITNRIKFKVL 240

Qy 241 HTIGDNLDSMEIREKYYAVYDMVVRGNCFCYGHASCAPVDGFNEVEGMVHGHCWC 300

Db 241 HTIGDNLDSMEIREKYYAVYDMVVRGNCFCYGHASCAPVDGFNEVEGMVHGHCWC 300

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Db 301 RHNTKGLNCLMDFYHDLFPWPAEGRNSNACKKCNNEHSISCHFDMAVYLATGVSG 360

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Db 361 VCDCCQHTNGRNCCECKPFYQHPERDTRDNFCERCTCDPAGSONEGICDSTDFSTG 420

Qy 421 LIAGQCRCKLNVEGERCDVCKEGFYDLSBEDPFGCKSCACNPLGTTIPGNCDSETHCY 480

Db 421 LIAGQCRCKLNVEGERCDVCKEGFYDLSBEDPFGCKSCACNPLGTTIPGNCDSETHCY 480

Qy 481 CKSLVTVGQCHDCQCLPEHWGLSNDLDCRCDCDCLGGALNNSCFABSGQSCRFPHMIGROC 540

Db 481 CKSLVTVGQCHDCQCLPEHWGLSNDLDCRCDCDCLGGALNNSCFABSGQSCRFPHMIGROC 540

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Db 541 NEVEGSGYFTTLDHYLYEAEANLPGVSVISERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600
QY 601 IDNIPYSMEVDILIRVEPOLPDHWEKAVITVQPGRIPTSSRCGNTIPDDNQVLSLSPG 660
Db 601 IDNIPYSMEVDILIRVEPOLPDHWEKAVITVQPGRIPTSSRCGNTIPDDNQVLSLSPG 660
QY 661 SRYVVLPRPVCFFKGTNTYVRLELPQVTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGG 720
Db 661 SRYVVLPRPVCFFKGTNTYVRLELPQVTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGG 720
QY 721 SGQGVNTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALLHOTGLACECDPQGS 780
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QY 781 LSSVCDPNGQCQCRPNVVGRTCNRCAPGTFGFGPGCKPCECHLOGSVNAFCNPVTGQC 840
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QY 901 GYVGDPIIGSDHCRPCPCPDGSDGPOFARSCVQDPVTLQACVCDPVGVIISRCDDCAS 960
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QY 961 GYFNPSEVGSGCQPCQCHNNIDTTPDPAKXETGRCLKCLYHTEGHEQCFRFGYGBA 1020
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QY 1381 LAGLKQLSLDLASAAEMTCGTPPGASCSETGCGPNCRTDGERKCGGPGCGGLVTVAHNA 1440
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QY 1441 WQKAMLDODVLSALAEVQSLKMWSEAKLPADEAKQSAEDILIKTNATKMKDKNEEL 1500
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QY 1501 RNLIKQIRNFILTPSDADLDSIEAVANEVLKMEPSTPQQLQNLNTEDIRREVESLSQVEVI 1560
Db 1501 RNLIKQIRNFILTPSDADLDSIEAVANEVLKMEPSTPQQLQNLNTEDIRREVESLSQVEVI 1560
QY 1561 LQSSAADTARAEMLLEAEKRAKSKATDVKTVDVADVMVKALBEAEKAQVAEKAIKQADEDI 1620
Db 1561 LQSSAADTARAEMLLEAEKRAKSKATDVKTVDVADVMVKALBEAEKAQVAEKAIKQADEDI 1620
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QY 1621 QGTQNLTLTSESTFAAEEITLFNASQRISELERNVBELKRAAQNSEAEYIEKVYTVK 1680
Db 1621 QGTQNLTLTSESTFAAEEITLFNASQRISELERNVBELKRAAQNSEAEYIEKVYTVK 1680
QY 1681 QSAEDVKTLDGELDEKVKVENLIAKTBESADARRKAEMLQNEAKTLLAQANSKIQLL 1740
Db 1681 QSAEDVKTLDGELDEKVKVENLIAKTBESADARRKAEMLQNEAKTLLAQANSKIQLL 1740
QY 1741 KDLERKVEDNORYLEDKAEQELARLEGEVRSLLKDISOKVAVYSTCL 1786
Db 1741 EDLERKVEDNORYLEDKAEQELARLEGEVRSLLKDISOKVAVYSTCL 1786

RESULT 3
WARNS
laminin beta-2 chain precursor - rat
N.Alterate names: laminin chain B3; S-laminin
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C.Accession: S03539
R.Hunter: D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A.Article: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurite
A.Reference number: S03539; PMID:89159410; PMID:2922051
A.Accession: S03539
A.Molecule type: mRNA
A.Residues: 1-1801 <HUN>
A.Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C.Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C.Function:
A.Description: Interact with cells and with other basement membrane proteins to promote
C.Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C.Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F.1-35/Domain: signal sequence #status predicted <SIG>
F.36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F.36-285/Domain: VI <DOM5>
F.286-555/Domain: V <DOM5>
F.286-347/Domain: laminin-type EGF-like homology <LE01>
F.350-410/Domain: laminin-type EGF-like homology <LE02>
F.413-470/Domain: laminin-type EGF-like homology <LE03>
F.473-522/Domain: laminin-type EGF-like homology <LE04>
F.525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F.556-784/Domain: IV <DOM4>
F.786-831/Domain: laminin-type EGF-like homology <LE06>
F.788-1196/Domain: III <DOM3>
F.834-877/Domain: laminin-type EGF-like homology <LE07>
F.880-927/Domain: laminin-type EGF-like homology <LE08>
F.930-986/Domain: laminin-type EGF-like homology <LE09>
F.989-1038/Domain: laminin-type EGF-like homology <LE10>
F.1041-1095/Domain: laminin-type EGF-like homology <LE11>
F.1098-1143/Domain: laminin-type EGF-like homology <LE12>
F.1146-1190/Domain: laminin-type EGF-like homology <LE13>
F.1197-1412/Domain: II <DOM2>
F.1197-1412/Region: heptad repeats
F.1413-1445/Domain: alpha <ALP>
F.1446-1801/Region: heptad repeats
F.1448-1801/Domain: I <DOM1>
F.45-50/Disulfide bonds: #status predicted
F.151-371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F.1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.2%; Score 5088.5; DB 1; Length 1801;
Best Local Similarity 51.2%; Pred. No. 3.3e-186;
Matches 916; Conservative 303; Mismatches 550; Indels 21; Gaps 9;
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QY 7 LAFSFLACRAVRARQEPFSY-GCAEGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPVC 65
Db 21 LRLGLLSVLATLAQAQVPSLDVPGCGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPVC 80
QY 66 IVSHLQDEKQKFCICNSQDPYHETLNPDSHLIENVTVPAPNRLKIWMQSENGVENVTIQL 125
Db 81 IVSHLQDEKQKFCICNSQDPYHETLNPDSHLIENVTVPAPNRLKIWMQSENGVENVTIQL 140
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: May 18, 2004, 14:26:08 / Search time 10.1546 Seconds  
(without alignments)  
9158.169 Million cell updates/sec  
Title: US-10-037-182-6  
Perfect score: 9754  
Sequence: 1 MGLQLLAFLAFSLALCRARV.....EVRSLKDISQKVAVYSTCL 1786  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42:\*

Result No.	Score	Query Match	Length	DB ID	Description
1	9754	100.0	1786	1 LMB1_HUMAN	P07942 homo sapien
2	9144	93.7	1786	1 LMB1_MOUSE	P02469 mus musculus
3	5088.5	52.2	1801	1 LMB2_RAT	P15800 rattus norv
4	5052.5	51.8	1798	1 LMB2_HUMAN	P58268 homo sapien
5	5051.5	51.8	1799	1 LMB2_MOUSE	Q61292 mus musculus
6	3846	39.4	1790	1 LMB1_DROME	P11046 drosophila
7	1762.5	18.1	1639	1 LMB1_DROME	P15215 drosophila
8	1729.5	17.7	3672	1 LMB2_CABEL	Q13133 caenorhabdi
9	1696.5	17.4	1535	1 LMB1_HUMAN	Q18823 homo sapien
10	1676.5	17.2	1609	1 LMB1_HUMAN	P11047 homo sapien
11	1658	17.0	1607	1 LMB1_MOUSE	P02468 mus musculus
12	1645.5	16.9	3712	1 LMB1_DROME	Q00174 drosophila
13	1617	16.6	3718	1 LMB1_MOUSE	Q61001 mus musculus
14	1583	16.2	303	1 LMB1_CHICK	Q01635 gallus gall
15	1569.5	16.1	3695	1 LMB5_HUMAN	Q15230 homo sapien
16	1566	16.1	3110	1 LMB2_HUMAN	P24043 homo sapien
17	1559	16.0	1581	1 LMB3_MOUSE	Q97066 mus musculus
18	1557.5	16.0	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1539	15.8	3106	1 LMB2_MOUSE	Q60675 mus musculus
20	1529.5	15.7	3075	1 LMB1_HUMAN	P25391 homo sapien
21	1515.5	15.5	1587	1 LMB3_HUMAN	Q99616 homo sapien
22	1510	15.5	3084	1 LMB1_MOUSE	P19137 mus musculus
23	1483.5	15.2	1168	1 LMB3_MOUSE	Q61087 mus musculus
24	1372	14.1	3333	1 LMB3_MOUSE	Q61789 mus musculus
25	891	9.1	1191	1 LMB2_MOUSE	Q61092 mus musculus
26	873	9.0	1193	1 LMB2_HUMAN	Q13753 homo sapien
27	695.5	7.1	604	1 NET1_HUMAN	Q95631 homo sapien
28	695.5	7.1	604	1 NET1_MOUSE	Q09118 mus musculus
29	692	7.1	606	1 NET1_CHICK	Q90922 gallus gall
30	666	6.8	3707	1 PGSM_MOUSE	Q05793 mus musculus
31	657	6.7	4391	1 PGSM_HUMAN	P98160 homo sapien
32	608	6.2	581	1 NET2_CHICK	Q90923 gallus gall
33	582.5	6.0	1816	1 LMB4_HUMAN	Q16363 homo sapien

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9754	100.0	1786	1 LMB1_HUMAN	P07942 homo sapien
2	9144	93.7	1786	1 LMB1_MOUSE	P02469 mus musculus
3	5088.5	52.2	1801	1 LMB2_RAT	P15800 rattus norv
4	5052.5	51.8	1798	1 LMB2_HUMAN	P58268 homo sapien
5	5051.5	51.8	1799	1 LMB2_MOUSE	Q61292 mus musculus
6	3846	39.4	1790	1 LMB1_DROME	P11046 drosophila
7	1762.5	18.1	1639	1 LMB1_DROME	P15215 drosophila
8	1729.5	17.7	3672	1 LMB2_CABEL	Q13133 caenorhabdi
9	1696.5	17.4	1535	1 LMB1_HUMAN	Q18823 homo sapien
10	1676.5	17.2	1609	1 LMB1_HUMAN	P11047 homo sapien
11	1658	17.0	1607	1 LMB1_MOUSE	P02468 mus musculus
12	1645.5	16.9	3712	1 LMB1_DROME	Q00174 drosophila
13	1617	16.6	3718	1 LMB1_MOUSE	Q61001 mus musculus
14	1583	16.2	303	1 LMB1_CHICK	Q01635 gallus gall
15	1569.5	16.1	3695	1 LMB5_HUMAN	Q15230 homo sapien
16	1566	16.1	3110	1 LMB2_HUMAN	P24043 homo sapien
17	1559	16.0	1581	1 LMB3_MOUSE	Q97066 mus musculus
18	1557.5	16.0	1172	1 LMB3_HUMAN	Q13751 homo sapien
19	1539	15.8	3106	1 LMB2_MOUSE	Q60675 mus musculus
20	1529.5	15.7	3075	1 LMB1_HUMAN	P25391 homo sapien
21	1515.5	15.5	1587	1 LMB3_HUMAN	Q99616 homo sapien
22	1510	15.5	3084	1 LMB1_MOUSE	P19137 mus musculus
23	1483.5	15.2	1168	1 LMB3_MOUSE	Q61087 mus musculus
24	1372	14.1	3333	1 LMB3_MOUSE	Q61789 mus musculus
25	891	9.1	1191	1 LMB2_MOUSE	Q61092 mus musculus
26	873	9.0	1193	1 LMB2_HUMAN	Q13753 homo sapien
27	695.5	7.1	604	1 NET1_HUMAN	Q95631 homo sapien
28	695.5	7.1	604	1 NET1_MOUSE	Q09118 mus musculus
29	692	7.1	606	1 NET1_CHICK	Q90922 gallus gall
30	666	6.8	3707	1 PGSM_MOUSE	Q05793 mus musculus
31	657	6.7	4391	1 PGSM_HUMAN	P98160 homo sapien
32	608	6.2	581	1 NET2_CHICK	Q90923 gallus gall
33	582.5	6.0	1816	1 LMB4_HUMAN	Q16363 homo sapien

ALIGNMENTS

RESULT 1

ID	LMB1_HUMAN	STANDARD	PRT	1786 AA
AC	P07942			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Laminin beta-1 chain precursor (Laminin B1 chain).			
GN	LAMB1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90368768; PubMed=1975589;			
RA	Vuolteenaho R., Chow L.T., Tryggvason K.;			
RT	"Structure of the human laminin B1 chain gene.";			
RL	J. Biol. Chem. 265:15611-15616(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=87280037; PubMed=3611077;			
RA	Pikkariainen T., Eddy R., Fukushima Y., Byers M., Shows T.,			
RA	Phalajanemi T., Saraste M., Tryggvason K.;			
RT	"Human laminin B1 chain. A multidomain protein with gene (LAMB1)			
RL	locus in the q22 region of chromosome 7.";			
RN	[3]			
RP	SEQUENCE OF 1276-1709 FROM N.A.			
RA	MEDLINE=88021029; PubMed=3661559;			
RA	Jaye M., Modi W.S., Ricca G.A., Mudd R., Chiu I.M., O'Brien S.J.,			
RA	Dröhan W.N.;			
RT	"Isolation of a cDNA clone for the human laminin-B1 chain and its			
RL	gene localization.";			
RL	Am. J. Hum. Genet. 41:605-615(1987).			
CC	-I- FUNCTION: Binding to cells via a high affinity receptor, laminin			
CC	is thought to mediate the attachment, migration and organization			
CC	of cells into tissues during embryonic development by interacting			
CC	with other extracellular matrix components.			
CC	-I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three			
CC	different polypeptide chains (alpha, beta, gamma), which are bound			
CC	to each other by disulfide bonds into a cross-shaped molecule			
CC	comprising one long and three short arms with globules at each			
CC	end. The beta-1 chain is a subunit of laminin-1 (EHS laminin),			
CC	-I- SUBCELLULAR LOCATION: Extracellular.			
CC	-I- TISSUE SPECIFICITY: Found in the basement membranes (major			
CC	component).			
CC	-I- DOMAIN: The alpha-helical domains I and II are thought to interact			
CC	with other laminin chains to form a coiled coil structure.			
CC	-I- DOMAIN: Domains VI and IV are globular.			
CC	-I- SIMILARITY: Contains 1 laminin N-terminal domain.			
CC	-I- SIMILARITY: Contains 13 laminin EGF-like domains.			
CC	-I- SIMILARITY: Contains 1 laminin IV domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			

SIGNAL	1	21	22	1786	LAMININ BETA-1 CHAIN
CHAIN	22	1786	22	1786	LAMININ N-TERMINAL (DOMAIN VI).
DDOMAIN	22	1786	22	1786	LAMININ EGF-LIKE 1.
DDOMAIN	271	334	271	334	LAMININ EGF-LIKE 2.
DDOMAIN	335	397	335	397	LAMININ EGF-LIKE 3.
DDOMAIN	398	457	398	457	LAMININ EGF-LIKE 4.
DDOMAIN	458	509	458	509	LAMININ EGF-LIKE 5 (INCOMPLETE).
DDOMAIN	510	540	510	540	LAMININ DOMAIN IV
DDOMAIN	541	771	541	771	LAMININ EGF-LIKE 6.
DDOMAIN	773	820	773	820	LAMININ EGF-LIKE 7.
DDOMAIN	821	866	821	866	LAMININ EGF-LIKE 8.
DDOMAIN	867	916	867	916	LAMININ EGF-LIKE 9.
DDOMAIN	917	975	917	975	LAMININ EGF-LIKE 10.
DDOMAIN	976	1027	976	1027	LAMININ EGF-LIKE 11.
DDOMAIN	1028	1083	1028	1083	LAMININ EGF-LIKE 12.
DDOMAIN	1084	1131	1084	1131	LAMININ EGF-LIKE 13.
DDOMAIN	1132	1177	1132	1177	DOMAIN II.
DDOMAIN	1179	1398	1179	1398	DOMAIN ALPHA.
DDOMAIN	1398	1430	1398	1430	DOMAIN I.
DDOMAIN	1431	1786	1431	1786	COILED COIL (POTENTIAL).
DDOMAIN	1216	1315	1216	1315	COILED COIL (POTENTIAL).
DDOMAIN	1353	1388	1353	1388	COILED COIL (POTENTIAL).
DDOMAIN	1442	1781	1442	1781	BY SIMILARITY.
DDOMAIN	271	280	271	280	BY SIMILARITY.
DISULFID	271	280	271	280	BY SIMILARITY.
DISULFID	273	298	273	298	BY SIMILARITY.
DISULFID	300	309	300	309	BY SIMILARITY.
DISULFID	312	332	312	332	BY SIMILARITY.
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DISULFID	337	362	337	362	BY SIMILARITY.
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DISULFID	377	395	377	395	BY SIMILARITY.
DISULFID	398	411	398	411	BY SIMILARITY.
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DISULFID	428	437	428	437	BY SIMILARITY.
DISULFID	440	455	440	455	BY SIMILARITY.
DISULFID	458	472	458	472	BY SIMILARITY.
DISULFID	460	479	460	479	BY SIMILARITY.
DISULFID	481	490	481	490	BY SIMILARITY.
DISULFID	493	507	493	507	BY SIMILARITY.
DISULFID	773	785	773	785	BY SIMILARITY.
DISULFID	775	792	775	792	BY SIMILARITY.
DISULFID	794	803	794	803	BY SIMILARITY.
DISULFID	806	818	806	818	BY SIMILARITY.
DISULFID	821	833	821	833	BY SIMILARITY.
DISULFID	823	840	823	840	BY SIMILARITY.
DISULFID	842	851	842	851	BY SIMILARITY.
DISULFID	854	864	854	864	BY SIMILARITY.
DISULFID	867	876	867	876	BY SIMILARITY.
DISULFID	869	883	869	883	BY SIMILARITY.
DISULFID	886	895	886	895	BY SIMILARITY.
DISULFID	898	914	898	914	BY SIMILARITY.
DISULFID	917	933	917	933	BY SIMILARITY.
DISULFID	919	944	919	944	BY SIMILARITY.
DISULFID	946	955	946	955	BY SIMILARITY.

SIGNAL	1	21	22	1786	LAMININ BETA-1 CHAIN
CHAIN	22	1786	22	1786	LAMININ N-TERMINAL (DOMAIN VI).
DDOMAIN	22	1786	22	1786	LAMININ EGF-LIKE 1.
DDOMAIN	271	334	271	334	LAMININ EGF-LIKE 2.
DDOMAIN	335	397	335	397	LAMININ EGF-LIKE 3.
DDOMAIN	398	457	398	457	LAMININ EGF-LIKE 4.
DDOMAIN	458	509	458	509	LAMININ EGF-LIKE 5 (INCOMPLETE).
DDOMAIN	510	540	510	540	LAMININ DOMAIN IV
DDOMAIN	541	771	541	771	LAMININ EGF-LIKE 6.
DDOMAIN	773	820	773	820	LAMININ EGF-LIKE 7.
DDOMAIN	821	866	821	866	LAMININ EGF-LIKE 8.
DDOMAIN	867	916	867	916	LAMININ EGF-LIKE 9.
DDOMAIN	917	975	917	975	LAMININ EGF-LIKE 10.
DDOMAIN	976	1027	976	1027	LAMININ EGF-LIKE 11.
DDOMAIN	1028	1083	1028	1083	LAMININ EGF-LIKE 12.
DDOMAIN	1084	1131	1084	1131	LAMININ EGF-LIKE 13.
DDOMAIN	1132	1177	1132	1177	DOMAIN II.
DDOMAIN	1179	1398	1179	1398	DOMAIN ALPHA.
DDOMAIN	1398	1430	1398	1430	DOMAIN I.
DDOMAIN	1431	1786	1431	1786	COILED COIL (POTENTIAL).
DDOMAIN	1216	1315	1216	1315	COILED COIL (POTENTIAL).
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DDOMAIN	1442	1781	1442	1781	BY SIMILARITY.
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DISULFID	273	298	273	298	BY SIMILARITY.
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DISULFID	898	914	898	914	BY SIMILARITY.
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Query Match				100.08; Score 9754; DB 1; Length 1786;			
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Matches 1786; Conservative				0; Mismatches			
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				0; Gaps			
Qy	1	MGLQLLAFSLALCRARVRAQAEPEFSYCGAEGSCYPATGDLILIGRAQKLSVTSTGLHK	60				
Db	1	MGLQLLAFSLALCRARVRAQAEPEFSYCGAEGSCYPATGDLILIGRAQKLSVTSTGLHK	60				
Qy	61	PEPYCIUSHLQEDKKCFICNSODPVHETLNDPSHLIENVTTPAPNRLKIWQSENGVEN	120				
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Qy	121	VTIQLDLAEAEHFTHLIMTFKTFPAAMLIERSSDFGKTWGVYFYAYDCEASPPGISTG	180				
Db	121	VTIQLDLAEAEHFTHLIMTFKTFPAAMLIERSSDFGKTWGVYFYAYDCEASPPGISTG	180				
Qy	181	PMKKVDDIICDSRYSIDIEPSTEGEVIIPALDPAKIEDPYSPIRNLKIINLKIKFVKL	240				
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Qy	241	HTLGDNLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVGWHGCMC	300				
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Qy	301	RHNTKGLNCELMDPYHDLPMRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG	360				
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Qy	361	VCDCHNTMGRNCQCKPFYQHPERDIRDPNFCERTCDPAGSQNEGICDSYDFSTG	420				
Db	361	VCDCHNTMGRNCQCKPFYQHPERDIRDPNFCERTCDPAGSQNEGICDSYDFSTG	420				
Qy	421	LIAGCRCKLVNVEGHCVDVCEGFDYLSSEDPFGCKSCACNPLGTIPGGNPNCDSETHGY	480				
Db	421	LIAGCRCKLVNVEGHCVDVCEGFDYLSSEDPFGCKSCACNPLGTIPGGNPNCDSETHGY	480				
Qy	481	CKRLVTGHCOCICPEHGLNSLDGCRPCDCLGGALNNSCFAESGCCSRPHMIGROC	540				
Db	481	CKRLVTGHCOCICPEHGLNSLDGCRPCDCLGGALNNSCFAESGCCSRPHMIGROC	540				
Qy	541	NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIDRIPSWTGAGFVRPEGAYLEFF	600				
Db	541	NEVEPGYFATLDHYLYEAEANLPGVSIIVERQYIDRIPSWTGAGFVRPEGAYLEFF	600				
Qy	601	IDNIPYSMEYDILIRYEPOLPDHNEKAVITVQRGRIPTSRRCNTIPDDNQVVSLSPG	660				
Db	601	IDNIPYSMEYDILIRYEPOLPDHNEKAVITVQRGRIPTSRRCNTIPDDNQVVSLSPG	660				
Qy	661	SRVVLPRPVCPEKGTNTVRLLEPQYTSDDVESPYTLIDSLVLMYPYCKSLDIFTVGG	720				
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Qy	721	SGDGVVTSNASETFORRYCLENRSVVKTPMTDVCNRIIFSIALLHQTGLACEDPQGS	780				
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Qy	781	LSSVCDPNGGOCQCPNVVGRTCNRCAPGTGFGSGCKPCBCHLQGSVNAFCNPVTGQC	840				
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Qy	841	HCFOGVYARQDCRLCPGHGWFPSQPCQCNHADDCDPVTGECNCDQYTMGHNCERCLA	900				
Db	841	HCFOGVYARQDCRLCPGHGWFPSQPCQCNHADDCDPVTGECNCDQYTMGHNCERCLA	900				
Qy	901	GYGDPPIIGSDHCHRCPCPCDPSGROFASCSYQDPVTQLQACVCDPGYIGSRCDCCAS	960				
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Qy	961	GYFGNPFVGGSCQPCQCHNNIDTTDPEACDKETGRCLKLYHTEGEHCQCFRFGYTGDA	1020				
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Qy	1021	LRODCRKCVCNYLGTIVQBEHNGSCQCDKATQCCQLCLPNVIGQNCDCRCAPNWTQIASGTG	1080
Db	1021	LRODCRKCVCNYLGTIVQBEHNGSCQCDKATQCCQLCLPNVIGQNCDCRCAPNWTQIASGTG	1080
Qy	1081	CDPCNNAHSGPCSCNFTGOCQCMPCGPGGRTCSCECELFWGDDPVECRACDCDPRGIE	1140
Db	1081	CDPCNNAHSGPCSCNFTGOCQCMPCGPGGRTCSCECELFWGDDPVECRACDCDPRGIE	1140
Qy	1141	TPQCDOSTQCCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFAWDVIIAELTNRTHRF	1200
Db	1141	TPQCDOSTQCCVCEGVGPRCDKCTRGYSGVFPDCTPCHQCFAWDVIIAELTNRTHRF	1200
Qy	1201	LEKAKALKISVIGPYRETVDSVERKSEIKDILAQSPAAPAEPLKNIGNLFEAEKLIKDV	1260
Db	1201	LEKAKALKISVIGPYRETVDSVERKSEIKDILAQSPAAPAEPLKNIGNLFEAEKLIKDV	1260
Qy	1261	TEMMAQVEVKLSDTTSSQNSTAKELDSLQTEAESLDNTVKELAEQLFTKNSDIRGALDS	1320
Db	1261	TEMMAQVEVKLSDTTSSQNSTAKELDSLQTEAESLDNTVKELAEQLFTKNSDIRGALDS	1320
Qy	1321	ITKYFQMSLEABERNVASTTEPNSTVEQSALMRDRVEDVMERESQFKEKQEQEARLLDE	1380
Db	1321	ITKYFQMSLEABERNVASTTEPNSTVEQSALMRDRVEDVMERESQFKEKQEQEARLLDE	1380
Qy	1381	LAKGLOSLLSAAAEWTCGTPPGASCSETECGGPNCRDTDEGERKCGGCGGLVVAHNA	1440
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Qy	1441	WQKAMLDQDLVSALAEBEQLSKMYSEAKLRADAEKQSAEDILLKTNATKEXDKNSBEL	1500
Db	1441	WQKAMLDQDLVSALAEBEQLSKMYSEAKLRADAEKQSAEDILLKTNATKEXDKNSBEL	1500
Qy	1501	RNLKQIRNFLTQDSADLDSIEAVANVLKMEPSTPOOLQNLTEDIRERVESLSQVEVI	1560
Db	1501	RNLKQIRNFLTQDSADLDSIEAVANVLKMEPSTPOOLQNLTEDIRERVESLSQVEVI	1560
Qy	1561	LQHSADIAARAEMLLEAEKXASKSATDVKTADVMYKEALEEAEKQAAAEKAIKQADEDI	1620
Db	1561	LQHSADIAARAEMLLEAEKXASKSATDVKTADVMYKEALEEAEKQAAAEKAIKQADEDI	1620
Qy	1621	QGTQNLTSIESETAASBETLFNASORISELERNVEELKRAQNSGEAEYIEKVYVTVK	1680
Db	1621	QGTQNLTSIESETAASBETLFNASORISELERNVEELKRAQNSGEAEYIEKVYVTVK	1680
Qy	1681	QSAEDVKTLTDLGELDEKYKKVENLAKTTEESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
Db	1681	QSAEDVKTLTDLGELDEKYKKVENLAKTTEESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
Qy	1741	KOLERYEDNQRYLEDKQAEELARLEGEVESLLKDISQKVAVYSTCL	1786
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RESULT 2  
LMB1\_MOUSE  
ID LMB1\_MOUSE STANDARD; PRT; 1786 AA.  
AC P02469;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin beta-1 chain precursor (Laminin B1 chain).  
GN LAMB1-1 OR LAMB-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87147212; PubMed=3493487;  
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;  
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a  
RT multidomain protein containing cysteine-rich repeats."  
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939 (1987).

[2]  
 RP SEQUENCE OF 1292-1786 FROM N.A.  
 RA MEDLINE=85051302; PubMed=6209134;  
 RX Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;  
 RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of  
 coiled-coil alpha-helix";  
 RL EMBO J. 3:2355-2362(1984).  
 RN [3]  
 RP SEQUENCE OF 165-172; 539-547 AND 712-719.  
 RX STRAIN=BALB/c; TISSUE=Endothelial cells;  
 RC MEDLINE=97363207; PubMed=9219532;  
 RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,  
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of  
 endothelium";  
 RL Eur. J. Biochem. 246:727-735(1997).  
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
 is thought to mediate the attachment, migration and organization  
 of cells into tissues during embryonic development by interacting  
 with other extracellular matrix components.  
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
 different polypeptide chains (alpha, beta, gamma), which are bound  
 to each other by disulfide bonds into a cross-shaped molecule  
 comprising one long and three short arms with globules at each  
 end. The beta-1 chain is a subunit of laminin-1 (BHS laminin),  
 laminin-2 (merosin), and laminin-6 (K-laminin).  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: Found in the basement membranes (major  
 component).  
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.  
 CC -1- SIMILARITY: Contains 13 laminin EGF-like domains.  
 CC -1- SIMILARITY: Contains 1 laminin IV domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M15525; AAA39407.1; ALT\_INIT.  
 DR EMBL; X05212; CAA38839.1; -.  
 DR PIR; A26413; MMSB1.  
 DR HSSP; P02468; 1KJO.  
 DR MGD; MGI:96743; Lamb1-1.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR008211; LamNT.  
 DR Pfam; PF00053; laminin\_EGF; 13.  
 DR PRINTS; PR00011; EGF/LAMININ.  
 DR SMART; SM00180; EGF\_Lam; 11.  
 DR SMART; SM00136; LamNT; 1.  
 DR PROSITE; PS00022; EGF\_1; 9.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01248; LAMININ TYPE\_EGF\_11.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.  
 FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).  
 FT DOMAIN 271 334 LAMININ EGF-LIKE 1.  
 FT DOMAIN 335 397 LAMININ EGF-LIKE 2.  
 FT DOMAIN 398 457 LAMININ EGF-LIKE 3.  
 FT DOMAIN 458 509 LAMININ EGF-LIKE 4.  
 FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 FT DOMAIN 541 772 LAMININ DOMAIN IV.  
 FT DOMAIN 773 820 LAMININ EGF-LIKE 6.  
 FT DOMAIN 821 866 LAMININ EGF-LIKE 7.  
 FT DOMAIN 867 916 LAMININ EGF-LIKE 8.  
 FT DOMAIN 917 975 LAMININ EGF-LIKE 9.  
 FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.

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Query Match 93.7%; Score 9144; DB 1; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLIQLLAFSFLACRAVRAQEPFSGCAGSGCYPATGDLIGRAQKLSVITSCGLHK 60  
DB 1 MGLLOVAFAGVALMGTRVCAQEPFSGCAGSGCYPATGDLIGRAQKLSVITSCGLHK 60  
QY 61 PEPYCVSHLQBDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGYEN 120  
DB 61 PEPYCVSHLQBDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGYEN 120  
QY 121 VTIQDLLEAFHFTLHMTKTFRAAMLIERSDFGKTWGYRYFAYDCASRPGISTG 180  
DB 121 VTIQDLLEAFHFTLHMTKTFRAAMLIERSDFGKTWGYRYFAYDCASRPGISTG 180  
QY 181 PMKVVDDIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPYSPRIQNLKIINLRIKFVKL 240  
DB 181 PMKVVDDIICDSRYSDIEPSTEGEYIFRALDPAFKIEDPYSPRIQNLKIINLRIKFVKL 240  
QY 241 HTLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCMC 300  
DB 241 HTLGNLLDSRMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCMC 300  
QY 301 RNTKGLNCELCEMDFYHDLFWRPAPGRNSNACKCNNEHSSCHFDMAVFLATGNVSGG 360  
DB 301 RNTKGLNCELCEMDFYHDLFWRPAPGRNSNACKCNNEHSSCHFDMAVFLATGNVSGG 360  
QY 361 VCDCCOHNMTGNRCQCKPFFYQHPERDIRDNFCERCTCDPAGSQNGICDSYDFSTG 420  
DB 361 VCDCCOHNMTGNRCQCKPFFYQHPERDIRDNFCERCTCDPAGSQNGICDSYDFSTG 420  
QY 421 LIAGQCRKLVGEGHCDVKEGFFYDLSSEDPFGCKSCACNPLGTIPGNCDCSETGHY 480  
DB 421 LIAGQCRKLVGEGHCDVKEGFFYDLSSEDPFGCKSCACNPLGTIPGNCDCSETGHY 480  
QY 481 CKRLVTGQCDQCLPEHMGSLNDLDCRCPDCLGALNNSCFABSGQSCSRPHMIGRQC 540  
DB 481 CKRLVTGQCDQCLPEHMGSLNDLDCRCPDCLGALNNSCFABSGQSCSRPHMIGRQC 540  
QY 541 NEVEGYFYATLDHYLYEAEANLPGVSVIYERQVQIDRIPSWTCAGVRVPEGAYLEFF 600  
DB 541 NEVEGYFYATLDHYLYEAEANLPGVSVIYERQVQIDRIPSWTCAGVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGRIPTSRRCNGNTIPDDDNQVVSLSFG 660  
DB 601 IDNIPYSMEYDILIRYEPOLPDHWEKAVITVORPGRIPTSRRCNGNTIPDDDNQVVSLSFG 660  
QY 661 SRYVLPVPRVCEKGTNYVRLLELPQYTSDDSDVESPYTLDSLVIMPYCKSLDIFTVGG 720  
DB 661 SRYVLPVPRVCEKGTNYVRLLELPQYTSDDSDVESPYTLDSLVIMPYCKSLDIFTVGG 720  
QY 721 SGDGVTNSAWETTFORYRCLNSRSVVKTPMTDVCNIIIFSISALLHOTGLACEDPOGS 780  
DB 721 SGDGVTNSAWETTFORYRCLNSRSVVKTPMTDVCNIIIFSISALLHOTGLACEDPOGS 780  
QY 781 LSSVCDPNQGQCCQCPNPNVVRGTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840  
DB 781 LSSVCDPNQGQCCQCPNPNVVRGTCNRCAPGTGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840  
QY 841 HCFQGYARQDRCLPGHGFSPSCPCOCNGHADDCTPVTGECNCDYTWGHCERCLA 900  
DB 841 HCFQGYARQDRCLPGHGFSPSCPCOCNGHADDCTPVTGECNCDYTWGHCERCLA 900  
QY 901 GYVGPPIIGSGDHCRPCPCPDGPDGSRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAS 960  
DB 901 GYVGPPIIGSGDHCRPCPCPDGPDGSRQFARSQYQDPVTLQACVCDPGYIGSRCDCCAS 960  
QY 961 GYFAGNPSVGGSCQPCQCHNIDTTPDACDKETGRCLKCLYHTEGHCQCRGGYVYDA 1020  
DB 961 GYFAGNPSVGGSCQPCQCHNIDTTPDACDKETGRCLKCLYHTEGHCQCRGGYVYDA 1020  
QY 1021 LRQDCKKVCNLYGTVKEHCNGSDCHCDKATQCCLPNVIGQNCDCRCAPTWQLASGTG 1080

DB 1021 LRQDCKKVCNLYGTVKEHCNGSDCHCDKATQCCLPNVIGQNCDCRCAPTWQLASGTG 1080  
QY 1081 CDPCNCAHSGFSPSCNEFTGQCCQMPFGGRTSCQELFWGDDPVECRACDDCPRGIE 1140  
DB 1081 CDPCNCAHSGFSPSCNEFTGQCCQMPFGGRTSCQELFWGDDPVECRACDDCPRGIE 1140  
QY 1141 TPOCDOSTGQCVGVEGPRCDKTRGYSVUPPDCPTPCQCFALWDVILIAELTNTHRP 1200  
DB 1141 TPOCDOSTGQCVGVEGPRCDKTRGYSVUPPDCPTPCQCFALWDVILIAELTNTHRP 1200  
QY 1201 LEKAKALKISGVTGPYRETVDVSVERKVSBEIKOILAQSPAAEPLKNIGNLFEAEKLIKDV 1260  
DB 1201 LEKAKALKISGVTGPYRETVDVSVERKVSBEIKOILAQSPAAEPLKNIGNLFEAEKLIKDV 1260  
QY 1261 TEMMAQVEVKLSSTTSQSNSTAKELDSLOTEABSLDNTVKELAEQLEFINKSDIRGALDS 1320  
DB 1261 TEMMAQVEVKLSSTTSQSNSTAKELDSLOTEABSLDNTVKELAEQLEFINKSDIRGALDS 1320  
QY 1321 ITKYFQMSLEAEERVNASTTPEPNSVTVEQSALMRDVEDVMERESQFKEQEOEARLLDE 1380  
DB 1321 ITKYFQMSLEAEERVNASTTPEPNSVTVEQSALMRDVEDVMERESQFKEQEOEARLLDE 1380  
QY 1381 LAGKLOSLLDSAAAEAMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
DB 1381 LAGKLOSLLDSAAAEAMTCGTPPGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
QY 1441 WQKAMLDODVLSALAEVEQLSKWVSEAKLRADAEAKOSAEEDILLKTNAKEMDKSNEEL 1500  
DB 1441 WQKAMLDODVLSALAEVEQLSKWVSEAKLRADAEAKOSAEEDILLKTNAKEMDKSNEEL 1500  
QY 1501 RNLIKOIRNELTQDSADLDSIEAVANVELKMPSTPQOLQNLITEDIRREVESLSQVEVI 1560  
DB 1501 RNLIKOIRNELTQDSADLDSIEAVANVELKMPSTPQOLQNLITEDIRREVESLSQVEVI 1560  
QY 1561 LQHSADIAPAEMLLEBAKRAKSKSATDVKTADMTVKEALEBAEKAQVAEKAQKADEI 1620  
DB 1561 LQHSADIAPAEMLLEBAKRAKSKSATDVKTADMTVKEALEBAEKAQVAEKAQKADEI 1620  
QY 1621 QGTQNLITSTESATAASEETLFNASQRISELERNEVEELKRAQAQNSGEAEYIEKVYTVK 1680  
DB 1621 QGTQNLITSTESATAASEETLFNASQRISELERNEVEELKRAQAQNSGEAEYIEKVYTVK 1680  
QY 1681 QSAEDVVKTLGDBELDKYKVENLIAKTTESADARRKAEMLQNEAKTLLAQAQNSKLQLL 1740  
DB 1681 QSAEDVVKTLGDBELDKYKVENLIAKTTESADARRKAEMLQNEAKTLLAQAQNSKLQLL 1740  
QY 1741 KDLERKVEDNORYLEDKAQLAELEGEVRSLLKDISQKVAVYSTCL 1786  
DB 1741 KDLERKVEDNORYLEDKAQLAELEGEVRSLLKDISQKVAVYSTCL 1786  
RESULT 3  
LMB2 RAT  
ID LMB2 RAT STANDARD; PRT; 1801 AA.  
AC P15800; 1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).  
GN LAMB2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RC MEDLINE=89159410; PubMed=2922051;  
EX Hunter D.D.; Shah V.; Merlie J.P.; Sanes J.R.;  
RA "A laminin-like adhesive protein concentrated in the synaptic clef  
RT "Nature 338:229-234 (1989).  
RL Nature 338:229-234 (1989).



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 48.4494 Seconds  
(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-6

Perfect score: 9754  
Sequence: 1 MGLQLLAFLACRARVR.....EVRSLKDLSKVAVYSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.25.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriopl.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6811.5	69.8	1785	13 Q8JHV7	Q8JHV7 brachydanio
2	5808	59.5	1086	4 Q8TAS6	Q8TAS6 homo sapien
3	5325	54.6	1792	13 Q57484	Q57484 gallus gall
4	5074.5	52.0	1799	11 Q830Y0	Q830Y0 mus musculus
5	4891	50.1	984	11 Q8K271	Q8K271 mus musculus
6	4527	46.4	911	11 Q9CRX6	Q9CRX6 mus musculus
7	3832.5	39.3	1761	4 Q86XN2	Q86XN2 homo sapien
8	3797.5	38.9	1827	13 Q8JHV6	Q8JHV6 brachydanio
9	3625.5	37.2	1631	4 Q9Y6U6	Q9Y6U6 homo sapien
10	2842.5	29.1	1067	5 Q4565	Q4565 caenorhabdi
11	2297.5	23.6	1168	5 Q967S8	Q967S8 schistocerc
12	2034	20.9	1781	4 Q9UHI2	Q9UHI2 homo sapien
13	1921	19.7	1026	5 Q8SWI0	Q8SWI0 bomyx mori
14	1847	18.9	1069	5 Q9BPS2	Q9BPS2 caenorhabdi
15	1729.5	17.7	3704	5 P91904	P91904 caenorhabdi
16	1684.5	17.3	1593	13 Q8JHV8	Q8JHV8 brachydanio

17	1674.5	17.2	1623	5 Q9U3U7	Q9U3U7 anopheles g
18	1641.5	16.8	3712	5 Q9VRW0	Q9VRW0 drosophila
19	1573.5	16.1	3695	4 Q8TDF8	Q8TDF8 homo sapien
20	1491.5	15.3	1168	11 Q91V90	Q91V90 mus musculus
21	1380	14.1	1007	13 Q90ZN3	Q90ZN3 gallus gall
22	1307.5	13.4	3102	5 Q45614	Q45614 caenorhabdi
23	1217	12.5	2731	5 Q9VJT5	Q9VJT5 drosophila
24	1217	12.5	3367	5 Q9XZC9	Q9XZC9 drosophila
25	1217	12.5	3375	5 Q8IF51	Q8IF51 drosophila
26	1101.5	11.3	1546	4 Q9NS27	Q9NS27 homo sapien
27	1099.5	11.3	1546	4 Q75445	Q75445 homo sapien
28	1064	10.9	1486	4 Q14637	Q14637 homo sapien
29	1041.5	10.7	1461	11 Q9JLP3	Q9JLP3 mus musculus
30	1040	10.7	750	4 Q86TP7	Q86TP7 homo sapien
31	1001.5	10.3	616	4 Q15483	Q15483 mus musculus
32	1001	10.3	628	11 Q9J133	Q9J133 mus musculus
33	993	10.2	628	4 Q9HB63	Q9HB63 homo sapien
34	991	10.2	628	4 Q9BZP1	Q9BZP1 homo sapien
35	975	10.0	605	4 Q7Z5B6	Q7Z5B6 homo sapien
36	964	9.9	1512	11 Q8K3K1	Q8K3K1 rattus norv
37	889	9.1	1190	6 Q8HZ19	Q8HZ19 equus cabal
38	880	9.0	1196	6 Q867A2	Q867A2 canis famil
39	695.5	7.1	604	11 Q9Z4Z9	Q9Z4Z9 rattus norv
40	680	7.0	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi
41	678.5	7.0	569	13 Q57339	Q57339 xenopus lae
42	678	7.0	602	13 Q42203	Q42203 brachydanio
43	675.5	6.9	529	4 Q8N2D6	Q8N2D6 homo sapien
44	675	6.9	603	13 Q42140	Q42140 brachydanio
45	669.5	6.9	1574	11 Q88281	Q88281 rattus norv

#### ALIGNMENTS

#### RESULT 1

Q8JHV7	Q8JHV7	PRELIMINARY;	PRT; 1785 AA.
ID	Q8JHV7		
AC	Q8JHV7;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Laminin beta 1.		
GN	LAME1		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22065263; PubMed=12070089;		
RA	Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P.,		
RA	Hirst E.M., Stemple D.L.;		
RT	"Zebrafish mutants identify an essential role for laminins in		
RT	notochord formation."		
RL	Development 129:3137-3146(2002).		
DR	EMBL; AF468049; AAW61767.1;		
DR	GO; GO:0005578; C:extracellular matrix; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR003049; Laminin_EGF.		
DR	InterPro; IPR008211; LamNT.		
DR	Pfam; PF00053; laminin_EGF; 13.		
DR	Pfam; PF00055; laminin_Nterm; 1.		
DR	PRINTS; PR00011; EGF_Lam; 13.		
DR	SMART; SM00180; EGF_Lam; 13.		
DR	SMART; SM00136; LamNT; 1.		
DR	PROSITE; PS00022; EGF_1; 10.		
DR	PROSITE; PS01186; EGF_2; 2.		
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 12.		
KW	Laminin EGF-like domain.		
SEQUENCE	1785 AA; 137279 MW; 1BD338A0B6AB9F26 CRC64;		



Query Match	69.84;	Score	6811.5;	DB	13;	Length	1785;
Best Local Similarity	67.04;	Pred. No.	9.3e-290;				
Matches	1198;	Conservative	253;	Mismatches	328;	Indels	9;
Gaps	7;						
QY	3	LLQLAFALCARVRAQEPFSGCAEGSCYPATGDLIGRAOKLSVTSGLHKPE	62				
DB	2	LLQLAALSILG---AWALADVPBLGDVCTEGSCYPATGDLIGRAOQLLATSTCGVHKPE	58				
QY	63	PYCVISHLODKKCFICNSQDPYHETLNP--DSHLIENVVTTTAPNRLKIWQSENGVENY	121				
DB	59	PFCLVSHLODKKCFVCDSCQAINEAHOVTSHSIENVVTTTAPNRLKIWQSENGLENV	118				
QY	122	TIQLDLAEHPHFLIMFTFPPAAMLIERSDFGKTGWVRYPAYDEAFPGISTGP	181				
DB	119	TIQLDLAEHPHFLIMFTFPPAAMLIERSDFGKTGWVRYPAYDEAFPGISTGP	178				
QY	182	MKVVDIICDSRYSDIPESTGEVIFRALDPAFKIEDPSPRIONLLKTNIRIKFVKLH	241				
DB	179	MTKVDDVICDTRSDIPESTGEVIFRVLDPARIEDPSPRIONLLKTNIRIKFVKLH	238				
QY	242	TLGNLLDSRMEIREKYYIAYDMVVRGNCFCYGHASACAPVDGFMVEVGMVHGCMCR	301				
DB	239	TLGNLLDSRMEIREKYYIAYDMVVRGNCFCYGHASACAPVDGFMVEVGMVHGCMCN	298				
QY	302	HNTKGLNCELMDPVDHLPWRPAEGRNSNACKNCNNEHSISCHFDMAVYLATGNVSGV	361				
DB	299	HNTKGLNCECDPVDHLPWRPAEGRNTNACKCHCNHSHSCHFDMVYRASGNVSGV	358				
QY	362	CDQCQHTMGRNCRCQKPFYYQHPERDIRDPNFCERCTCDPAGSNEGICDSVDFSTGL	421				
DB	359	CDQCQHTMGRNCRCQKPFYYQHPERDIRDPNFCERCTCDPAGSNEGICDSVDFSTGL	418				
QY	422	IAGCRCKLVNVEGHCDVCEGFDYLSSEDPFCCKSCACNPLGTIPGNPCDSETHCYC	481				
DB	419	ISGCRCKLVNVEGHCDVCEGFDYLSSEDPFCCKSCACNPLGTIPGNPCDSETHCYC	477				
QY	482	KRLVTGHCDCCLPEHMGSLNDLGRPCDCDGLGALNNSCFAESGQCSCRPHMIGRCN	541				
DB	478	KRLVTGRNCDCCLPEHMGSLNDLGRPCDCDGLGALNNSCFAESGQCSCRPHMIGRCN	537				
QY	542	EVEGYPYATLDHYLYAEANLPGVSIYVERQVIOIRIPSWTGAQVRYPEGAYLEFFI	601				
DB	538	QVESGFYIALDHYLYAEANLPGVSIYVERQVIOIRIPSWTGAQVRYPEGAYLEFSI	597				
QY	602	DNIPIYSMEYDILRIYEPOLPHWEKAVITVORPQRIPTSRGCGNTIPDDNQVVSLSPGS	661				
DB	598	DNIPIYSMEYDILRIYEPOLPEQWEEVLVTIPRVITADSRCAANTMPDDNQVVSLSPGS	657				
QY	662	RYVLPVPCFEKGTNYTVRLLEQYTSDDSDVESPTLIDSLVMPYCKSLDIFTVGS	721				
DB	658	RYVLPVPCFEKGTNYTVRLLSLY--SALSDVQSPYTLIDSLVLMFHCRLDIFSGSGT	716				
QY	722	-GDGVVNSAMETFORVRCLENSRVVKTMTDVCNRIIFSISALLHOTGLACECDPQGS	780				
DB	717	EGGNLVNSAMENFORVRCLENSQAVVKTMTDVCNRIIFSISALLHOTGLACECDPQGS	776				
QY	781	LSSVCDPNGGQCQCRPNVVGTRNRCAPGTFGFGSGCKPCCECHLOGSNVAFNCPVTGQC	840				
DB	777	LSTVCDPNGGQCQCRPNVVGTRNRCAPATFUXPGCRPCDCSPGSGVSHSICHEATGQC	836				
QY	841	HCFCQVYARQCDRLCPGHGWFPSQPCOCNCHADDQDPVTGECINCDQYTMGNHNCERCLA	900				
DB	837	ECTAGYGRQCDRLCPGHGWFPSQPCOCNCHADDQDPVTGECINCDQYTMGNHNCERCLG	896				
QY	901	GYGDPFIIGSGDHCRFCPCPDGSGRQFARSQVDPVTLOLACVDPGYIGSRCDPCAS	960				
DB	897	GYGDPFVLGSGDHCRFCPCPDGSGRQFARSQVDPVTLOLACVDPGYIGSRCDPCAS	956				
QY	961	GYFGNPSVGGSCQCCQCHNIDITDPEACDKETGRCLKCLVHTGEGHCQCFRGYVGDA	1020				
DB	957	GYFGNPSVGGSCQCCQCHNIDITDPEACDKETGRCLKCLVHTGEGHCQCFRGYVGN	1016				
QY	1021	LQDRCRKCVCNVLGTQVQEH--NGSDCQCDKATGQCCLPNNVIGONCDRCAPNTWLQASGT	1079				

Db	1017	LTQSCRKVCNONGTVEMCPSGNCNDLTSQCCLCLPNNVVGHCDCQCAPDTWNASGK	1076
QY	1080	GDPCPCNAAHSPGSCNEFTGCQCMPOFGGRTCSBQCLLFWGPDVYECRACDCDPGSI	1139
DB	1077	GCSDCDPDPHSPGSSCNEIMGQCSCKPFGGRTCRECLFWGPNPKVCHACDCDPGSI	1136
QY	1140	ETPOCDSTGCVCVGVGPRCDKTCRQYSGVFPDCTPCHQCFALMDVIIAELTNRTHR	1199
DB	1137	AEQCNKVTHGVCVGVGPRCDTCARGYTGFEFQCHOCFAEWDLIVGDLNQTHR	1196
QY	1200	FLEKAKALKISGVIGPYRETVDOSVERKVSEIKDIIAQSAPAPLKNIGNLFEASKLKD	1259
DB	1197	LVQKVNTIKATGTYGTYQATINNVSANSIRNIIAQNAPATPLTEIOGLEQATLMAE	1256
QY	1260	VTEMAQVEVKLSDDTYSQSNSTAKELDSLQTAESLDNTVKELAEQLEFKNSDIRGALD	1319
DB	1257	MNSHNLNTEETLEISDNNSTDTKLKSLKEBAQKLEQTVKDLRQVFPVKNSDIRGARA	1316
QY	1320	SITKYFQMSLEABERVNNASTTEPNSTVEQSALMRQVEDVMMERESQFKKEQEQARLLD	1379
DB	1317	SVTRYEQSQNABIRANASTTDPYNLVQNSATLRTETEELMNQTKKEFNQRODEFKSLD	1376
QY	1380	ELAGKQSLDLSAAAEWTCGTPPGA--SCSETECGGPNCRITDGERKCGPGGCGGLVTVAH	1438
DB	1377	NLAGQLETLDELSEKTCGSPAGSNCADSRCCGLSCVDMQGRKCGGEGCGGLTTLAH	1436
QY	1439	NAMQKAMDLDQDVLASALAEVQSLKMWSEAKURADEAKASABDILLKTNATKMKDKNE	1498
DB	1437	NAMQKAXDFLEIISAMEEVDKLSKMWSEAKURADEAKLNAQEVLAKTNETKRYDSSNE	1496
QY	1499	ELRNLIIQIIRNFLTQDSADLDSIEAVANEVLKMWEPSTPOQLNLTEDIRERVESLSOVE	1558
DB	1497	ELRQLIIQIIRDFLTQDGADLESIEAVANEVLQMWETTPAQQLNLTETIRERVGSITDVE	1556
QY	1559	VILQHSAADIRARAEMLLLEAKRASKSATVDYKVTADMVKEALPEAKAQAQVAEKALKQADE	1618
DB	1557	DILQSAADILRAESLLEQARKARKEASDVKSTAEWVKEALQHAERAQNSVAEALKQAAV	1616
QY	1619	DIQGTQMLTISISSETAASEETLFPNASQISELERNVVELKBAQNSGEAEVIEKVVYT	1678
DB	1617	DIKGTQDLVSEBSETSDSELKSNATRLKLESVDALKKALNWSISANSTKEAES	1676
QY	1679	VKQSAEDVKTLDGELDEKYKKVENIATKTEBSADARRKAEMLQNEAKTLQAQNSKLQ	1738
DB	1677	INALAEQLKDLSELKDKYSTVEELLITQKAEQVAEKAKRAEKLEQEARNLLQASEKLQ	1736
QY	1739	LLKOLERYEDNQRYLEDKQAEARLEGEVRSLLKDISQKAVYVYSTCL	1786
DB	1737	LLKQNKRYDNQKLLDKANELVDLEKAVKLEQIESHKVTVYSTCL	1784

RESULT 2

Q8TAS6

PRELIMINARY; PRT; 1086 AA.

Q8TAS6; AC Q8TAS6; DT 01-JUN-2002 (TREMBLrel. 21, Created) DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DE Similar to laminin, beta 1 (Fragment). OS Homo sapiens (human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI\_TaxId=9606; RN [1] SEQUENCE FROM N.A. RP TISSUE=Muscle; RC Straussberg R.; RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. DR EMBL; BC026018; AAH26018.1; DR GO; GO:0005198; F:structural molecule activity; IEA. DR InterPro; IPR006209; BGF like. DR InterPro; IPR002049; Laminin\_BGF.

RESULT 2

Q8TAS6

ID	Q8TAS6	PRELIMINARY;	PRT;	1086	AA.
AC	Q8TAS6;				
DT	01-JUN-2002 (TREMELrel. 21, Created)				
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)				
DT	01-JUN-2003 (TREMELrel. 24, Last annotation update)				
DE	Similar to laminin, beta 1 (fragment).				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Muscle;				
RA	Strausberg R.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC026018; AAH26018.1;				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro; IPR006209; EGF like.				
DR	InterPro; IPR002049; Laminin_EGF.				

1017 LTQSCRKVCNQMGTVEEMCPGNCNCNCDLTSGCCLPLNVVGHQDQCAPDTWNMASGK 1076

1080 GCDPCNCAHAFSGPSNEFTGQCQCMFPGGRTSCQBELFWGDPDVEACDCDPRGI 1139

1077 GCEBCDCDHPHSGFSSCNEIMGQSCCKPFGGRTCRECLFWGPNVFKACHACDCDPRGI 1136

1140 ETPOCDSTGQCVCEGVGPRCDKTRGSGVFPDCTPHQCQFALNDVIAELTNTTHR 1159

1137 AEQCNKVTGHCVCVGVSGPRCDTCARGTGEFPQCHQCFAEWDIIVGDLTNTTHR 1196

1200 FLEKAKALKISGVIGPYRETVDSEVERKVSSEIKOIAQSPAAEPKNIQNGNLFEEAEKLIK 1259

1197 LVQKNITKATIGTPQATINNVENSANSIRNLAQNPATOPTLEIQGLEQATALMAE 1256

1260 VTEMAQVVEVKLSTTQSSNTAKELSLQTEAESLONTVELAEQLEFKNSDIRGALD 1319

1257 MNSNLNLTETLSEISSDNNSTDTKLKSLKEAQLEQTVKDLREQVEFVKNSDIRGARA 1316

1320 SITKYFOMSLAEERVNASTTTPNSTVTEQSAIMDRVEDVNMERESOFKEQEQAQRLD 1379

1317 SVTRYEOSQNAETRANASTTDPYLVNQSATLATETELMNQTKKEFNQDEFSKKLD 1376

1380 ELAGKLQSLDLSAAEMTCGTPPGA--SCSETECGPNCRTDEGERKCGGCGGLVTVAH 1438

1377 NLAGQLETLDLSELSEKTCGSPAGSNCADSRGCGLSCVDMQSGKCGGEGCDGLTTLAH 1436

1439 NAWQAMLDODVLSALAEVQLSQVSEAKLRADAEKQSAEDILLKTNATKEXDKSNE 1498

1437 NAWQAKAFDLEISAMEEVKLSQVSEAKVKADEAKLNAQEVLAQTNETKKEVDSSNE 1496

1499 ELRNLIKQIRNPLTODSADLDSIEAVANVLKJMSNPSTPOQLQNLTEDIRERVSLSQVE 1558

1497 ELRQLIKQIRDFLTQDQADLESIEAVANVLQMQMPTTPAQLQNLTEIRERVSLSQVE 1556

1559 VILQHSADIAEAEMLEAEKRAKSDATDVKTADVKEALEAEAKQAQAAEKAQKQADE 1618

1557 DILNQSAADIIRAEELLEQAKRAKESADVSTAEVKEALQHAERQNSVAEALKQAQV 1616

1619 DIQGTQNLTSIESSTAASEETLFPNASORISELERNVEELKRAQAQNSGEAEYIEKVYVT 1678

1617 DIKGTQDLVSVESSETSELKLSNATRLKLSVALLKEKALNTSISANSTEKEAES 1676

1679 VKQSAEDVKTLIDGDEKVKVENLIAKTEESADARRKAEMLQNEAKTLLAQANSKIQ 1738

1677 INALAEQKQKQDLSELKQKYSTVEELITQKAEQVAAEKRAEKLOEARNLLQASEKIQ 1736

1739 LKDLERKYEDNQRYLEKQAELEGEVRSLKMDISQKVAVYSTCL 1786

1737 LKLNLEKNYDQKQKLELQKANELVLEKAVKELLQEISHKVTYVSTCL 1784

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 47.8797 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-8  
Perfect score: 9654  
Sequence: 1 QPERSYGCAGSCYPATGD.....EVRSLKDISQKAVYSICL 1765

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Length	DB ID	Description
1	9654	100.0	1765	3 AAB19798	Aab19798 Human lam
2	9654	100.0	1765	3 AAB48449	Aab48449 Human lam
3	9654	100.0	1765	5 ABB81591	Abb81591 Human lam
4	9654	100.0	1786	2 AAW50893	Aaw50893 Human lam
5	9654	100.0	1786	3 AAB16522	Aab16522 Human lam
6	9654	100.0	1786	3 AAB19797	Aab19797 Human lam
7	9654	100.0	1786	3 AAB48448	Aab48448 Human lam
8	9654	100.0	1786	4 AAB30788	Aab30788 Human she
9	9654	100.0	1786	5 ABB81590	Abb81590 Human lam
10	9638	99.8	1786	5 AAM48896	Aam48896 Laminin p
11	9618.5	99.6	1785	2 AAY15461	Aay15461 Human lam
12	9092	94.2	1786	3 AAB19799	Aab19799 Mouse lam
13	9092	94.2	1786	3 AAB48450	Aab48450 Mouse lam
14	9092	94.2	1786	5 ABB81592	Abb81592 Mouse lam
15	9035	93.6	1776	2 AAW50894	Aaw50894 Mouse lam
16	8967.5	92.9	1764	1 AAP1672	Aap1672 Primary a
17	8873	91.9	1725	3 AAB19800	Aab19800 Mouse lam
18	8873	91.9	1725	3 AAB48451	Aab48451 Mouse lam
19	8873	91.9	1725	5 ABB81593	Abb81593 Mouse lam
20	5084	52.7	1801	2 AAW50895	Aaw50895 Rat lamin
21	5084	52.7	1801	7 ADE60383	Ade60383 Rat Prote
22	5048	52.3	1798	2 AAW50896	Aaw50896 Human lam
23	5048	52.3	1798	7 ADE60385	Ade60385 Human Pro
24	5046	52.3	1799	5 AAM50359	Aam50359 Mouse lam
25	4918	50.9	1798	5 AAU84346	Aau84346 Protein L

26	4918	50.9	1798	5 AAM50360	Aam50360 Human lam
27	3881	40.2	822	5 AAM48897	Aam48897 Laminin p
28	3850.5	39.9	1788	4 ABB62995	Abb62995 Drosophil
29	3832.5	39.7	1761	2 AAY15457	Aay15457 Human lam
30	3625.5	37.6	1670	7 ADE07851	Ade07851 Novel pro
31	3076.5	31.9	1101	7 ADE28641	Ade28641 Human NOV
32	3044.5	31.5	1105	2 AAY15459	Aay15459 SEQ ID 5
33	2776	28.8	466	2 AAR07447	Aar07447 Human lam
34	2348	24.3	527	3 AAB58995	Aab58995 Breast an
35	2115	21.9	434	1 AAP60109	Aap60109 Human Bl
36	1787	18.5	315	6 ABU70520	Abu70520 Human adi
37	1759	18.2	1639	4 ABB59807	Abb59807 Drosophil
38	1680.5	17.4	1609	3 AAB19801	Aab19801 Human lam
39	1680.5	17.4	1609	3 AAB48452	Aab48452 Human lam
40	1680.5	17.4	1609	5 ABB81594	Abb81594 Human lam
41	1680.5	17.4	1609	7 ADC01887	Adc01887 Human lam
42	1680.5	17.4	1617	3 AAB19803	Aab19803 Human lam
43	1677	17.4	1572	3 AAB19806	Aab19806 Mouse lam
44	1677	17.4	1572	3 AAB48455	Aab48455 Mouse lam
45	1677	17.4	1572	5 ABB81597	Abb81597 Mouse lam

ALIGNMENTS

RESULT 1  
AAB19798  
ID AAB19798 standard; protein; 1765 AA.  
XX  
AC AAB19798;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Human laminin 2 mature beta-1 chain.  
XX  
KW Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200066730-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011378.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 15-JUN-1999; 99US-0139198P.  
PR 12-JUL-1999; 99US-0143289P.  
PR 24-SEP-1999; 99US-0155945P.  
(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Yurchenco P;  
WPI: 2000-687537/57.  
N-PSDB; AAB88898.  
Purified laminin 2 protein, useful for research and therapeutic purposes including peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, and ex vivo cell therapy.  
Claim 5; Page 199-204; 305pp; English.  
The present sequence is that of the human laminin 2 beta-1 chain mature protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1 (100 kDa) chains. It is thought to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis. Genetic defects in its structure or expression are associated with a major type of congenital muscular dystrophy. Laminin 2 is also thought to be important in Schwann cell/basal lamina interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding

CC them (see AAA8891-906), methods for making recombinant laminin 2, cells  
 CC that express recombinant laminin 2, and methods for using purified  
 CC laminin 2 for research and therapeutic purposes including peripheral  
 CC nerve regeneration, treatment of degenerative muscle disorders,  
 CC angiogenesis regulation, promoting cell attachment and migration, ex vivo  
 CC cell therapy, improving the take of grafts, improving the  
 CC biocompatibility of medical devices and preparing improved culture  
 CC devices and media  
 XX  
 SQ Sequence 1765 AA;  
 Query Match 100.0%; Score 9654; DB 3; Length 1765;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QEPFFSGCAGSCYPATGDLIGRAOKLSVTSCGLHKPEPYCIIVSHLOEDKKFCINS 60  
 DB 1 QEPFFSGCAGSCYPATGDLIGRAOKLSVTSCGLHKPEPYCIIVSHLOEDKKFCINS 60  
 QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEAFPHFLIMTFK 120  
 DB 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEAFPHFLIMTFK 120  
 QY 121 TFRPAALMIESSDPFGKTVGYRYPAYDCASPGISTGPMKVVDDIICDSRYSDIEPST 180  
 DB 121 TFRPAALMIESSDPFGKTVGYRYPAYDCASPGISTGPMKVVDDIICDSRYSDIEPST 180  
 QY 181 EGEVIFRALDPAFKIEDPYSPRIQNLKILNRIKFKVYKLTLDGNLDSMEIREYVYA 240  
 DB 181 EGEVIFRALDPAFKIEDPYSPRIQNLKILNRIKFKVYKLTLDGNLDSMEIREYVYA 240  
 QY 241 YDMVVRGNCFYCHASECAPVDGFNEEVGMVGHCHCHNTKGLNCELMDFYHDLPW 300  
 DB 241 YDMVVRGNCFYCHASECAPVDGFNEEVGMVGHCHCHNTKGLNCELMDFYHDLPW 300  
 QY 301 RPAGRNSNACKCNNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360  
 DB 301 RPAGRNSNACKCNNEHSISCHFDMAVYLATGNVSGGVCDCCQHNMTGRNCEQCKPFY 360  
 QY 361 YQHPERIDRPNFCERTCTCPAGSQNEGICDSYDTPSTGLIAGCCRCKLNVGEHCDCVK 420  
 DB 361 YQHPERIDRPNFCERTCTCPAGSQNEGICDSYDTPSTGLIAGCCRCKLNVGEHCDCVK 420  
 QY 421 EGFYDLSSDPFGCKSCACNPLGTIPGNPCDSETHCYCKRLVTGQHCDOCLPEHWGLS 480  
 DB 421 EGFYDLSSDPFGCKSCACNPLGTIPGNPCDSETHCYCKRLVTGQHCDOCLPEHWGLS 480  
 QY 481 NDLGCRPCDCDLGALNNSCFABSGQSCSRPHMIGRCQNEVEPGYVYFATLDHYLYEABE 540  
 DB 481 NDLGCRPCDCDLGALNNSCFABSGQSCSRPHMIGRCQNEVEPGYVYFATLDHYLYEABE 540  
 QY 541 ANLGGVSIIVERQYIQRISWTGAGFVRPEGAYLEFFDNIPIYSMEYDILIRYEPQLP 600  
 DB 541 ANLGGVSIIVERQYIQRISWTGAGFVRPEGAYLEFFDNIPIYSMEYDILIRYEPQLP 600  
 QY 601 DHWEKAVITVQRPRIPTSSRCGNTIPDDNQVVSLSFGSRYYVLPFPVCFEKGNTYVR 660  
 DB 601 DHWEKAVITVQRPRIPTSSRCGNTIPDDNQVVSLSFGSRYYVLPFPVCFEKGNTYVR 660  
 QY 661 LELQYTSDDSDVSPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNSAWETQRYRCLE 720  
 DB 661 LELQYTSDDSDVSPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNSAWETQRYRCLE 720  
 QY 721 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDCDPQGSLSVCDPNGGQCQCPNVVGR 780  
 DB 721 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDCDPQGSLSVCDPNGGQCQCPNVVGR 780  
 QY 781 TCNRCAPGTFGFGSGCKPECHIQGSVNAFCNPVTPCQCHCFQGVYARQCDCRCLPGHWGF 840  
 DB 781 TCNRCAPGTFGFGSGCKPECHIQGSVNAFCNPVTPCQCHCFQGVYARQCDCRCLPGHWGF 840  
 QY 841 PSCQPCQCNHADDPCDPTVTECLNCQDYTMGHNCERCLAGYVGPDIIGSGDHCRPCPCPD 900

DB 841 PSCQPCQCNHADDPCDPTVTECLNCQDYTMGHNCERCLAGYVGPDIIGSGDHCRPCPCPD 900  
 QY 901 GPDSSGRQFARSQYDPVTLQACVCDPGYIGSRCDDCASGYFNGPSEVGGSCQCCQCHNN 960  
 DB 901 GPDSSGRQFARSQYDPVTLQACVCDPGYIGSRCDDCASGYFNGPSEVGGSCQCCQCHNN 960  
 QY 961 IDTTPEACDKETGRCLKLYHTEGEHCQFCRFGYIGDALRQDCRCKVCNYLGTVOEHEN 1020  
 DB 961 IDTTPEACDKETGRCLKLYHTEGEHCQFCRFGYIGDALRQDCRCKVCNYLGTVOEHEN 1020  
 QY 1021 GSDCCQCDKATGOCICLCPNVIGQNCDCRCPANTWQLASGTGCDPCNCNAAHSFGPSCNEFTG 1080  
 DB 1021 GSDCCQCDKATGOCICLCPNVIGQNCDCRCPANTWQLASGTGCDPCNCNAAHSFGPSCNEFTG 1080  
 QY 1081 QCCQMPFGGRTCSBCQELFWGDDPVECRACDPCPRGIETPQCQSTQCQCVGVEGPR 1140  
 DB 1081 QCCQMPFGGRTCSBCQELFWGDDPVECRACDPCPRGIETPQCQSTQCQCVGVEGPR 1140  
 QY 1141 CDKTRGSGVPPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGIVGPVRETVD 1200  
 DB 1141 CDKTRGSGVPPDCTPCHQCFALWDVIAELTNRTHRFLEKAKALKISGIVGPVRETVD 1200  
 QY 1201 SVKRVKSIKDLAQSPAAEPKNIKNLFEAEKLIKDVTEMAQVEVKLSDTTSSQNST 1260  
 DB 1201 SVKRVKSIKDLAQSPAAEPKNIKNLFEAEKLIKDVTEMAQVEVKLSDTTSSQNST 1260  
 QY 1261 AKELDSLQTEAESLNTVKELAEOLFIKNSDIRGALDSITIKYFQMSLEAEERNVASTTE 1320  
 DB 1261 AKELDSLQTEAESLNTVKELAEOLFIKNSDIRGALDSITIKYFQMSLEAEERNVASTTE 1320  
 QY 1321 PNSTVEQALMRDVEDVMMERESQFKEQEAEQARLLDELAKLQSLDLSAAAEWTCGTP 1380  
 DB 1321 PNSTVEQALMRDVEDVMMERESQFKEQEAEQARLLDELAKLQSLDLSAAAEWTCGTP 1380  
 QY 1381 PGASCSSETECGPNCRITDEGERKCGGPGCGGLVTVAHNAWKAMDLDQDVLALAEVEQL 1440  
 DB 1381 PGASCSSETECGPNCRITDEGERKCGGPGCGGLVTVAHNAWKAMDLDQDVLALAEVEQL 1440  
 QY 1441 SKWSEAKLRADAEKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500  
 DB 1441 SKWSEAKLRADAEKQSAEDILLKTNATKEKMDKSNELRNLIKQIRNFLTQDSADLDSI 1500  
 QY 1501 EAVANEVLKMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADTARAEMLLEAKRA 1560  
 DB 1501 EAVANEVLKMPSTPQQLNLTEDIRERVESLSQVEVILQHSAAADTARAEMLLEAKRA 1560  
 QY 1561 SKSATDVKTADVMKVEALAEAKQVAEAKIKQADEDIQGTQNLTSISETAASBETL 1620  
 DB 1561 SKSATDVKTADVMKVEALAEAKQVAEAKIKQADEDIQGTQNLTSISETAASBETL 1620  
 QY 1621 FNASQRISELRNVEELKRAAQNQSGEAEYIEKVYTVKQSAEDVYKTLDGELDEKYKV 1680  
 DB 1621 FNASQRISELRNVEELKRAAQNQSGEAEYIEKVYTVKQSAEDVYKTLDGELDEKYKV 1680  
 QY 1681 ENLIAKKTESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKVEDNQRYLEDKQEL 1740  
 DB 1681 ENLIAKKTESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKVEDNQRYLEDKQEL 1740  
 QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765  
 DB 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765  
 RESULT 2  
 AAB48449  
 ID AAB48449 standard; protein; 1765 AA.  
 XX  
 AC AAB48449;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Human laminin 8 polypeptide, SEQ ID NO: 16.  
 XX

KW Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
XX vascular tissue injury; neural injury; angiogenesis regulation.  
XX Homo sapiens.  
XX WO200066732-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011543.  
XX 30-APR-1999; 99US-0131720P.  
XX 21-AUG-1999; 99US-0149738P.  
XX 24-SEP-1999; 99US-0155945P.  
XX 11-FEB-2000; 2000US-0182012P.  
XX (BIOS-) BIOTRATUM INC.  
XX Kortessmaa J, Tryggvason K;  
XX WPI; 2000-687539/67.  
XX N-PSDB; AAC83710.  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 163-168; 245pp; English.  
XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
XX family of heterotrimeric glycoproteins that function via binding  
XX interactions with neighboring cell receptors and by forming laminin  
XX networks. They are signalling molecules which influence cellular  
XX function. Laminin 8 is useful for treating injuries to tissue of  
XX mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
XX treating injuries to vascular tissue, promoting cell attachment and  
XX migration, ex vivo cell therapy, improving the biocompatibility of  
XX medical devices, and preparing improved cell culture devices and media.  
XX Laminin 8 is also useful for promoting re-endothelialisation at the site  
XX of vascular injuries, improving the take of grafts, improving the  
XX biocompatibility of medical devices, treating neural injuries (neural  
XX regeneration), regulating angiogenesis, and promoting cell attachment and  
XX migration  
SQ Sequence 1765 AA;  
Query Match 100.0%; Score 9654; DB 3; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCTVSHLQEDKXCFICNS 60  
DB 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKHPYCTVSHLQEDKXCFICNS 60  
QY 61 QDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVENVTIQLDLAEFHTLIMTFK 120  
DB 61 QDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVENVTIQLDLAEFHTLIMTFK 120  
QY 121 TTPRAAMLERSDGGKTGWVRYRAYDCEASFPGISGPMKKYDDIICDSRYSDIEPST 180  
DB 121 TTPRAAMLERSDGGKTGWVRYRAYDCEASFPGISGPMKKYDDIICDSRYSDIEPST 180  
QY 181 EGEVIFRALDPAFKIEDPYSPIQNLLKITNRIKFKVLHTLGNLDSRMEIREKYYA 240  
DB 181 EGEVIFRALDPAFKIEDPYSPIQNLLKITNRIKFKVLHTLGNLDSRMEIREKYYA 240  
QY 241 VYDMVVRGNCFCYGHASECAPVDGNEVEGVHGHGCMCRNTKGNLCELWDFHDLWP 300  
DB 241 VYDMVVRGNCFCYGHASECAPVDGNEVEGVHGHGCMCRNTKGNLCELWDFHDLWP 300  
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMTGRNCEQCKPFY 360

DB 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMTGRNCEQCKPFY 360  
QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGHECHDVCK 420  
DB 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGHECHDVCK 420  
QY 421 EGYDLSSEDPFCKSCACNPLGTTPGPNPCDSETHCYCKRLVTQCHQCDQLPEHWGLS 480  
DB 421 EGYDLSSEDPFCKSCACNPLGTTPGPNPCDSETHCYCKRLVTQCHQCDQLPEHWGLS 480  
QY 481 NDLDGCRPCDCLGGALNNSCFAESQSCSRPHMIGROCNQNEVEPGYFATLHLYEASE 540  
DB 481 NDLDGCRPCDCLGGALNNSCFAESQSCSRPHMIGROCNQNEVEPGYFATLHLYEASE 540  
QY 541 ANLGPVSVIVERQYIQDRIPSWTGAQFVRVPGAYLEFFIDNIPYSMEVDILLIRYEPQLP 600  
DB 541 ANLGPVSVIVERQYIQDRIPSWTGAQFVRVPGAYLEFFIDNIPYSMEVDILLIRYEPQLP 600  
QY 601 DHWEKAVITVQRPGRIPTSRCGNTIPDDDNQVSVSPGSRVYVLPVPCFEKGTNTYVR 660  
DB 601 DHWEKAVITVQRPGRIPTSRCGNTIPDDDNQVSVSPGSRVYVLPVPCFEKGTNTYVR 660  
QY 661 LELPQYTSDDSVESPYTLIDSLVLMYPCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720  
DB 661 LELPQYTSDDSVESPYTLIDSLVLMYPCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720  
QY 721 NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACBDDPQGLSSVCDPNGGQCCQCRPNVGR 780  
DB 721 NSRSVVKTPMTDVCRNIIIFSISALLHOTGLACBDDPQGLSSVCDPNGGQCCQCRPNVGR 780  
QY 781 TCMRCAPGTFGFGPSGCKPCCECHLQGSVNAFNPVTGQCHQFQGVYARQCDRLCPHMGF 840  
DB 781 TCMRCAPGTFGFGPSGCKPCCECHLQGSVNAFNPVTGQCHQFQGVYARQCDRLCPHMGF 840  
QY 841 PSCQPCQCNHADDQDPVTGECNLNCDQDYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900  
DB 841 PSCQPCQCNHADDQDPVTGECNLNCDQDYTMGNHCERCLAGYGDPIIGSGDHCRPCPCPD 900  
QY 901 GPDSGRQFARSQYQDPVTIQLACVCDPQYIGSRCDCCASGFGNPNSEVSGSQCCOCHNN 960  
DB 901 GPDSGRQFARSQYQDPVTIQLACVCDPQYIGSRCDCCASGFGNPNSEVSGSQCCOCHNN 960  
QY 961 IDTTDPEACDKETGRCLKCLYHTEGSHCQFCRFGYGDALRQDCRKCVCNLTGVQEHCN 1020  
DB 961 IDTTDPEACDKETGRCLKCLYHTEGSHCQFCRFGYGDALRQDCRKCVCNLTGVQEHCN 1020  
QY 1021 GSDCCDKATGQCLCLPNVIGQNCDCRCAPTNWLASGTGCDPCNCAHSGFSCNNEFTG 1080  
DB 1021 GSDCCDKATGQCLCLPNVIGQNCDCRCAPTNWLASGTGCDPCNCAHSGFSCNNEFTG 1080  
QY 1081 QCCQMFQGGRTCEQQLFWGDDPVECRACDPRGIEPTQCDQSTGQCVCEGVEGPR 1140  
DB 1081 QCCQMFQGGRTCEQQLFWGDDPVECRACDPRGIEPTQCDQSTGQCVCEGVEGPR 1140  
QY 1141 CDKCTRGSVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200  
DB 1141 CDKCTRGSVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRETVD 1200  
QY 1201 SVRKVSEIKDILAQSPAAEPKNIQNLPEAEKLIKDVTENMAQVEVKLSDTTQSNSST 1260  
DB 1201 SVRKVSEIKDILAQSPAAEPKNIQNLPEAEKLIKDVTENMAQVEVKLSDTTQSNSST 1260  
QY 1261 AKELDSLQTEAESLDNTVKELAEQLEFFIKNSDIRGALDSITKYFQMSLEABEVRNASTTE 1320  
DB 1261 AKELDSLQTEAESLDNTVKELAEQLEFFIKNSDIRGALDSITKYFQMSLEABEVRNASTTE 1320  
QY 1321 PNSTVQSALMRDRVDVMMERESQFKEQEOEARLLDELAKGLQSLDLISAAAEAMTCGTP 1380  
DB 1321 PNSTVQSALMRDRVDVMMERESQFKEQEOEARLLDELAKGLQSLDLISAAAEAMTCGTP 1380  
QY 1381 PGASCSETECGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440  
DB 1381 PGASCSETECGGNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASAEVEQL 1440

QY 1441 SKWVSEAKRADBAKQSAEDILLKTNATKEKMDKSNBEEENLKIQRNFLTQDSADLDSI 1500  
Db 1441 SKWVSEAKRADBAKQSAEDILLKTNATKEKMDKSNBEEENLKIQRNFLTQDSADLDSI 1500  
QY 1501 EAVANEVLKXEMESTPQQLNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLBEAKRA 1560  
Db 1501 EAVANEVLKXEMESTPQQLNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLBEAKRA 1560  
QY 1561 SKSATDVKTADVMKGALEBAEAEKAAQVAEAKAIKQADEDIQGTQNLNLTSESETAASEETL 1620  
Db 1561 SKSATDVKTADVMKGALEBAEAEKAAQVAEAKAIKQADEDIQGTQNLNLTSESETAASEETL 1620  
QY 1621 FNASQISELERNVEELKRAAONSGEAEVIEKVVTYVKAQSAEDVKKTLDDGLDEKVKV 1680  
Db 1621 FNASQISELERNVEELKRAAONSGEAEVIEKVVTYVKAQSAEDVKKTLDDGLDEKVKV 1680  
QY 1681 ENLIAXKTESADARRKAEMLQNEAKTLQAQNSKLQLLKDLERKYNQRYLEDKAQBL 1740  
Db 1681 ENLIAXKTESADARRKAEMLQNEAKTLQAQNSKLQLLKDLERKYNQRYLEDKAQBL 1740  
QY 1741 ARLEGEVRSLLKDIISOKVAVYSTCL 1765  
Db 1741 ARLEGEVRSLLKDIISOKVAVYSTCL 1765

RESULT 3  
ABB81591  
ID ABB81591 standard; protein; 1765 AA.  
XX ABB81591;  
AC ABB81591;  
DT 19-SEP-2002 (first entry)  
XX Human laminin 10 second chain protein sequence SEQ ID NO:8.  
DE Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
XX tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX Homo sapiens.  
OS WO200250111-A2.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P.  
XX 28-MAR-2001; 2001US-0279282P.  
XX 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
PI WPI; 2002-557650/59.  
XX N-PSDB; ABQ72909.  
XX New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX Claim 9; Page 126-132; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents a second chain protein of laminin 10, from the present  
XX invention  
QY Sequence 1765 AA;  
Query Match 100.0%; Score 9654; DB 5; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QEPFSGCGAGSGCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 60  
Db 1 QEPFSGCGAGSGCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIIVSHLQEDKKCFICNS 60  
QY 61 QDPYHEITLNPDSHLIENVTTFAPNRLKIWKQSENGVENVTIQLDLAEAFHFTLIMTFK 120  
Db 61 QDPYHEITLNPDSHLIENVTTFAPNRLKIWKQSENGVENVTIQLDLAEAFHFTLIMTFK 120  
QY 121 TFRPAAMLIERSSDFGTGWYRYFAYDCEASPGISTGPMKKVDDIICDSRYSDIEPST 180  
Db 121 TFRPAAMLIERSSDFGTGWYRYFAYDCEASPGISTGPMKKVDDIICDSRYSDIEPST 180  
QY 181 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGDNLDSRWEIREKYYA 240  
Db 181 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGDNLDSRWEIREKYYA 240  
QY 241 VYDMVRGNCFCYGHASECAPVDGFEVEGVMHGHCMCRHNTKGLNCELCEMDFYHDLPW 300  
Db 241 VYDMVRGNCFCYGHASECAPVDGFEVEGVMHGHCMCRHNTKGLNCELCEMDFYHDLPW 300  
QY 301 RPAEGRSNACKKCNCHSISCHFDMAVYATGNSGGVCCDCHNTGRNCEQCKPFY 360  
Db 301 RPAEGRSNACKKCNCHSISCHFDMAVYATGNSGGVCCDCHNTGRNCEQCKPFY 360  
QY 361 YOHERDIRDNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCLNVEGEHCDVCK 420  
Db 361 YOHERDIRDNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCLNVEGEHCDVCK 420  
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETHCYCKRLVTGQHCQCLPEHNGLS 480  
Db 421 EGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSETHCYCKRLVTGQHCQCLPEHNGLS 480  
QY 481 NDLGCRPCDCDILGALNNSCFAESGQSCRPNMGICQNEVEPGYFATLDHYLYEAE 540  
Db 481 NDLGCRPCDCDILGALNNSCFAESGQSCRPNMGICQNEVEPGYFATLDHYLYEAE 540  
QY 541 ANLQPGVSIYERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEQLP 600  
Db 541 ANLQPGVSIYERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEQLP 600  
QY 601 DHWEKAVITVORPGRIPTSRGCGNTIPDDNQVVSLSFGSRYVVLPRPVCFEKGNTYVR 660  
Db 601 DHWEKAVITVORPGRIPTSRGCGNTIPDDNQVVSLSFGSRYVVLPRPVCFEKGNTYVR 660  
QY 661 LELPQYTSDDSDVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVVTTNSAMETFORYCLE 720  
Db 661 LELPQYTSDDSDVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVVTTNSAMETFORYCLE 720  
QY 721 NSRSVVKTPMTDVCNRIIFISALLHGTGLACEDCDPGSSLSVCDPNGGQCCRPNVVGR 780  
Db 721 NSRSVVKTPMTDVCNRIIFISALLHGTGLACEDCDPGSSLSVCDPNGGQCCRPNVVGR 780  
QY 781 TCNRCAPGTGFGPGCKPCCECHLQGSVNAFCNPVTQCHCFQGVYARQCDRLPGHWGF 840  
Db 781 TCNRCAPGTGFGPGCKPCCECHLQGSVNAFCNPVTQCHCFQGVYARQCDRLPGHWGF 840  
QY 841 PSCQPCQNGHADDPCDVTGELNCDQYTWGNCERCLAGYVGPPIIGSGDHCPCPCPD 900  
Db 841 PSCQPCQNGHADDPCDVTGELNCDQYTWGNCERCLAGYVGPPIIGSGDHCPCPCPD 900  
QY 901 GPDGRQFARSQYQDPVTQLQACVCDPGYTGSRCDDCASGFFGNPSEVGSQPCQCHNN 960  
Db 901 GPDGRQFARSQYQDPVTQLQACVCDPGYTGSRCDDCASGFFGNPSEVGSQPCQCHNN 960

Db 901 GPDGQFARSCYQDVTIQLACVDPGYIGSRCDCCASGYFNPSEVGGSCQPCQCHNN 960  
Qy 961 IDTTDPEACDKETGKCLVHTEGHCQFCRFGYGGDALQDCKKVCNVLGTVQEHCH 1020  
Db 961 IDTTDPEACDKETGKCLVHTEGHCQFCRFGYGGDALQDCKKVCNVLGTVQEHCH 1020  
Qy 1021 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSHFGPSCNEFTG 1080  
Db 1021 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSHFGPSCNEFTG 1080  
Qy 1081 QCQCMFGGGRGSCSCQELFWGDDVEGRACDPRGLETPOCDOSTGQCVCVEGVEGR 1140  
Db 1081 QCQCMFGGGRGSCSCQELFWGDDVEGRACDPRGLETPOCDOSTGQCVCVEGVEGR 1140  
Qy 1141 CDKCTRGSGVFPDCTPCHQCFALMDVIIAELTNTRHFLFKAKALKISGVIPYRETVD 1200  
Db 1141 CDKCTRGSGVFPDCTPCHQCFALMDVIIAELTNTRHFLFKAKALKISGVIPYRETVD 1200  
Qy 1201 SYERKVEIKDILAQSPAERPLKNTGNLFEEAEKLIKVTENMAQVEVKLSDTTSQSNST 1260  
Db 1201 SYERKVEIKDILAQSPAERPLKNTGNLFEEAEKLIKVTENMAQVEVKLSDTTSQSNST 1260  
Qy 1261 AKELDSLOTAEBSLONTVKELAEQLEFFIKNSDIRGALDSITIKYFQMSLEAERVNASTTE 1320  
Db 1261 AKELDSLOTAEBSLONTVKELAEQLEFFIKNSDIRGALDSITIKYFQMSLEAERVNASTTE 1320  
Qy 1321 PNSTVEQSALMRDVEDVNMVERESQKEQEQEARLLDELACGLQSLDLSAAAEVTCGTP 1380  
Db 1321 PNSTVEQSALMRDVEDVNMVERESQKEQEQEARLLDELACGLQSLDLSAAAEVTCGTP 1380  
Qy 1381 PGASCSETCGGPNCRDTEGKCGGPGCGGLVTVAHNAQKAMLDQDVLSEAEVQQL 1440  
Db 1381 PGASCSETCGGPNCRDTEGKCGGPGCGGLVTVAHNAQKAMLDQDVLSEAEVQQL 1440  
Qy 1441 SKMVSAPKLRADPAKQSAEDILLKTNATKEKMDKNEELNLIKQIRNPLTQDSADLDSI 1500  
Db 1441 SKMVSAPKLRADPAKQSAEDILLKTNATKEKMDKNEELNLIKQIRNPLTQDSADLDSI 1500  
Qy 1501 EAVANVILKMEPSTPQQLONTEDIRERVESLSQVEVILQHSADIAEAEMLLBEAKRA 1560  
Db 1501 EAVANVILKMEPSTPQQLONTEDIRERVESLSQVEVILQHSADIAEAEMLLBEAKRA 1560  
Qy 1561 SKSATDVKVTADVMKEALBEAKQVAEAKAIKQADEDIQGTQNLITSIESSTAASEETL 1620  
Db 1561 SKSATDVKVTADVMKEALBEAKQVAEAKAIKQADEDIQGTQNLITSIESSTAASEETL 1620  
Qy 1621 FNASQRISELERNVEELKRAQNSGEAEYIEKVVYTVKQSAEDVKKTLGDLDEKYYKV 1680  
Db 1621 FNASQRISELERNVEELKRAQNSGEAEYIEKVVYTVKQSAEDVKKTLGDLDEKYYKV 1680  
Qy 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLQLKDLERKEDNQRYLEDKQAE 1740  
Db 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLQLKDLERKEDNQRYLEDKQAE 1740  
Qy 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765  
Db 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765

## RESULT 4

AAW50893 standard; protein; 1786 AA.

XX AC AAW50893;  
XX AC AAW50893;DT 07-DEC-1998 (first entry)  
XX DE Human laminin B1 chain.XX Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; Creutzfeldt-Jacob disease; CJD;KW Gertmann-Straussler syndrome; kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;  
KW Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;  
KW therapy.  
OS Homo sapiens.  
XX WO9815179-A1.  
XX 16-APR-1998.  
XX 08-OCT-1997; 97WO-US018145.  
XX 08-OCT-1996; 96US-0027981P.  
XX (UNIW ) UNIV WASHINGTON.  
XX Castillo G, Snow AD;  
XX WPI; 1998-240534/21.  
PT Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CJD.  
XX Claim 15; Page 86-89; 132pp; English.  
XX This is the amino acid sequence of the human laminin B1 chain. The  
XX primary object of the invention is to use laminin, laminin-derived  
XX protein fragments and/or laminin-derived polypeptides as potent  
XX inhibitors of amyloid formation, deposition, accumulation and/or  
XX persistence in Alzheimer's disease and other amyloidoses. The laminin  
XX products (see AAW5088-98) may include mouse or human laminin A or A1  
XX chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1  
XX chain, the globular repeats of the laminin A1 chain and the beta-amyloid  
XX binding domain of the laminin A chain. A claimed method for treating an  
XX amyloid disease comprises administering a polypeptide having a  
XX conformational similarity to a fragment of a laminin protein. A method  
XX for diagnosing an amyloid disease involves determining levels of laminin  
XX in a sample. Production of laminin or its fourth globular repeat in vivo  
XX provides a method for in vivo inhibition of beta-amyloid amyloidosis. The  
XX products and methods can be used for the diagnosis, prognosis, monitoring  
XX and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome  
XX and hereditary cerebral haemorrhage with amyloidosis of the Dutch type  
XX (where the specific amyloid is the beta-amyloid protein), the amyloidosis  
XX associated with chronic inflammation, various forms of malignancy and  
XX Familial Mediterranean Fever (AA amyloid or inflammation-association  
XX amyloidosis), the amyloidosis associated with multiple myeloma and other  
XX B-cell abnormalities (AL amyloid), the amyloidosis associated with type  
XX II diabetes (amylin or islet amyloid), the amyloidosis associated with  
XX prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Straussler  
XX syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis  
XX associated with long-term haemodialysis and carpal tunnel syndrome (beta  
XX 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
XX amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or  
XX transthyretin amyloid), and the amyloidosis associated with endocrine  
XX tumours such as medullary carcinoma of the thyroid (variant of  
XX procalcitonin).

## Sequence 1786 AA;

Query Match 100.0%; Score 9654; DB 2; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 QEPFSGYGCAGSCYPATGDLIGRAQKLSVTSTGLHKPEPCIVSHLQEDKKCFICNS 60  
Db 22 QEPFSGYGCAGSCYPATGDLIGRAQKLSVTSTGLHKPEPCIVSHLQEDKKCFICNS 81  
Qy 61 QDPVHETLNPDSHLIENVTTFAPNRLKIWQSGENVNTVIQDLAEAFHFLINTFK 120  
Db 82 QDPVHETLNPDSHLIENVTTFAPNRLKIWQSGENVNTVIQDLAEAFHFLINTFK 141

121 TFRPAAMLIRSSDFGKTGWYRYFAYDCASFGISTGPMKKVDDIIICDSRYSDIEPST 180  
142 TFRPAAMLIRSSDFGKTGWYRYFAYDCASFGISTGPMKKVDDIIICDSRYSDIEPST 201  
181 EGEVIFRALDPAKIEDIPYSPRIQNLKILNLAIKFVKLHTLGDNLDSRMEIREKYVA 240  
202 EGEVIFRALDPAKIEDIPYSPRIQNLKILNLAIKFVKLHTLGDNLDSRMEIREKYVA 261  
241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGVMVGHCHCMRHNTKGLNCELCDMPFYHDLWP 300  
262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGVMVGHCHCMRHNTKGLNCELCDMPFYHDLWP 321  
301 RPABGRNSACKKNCNCHSISCHFDMAVYLATGNSGGVCCDCHNTWGRNCEQCKPFY 360  
322 RPABGRNSACKKNCNCHSISCHFDMAVYLATGNSGGVCCDCHNTWGRNCEQCKPFY 381  
361 YQHPERIDIRPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRKLNVEGEHCDVCK 420  
382 YQHPERIDIRPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGQCRKLNVEGEHCDVCK 441  
421 EGFYDLSEDPFGCKSCACNPLGTHIPGNCPCDSETHCYCKRLVTHGOCHDCLPEHWGLS 480  
442 EGFYDLSEDPFGCKSCACNPLGTHIPGNCPCDSETHCYCKRLVTHGOCHDCLPEHWGLS 501  
481 NDLGCRPCDCLGALNNSCFABSGQSCRPMMIGRQCNEVEPGYFATLDHYLAEAE 540  
502 NDLGCRPCDCLGALNNSCFABSGQSCRPMMIGRQCNEVEPGYFATLDHYLAEAE 561  
541 ANLQGVSVIVERQYIQIRISWTGAGFVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600  
562 ANLQGVSVIVERQYIQIRISWTGAGFVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621  
601 DHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVVSLSFGSRVYVLPVPCFEKGTNYTVR 660  
622 DHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVVSLSFGSRVYVLPVPCFEKGTNYTVR 681  
661 LELPYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVWTSAMETQRYRCLE 720  
682 LELPYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVWTSAMETQRYRCLE 741  
721 NSRSVKTPTMTDVCNRIIFISALLHOTGLACEDPOGSLSSVCDPNNGOCQCRPNVVG 780  
742 NSRSVKTPTMTDVCNRIIFISALLHOTGLACEDPOGSLSSVCDPNNGOCQCRPNVVG 801  
781 TCNRCAPGTGFGSGCKPCCHLQGSVNAFCNPVTQCHCFQGVYARQCDRCLPGHWGF 840  
802 TCNRCAPGTGFGSGCKPCCHLQGSVNAFCNPVTQCHCFQGVYARQCDRCLPGHWGF 861  
841 PSCQPCQCNHADDCTPVTGCLNCQDYMTHGNCERCLAGYVGDPIIGSGDHCRCPCPD 900  
862 PSCQPCQCNHADDCTPVTGCLNCQDYMTHGNCERCLAGYVGDPIIGSGDHCRCPCPD 921  
901 GPDGQRFARSQYQDPVTLQACVCDPGYIGSRDCCDASGYFGNPFSEVGGSCQPCQCHN 960  
922 GPDGQRFARSQYQDPVTLQACVCDPGYIGSRDCCDASGYFGNPFSEVGGSCQPCQCHN 981  
961 IDTTDPEACDXTGKCLKLYHTGEGHQCFRFGYGDALRODCRKCVCNVLGTVOEHCN 1020  
982 IDTTDPEACDXTGKCLKLYHTGEGHQCFRFGYGDALRODCRKCVCNVLGTVOEHCN 1041  
1021 GSDCCDCKATGQCLCLPNVIGQNCDCRCAPIWTQALASGTGCDPCNCAHSPGSCNEFTG 1080  
1042 GSDCCDCKATGQCLCLPNVIGQNCDCRCAPIWTQALASGTGCDPCNCAHSPGSCNEFTG 1101  
1081 QCCQMPFGGRTSCQBELFWGDPVECRACDOPRGITETPCDQSQSTGCQVCVEGVGPR 1140  
1102 QCCQMPFGGRTSCQBELFWGDPVECRACDOPRGITETPCDQSQSTGCQVCVEGVGPR 1161  
1141 CDKCTRGVGVFPDCTPCQCFALMDVIIAELTNTRTHRFLEKAKALISGVIQYRTVD 1200  
1162 CDKCTRGVGVFPDCTPCQCFALMDVIIAELTNTRTHRFLEKAKALISGVIQYRTVD 1221  
1201 SVERKVSIEIKDILAQSPAAPLKNIGLNFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1260

1222 SVERKVSIEIKDILAQSPAAPLKNIGLNFEEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1281  
1261 AKELDSLQTEAESLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1320  
1282 AKELDSLQTEAESLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1341  
1321 FNSVTEQSAIMRDEVEDVMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380  
1342 FNSVTEQSAIMRDEVEDVMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401  
1381 PGASCSETGCGPNCRITDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLASAEVBQL 1440  
1402 PGASCSETGCGPNCRITDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLASAEVBQL 1461  
1441 SKWSEAKLRADAQKASAEEDILLKTNATKEXKWDKSNELRNLIKQIRNFLTQDSADLDSI 1500  
1462 SKWSEAKLRADAQKASAEEDILLKTNATKEXKWDKSNELRNLIKQIRNFLTQDSADLDSI 1521  
1501 EAVANEVLKMBMPSTPQQLNLTEDIRERVSLSQVEVILQHSAAADIAEAEMLJEEAKRA 1560  
1522 EAVANEVLKMBMPSTPQQLNLTEDIRERVSLSQVEVILQHSAAADIAEAEMLJEEAKRA 1581  
1561 SKSATDVVKTADMVKEALEBAEKAQVAABKAIKQADEDIQGTQNLITSIESETAASEETL 1620  
1582 SKSATDVVKTADMVKEALEBAEKAQVAABKAIKQADEDIQGTQNLITSIESETAASEETL 1641  
1621 FNASORISELERNVEELKXKAAQNSGEAEYIEKVYVTVKQSAEDVYKTLDELDEKYKV 1680  
1642 FNASORISELERNVEELKXKAAQNSGEAEYIEKVYVTVKQSAEDVYKTLDELDEKYKV 1701  
1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKOLERYEDNQRYLEDKAQEL 1740  
1702 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQLLKOLERYEDNQRYLEDKAQEL 1761  
1741 ARLEGEVRSLLKXDISQKVAVYSTCL 1765  
1762 ARLEGEVRSLLKXDISQKVAVYSTCL 1786

RESULT 5  
AAB16522  
ID AAB16522 standard; protein; 1786 AA.  
XX AAB16522;  
AC AAB16522;  
XX  
XX 27-OCT-2000 (first entry)  
XX Human laminin protein sequence.  
DE  
XX  
XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiotensin;  
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;  
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;  
KW Helicobacter related disease; fracture; cat scratch fever.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200032631-A2.  
XX  
XX 08-JUN-2000.  
XX  
XX 06-DEC-1999; 99WO-US028897.  
XX  
XX 04-DEC-1998; 98US-00206059.  
XX  
XX (ENTR-) ENTREMED INC.  
XX Macdonald NJ, Sim KL;  
XX WPI; 2000-412290/35.  
XX



PT New angiogenesis-inhibiting protein receptors, useful in methods for  
PT treating diseases and processes that are mediated by angiogenesis, such  
PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.  
XX  
XX Claim 1; Fig 6A; 100pp; English.  
XX  
XX This invention relates to angiogenesis-inhibiting protein receptors, and  
CC the DNA sequences encoding them. Angiogenesis is the generation of new  
CC blood vessels into a tissue, and normally occurs in wound healing, foetal  
CC and embryonal development and the formation of the corpus luteum,  
CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and  
CC AAA68202) involved in angiogenesis, and has an amino acid sequence  
CC similar to that of a plasminogen fragment (see murine plasminogen  
CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.  
CC Angiostatin is also an angiogenesis inhibiting protein (see AAB16451 and  
CC AAA68203). Sequences AAB68242 and AAB16532 represent coding and protein  
CC sequences of human laminin. Laminin is an angiostatin binding protein,  
CC and some of the peptides of the invention share homology with regions of  
CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the  
CC angiogenesis-inhibiting protein receptor fragments of the invention. The  
CC peptides bind either angiostatin or endostatin and can be used in methods  
CC for treating diseases and processes that are mediated by angiogenesis,  
CC such as solid tumors, psoriasis, scleroderma, myocardial angiogenesis,  
CC Crohn's disease, cerebral collaterals, arteriovenous malformations,  
CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,  
CC Helicobacter related diseases, fractures, placental and cat scratch  
CC fever. They are useful for the detection and prognosis of cancer. DNA  
CC sequences A628204-A628241 encode the peptides of the invention  
XX  
XX Sequence 1786 AA;

Query Match 100.0%; Score 9654; DB 3; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPEFSGCAEGSCYPATGDLIGRAQKLSVSTGGLHKPEPYCVSHLQEDKKCFICNS 60  
DB 22 QPPEFSGCAEGSCYPATGDLIGRAQKLSVSTGGLHKPEPYCVSHLQEDKKCFICNS 81  
QY 61 QDPYHTLNPDSHLIENVTTAPNRLKIWQSENGVENVTIQLDLEAFHFTHLIMTFK 120  
DB 82 QDPYHTLNPDSHLIENVTTAPNRLKIWQSENGVENVTIQLDLEAFHFTHLIMTFK 141  
QY 121 TTPPAAMLIERSDDFKTGWVRYFAYDCEAFPGISTGPMKKVDDIICDSRYSDIEPST 180  
DB 142 TTPPAAMLIERSDDFKTGWVRYFAYDCEAFPGISTGPMKKVDDIICDSRYSDIEPST 201  
QY 181 EGEVIFRALDPAPKIEDPYSPRIQNLKITNRIKFKVLTGDLNLSRMEIREKYIYA 240  
DB 202 EGEVIFRALDPAPKIEDPYSPRIQNLKITNRIKFKVLTGDLNLSRMEIREKYIYA 261  
QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCMCRHNTKGLNCELMDFYHDLPW 300  
DB 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCMCRHNTKGLNCELMDFYHDLPW 321  
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMGRNCEOCKPFPY 360  
DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDCCQHTMGRNCEOCKPFPY 381  
QY 361 YQHPEDIRDPNFCERCTCDPAGSONEGICDSYTFSTGLIAGQCRCKLNVEGEHCDCVK 420  
DB 382 YQHPEDIRDPNFCERCTCDPAGSONEGICDSYTFSTGLIAGQCRCKLNVEGEHCDCVK 441  
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHGYCKRLVTCQHCDCQLPHEWGLS 480  
DB 442 EGFYDLSSDDPFGCKSCACNPLGTIPGPNPCDSETHGYCKRLVTCQHCDCQLPHEWGLS 501  
QY 481 NDLGCRPCDCDLGGALNNSCFASQSCCRPHMTGRQCNVEPGYFATLDHLYEABE 540  
DB 502 NDLGCRPCDCDLGGALNNSCFASQSCCRPHMTGRQCNVEPGYFATLDHLYEABE 561  
QY 541 ANLPGVSVIVERYOIQDRIPSWTGAQVVRPBGAYLEFFIDNIPYSMEYDILIRYEPQLP 600

DB 562 ANLPGVSVIVERYOIQDRIPSWTGAQVVRPBGAYLEFFIDNIPYSMEYDILIRYEPQLP 621  
QY 601 DHWEKAVITVQRGRIPTSSRCGNTIPDDDNQVVSLSPGSRVYVLPBPVPCFEKGTNTYVR 660  
DB 622 DHWEKAVITVQRGRIPTSSRCGNTIPDDDNQVVSLSPGSRVYVLPBPVPCFEKGTNTYVR 681  
QY 661 LELPQYTSDDSDVESYTTILDSLVLMYPYKSLDIFVTGSGDGVVNTNSAWETFORVRCLE 720  
DB 682 LELPQYTSDDSDVESYTTILDSLVLMYPYKSLDIFVTGSGDGVVNTNSAWETFORVRCLE 741  
QY 721 NSRSVVKTPMTDVCNRNIIFISALLHOTGLACBDCPQGSLSVSSVCDPNGGQCCQCRPNVVG 780  
DB 742 NSRSVVKTPMTDVCNRNIIFISALLHOTGLACBDCPQGSLSVSSVCDPNGGQCCQCRPNVVG 801  
QY 781 TCRNRCAPGTGFGPFGCKPCECHLQGSVNAFCNPVVTGQCHCFQGVYVAROCDRCLPQHNGF 840  
DB 802 TCRNRCAPGTGFGPFGCKPCECHLQGSVNAFCNPVVTGQCHCFQGVYVAROCDRCLPQHNGF 861  
QY 841 PSCOPCCGCHADDOPVTEGCLNCCDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 900  
DB 862 PSCOPCCGCHADDOPVTEGCLNCCDYTMGHNCERCLAGYGDPIIGSGDHCRPCPCPD 921  
QY 901 GPDSGRQFARSQYQDPVTLQACVCDPGYIGSRCDPCASGYFGNPNSEVSGSCQPCQCHNN 960  
DB 922 GPDSGRQFARSQYQDPVTLQACVCDPGYIGSRCDPCASGYFGNPNSEVSGSCQPCQCHNN 981  
QY 961 IDTTPDACDKETGRCLKCLYHTEGHCQCFREGYVGDLARODCRKVCNLYLTGVOEHCN 1020  
DB 982 IDTTPDACDKETGRCLKCLYHTEGHCQCFREGYVGDLARODCRKVCNLYLTGVOEHCN 1041  
QY 1021 GSDCCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGDCPCNCAHASFPGSCNEFTG 1080  
DB 1042 GSDCCQCKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTGDCPCNCAHASFPGSCNEFTG 1101  
QY 1081 QCQMPFGGRTCSBCEQLFWGDPDVECRACDPRGIEPTQCDQSTGQCVCEVGEGR 1140  
DB 1102 QCQMPFGGRTCSBCEQLFWGDPDVECRACDPRGIEPTQCDQSTGQCVCEVGEGR 1161  
QY 1141 CDKCTRYSGVFPDCTPCHQCFALWDVITAEIENRTHRELEKAKALKISGVIPIYRETVD 1200  
DB 1162 CDKCTRYSGVFPDCTPCHQCFALWDVITAEIENRTHRELEKAKALKISGVIPIYRETVD 1221  
QY 1201 SVRKVSEIKDIIAQSPAAPLKNIGNLPEBAEKLIKDVTEMAQVEVKLSDTTSQNST 1260  
DB 1222 SVRKVSEIKDIIAQSPAAPLKNIGNLPEBAEKLIKDVTEMAQVEVKLSDTTSQNST 1281  
QY 1261 AKELDSLOTEAESIDNTVKELAEQLRKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320  
DB 1282 AKELDSLOTEAESIDNTVKELAEQLRKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341  
QY 1321 PNSTVEQSALMRDRVEDVMMERESQPKQEQEARLLDELQGLQSLDLSAAAEMTCGTP 1380  
DB 1342 PNSTVEQSALMRDRVEDVMMERESQPKQEQEARLLDELQGLQSLDLSAAAEMTCGTP 1401  
QY 1381 PGASCSSETCGGPNCRDTEGERKCGGPGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1440  
DB 1402 PGASCSSETCGGPNCRDTEGERKCGGPGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1461  
QY 1441 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1500  
DB 1462 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1521  
QY 1501 EAVANEVLKHEMSTPOOLQNLTEDIRVERVESISOVEVILQHSAAADIARAMELLEAKRA 1560  
DB 1522 EAVANEVLKHEMSTPOOLQNLTEDIRVERVESISOVEVILQHSAAADIARAMELLEAKRA 1581  
QY 1561 SKSATDVKVTADVMVKEALEEAKQAAEAKAIKQADEDIQGTQNLTSIESETAASEETL 1620  
DB 1582 SKSATDVKVTADVMVKEALEEAKQAAEAKAIKQADEDIQGTQNLTSIESETAASEETL 1641  
QY 1621 FNASQRISSELRNVEELKRKAAQNSGEAEYIEKVVTVKQSAEDVKTLDELDEYKKV 1680  
DB 1642 FNASQRISSELRNVEELKRKAAQNSGEAEYIEKVVTVKQSAEDVKTLDELDEYKKV 1701

Qy 1681 ENLIAKTESADARRAEMLQNEAKTLIAQANSKIQLLKDLKRYEDNORYLEDKAQEL 1740  
Db 1702 ENLIAKTESADARRAEMLQNEAKTLIAQANSKIQLLKDLKRYEDNORYLEDKAQEL 1761  
Qy 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765  
Db 1762 ARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 6

AAB19797  
ID AAB19797 standard; protein; 1786 AA.

XX AAB19797;  
AC (first entry)

DT 05-MAR-2001 (first entry)

XX Human laminin 2 beta-1 chain.

XX Laminin 2; human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /label= Signal\_peptide  
FT Protein 22..1786  
FT /label= Mature\_protein

XX WO200066730-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011378.

XX 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
XX 12-JUL-1999; 99US-0143289P.  
XX 24-SEP-1999; 99US-0155945P.

XX (UTNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

XX Yurchenco P;

XX WPI; 2000-687537/67.

XX N-PSDB; AAA88897.

XX Purified laminin 2 protein, useful for research and therapeutic purposes  
XX including peripheral nerve regeneration, treatment of degenerative muscle  
XX disorders, angiogenesis regulation, and ex vivo cell therapy.

XX Claim 5; Page 186-191; 305pp; English.

XX The present sequence is that of the beta-1 chain of human laminin 2.  
XX Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and gamma-1  
XX (100 kDa) chains. It is thought to be specifically required for  
XX stabilizing myotubes during skeletal muscle development, and for  
XX preventing apoptosis. Genetic defects in its structure or expression are  
XX associated with a major type of congenital muscular dystrophy. Laminin 2  
XX is also thought to be important in Schwann cell/basal lamina  
XX interactions. The invention provides laminin 2 alpha-2, beta-1 and gamma-  
XX 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding  
XX them (see AAA8891-906), methods for making recombinant laminin 2, cells  
XX that express recombinant laminin 2, and methods for using purified  
XX laminin 2 for research and therapeutic purposes including peripheral  
XX nerve regeneration, treatment of degenerative muscle disorders,  
XX angiogenesis regulation, promoting cell attachment and migration, ex vivo  
XX cell therapy, improving the take of grafts, improving the  
XX biocompatibility of medical devices and preparing improved culture  
XX devices and media

XX

SQ Sequence 1786 AA;		Query Match	100.0%; Score 9654; DB 3; Length 1786;
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1765; Conservative		0; Mismatches	0; Indels 0; Gaps 0;
Qy	1	QEPFYSYGCARGSCYPATGDLII	GRAQKLSVTSCGLHKPEPYCIVSHLQDKKCFICNS 60
Db	22	QEPFYSYGCARGSCYPATGDLII	GRAQKLSVTSCGLHKPEPYCIVSHLQDKKCFICNS 81
Qy	61	QDPYHETLNPDSHLIENVTTF	APNRLKIWQSENGVENVTIQDLAEFHTLIMTFK 120
Db	82	QDPYHETLNPDSHLIENVTTF	APNRLKIWQSENGVENVTIQDLAEFHTLIMTFK 141
Qy	121	TFRPAAMLIERSDFGKTGWY	RYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180
Db	142	TFRPAAMLIERSDFGKTGWY	RYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201
Qy	181	EGEVIFRALDPAPKIEDPYS	PRIONLLKIITNLRKFVKLHTLGNLDSRMEIREKYIYA 240
Db	202	EGEVIFRALDPAPKIEDPYS	PRIONLLKIITNLRKFVKLHTLGNLDSRMEIREKYIYA 261
Qy	241	VYDMVVRGNCFCYGHASE	CAVDGFNEBVEGVMHGHQWCRHNTKGLNCELQMDFYHDLPW 300
Db	262	VYDMVVRGNCFCYGHASE	CAVDGFNEBVEGVMHGHQWCRHNTKGLNCELQMDFYHDLPW 321
Qy	301	RPAGGRNSNACKKNCNEHS	ISCHFDMAVYLATNGVSGVCCDDCHNTMGNCCEQCKPFY 360
Db	322	RPAGGRNSNACKKNCNEHS	ISCHFDMAVYLATNGVSGVCCDDCHNTMGNCCEQCKPFY 381
Qy	361	YQHPERDIRDPNFCERCT	CDPAGSQNEGICDSYDFSTGLIAGQCRCKLVNVEGHCHDVCK 420
Db	382	YQHPERDIRDPNFCERCT	CDPAGSQNEGICDSYDFSTGLIAGQCRCKLVNVEGHCHDVCK 441
Qy	421	EGFYDLSSDPFGCKSKAC	NPLGTIPGNGPCDSTGHCYCKRLVTGQHCDOCLPEHNGLS 480
Db	442	EGFYDLSSDPFGCKSKAC	NPLGTIPGNGPCDSTGHCYCKRLVTGQHCDOCLPEHNGLS 501
Qy	481	NLDGCRPCDDCLGALNNS	CFABSGQSCRPBMIGRCQNEVEPGYFATLDHLYEABE 540
Db	502	NLDGCRPCDDCLGALNNS	CFABSGQSCRPBMIGRCQNEVEPGYFATLDHLYEABE 561
Qy	541	ANLGGVSIVERQYIQDRIP	SWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600
Db	562	ANLGGVSIVERQYIQDRIP	SWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621
Qy	601	DHWEKAVITVORPGRIPT	SSRCGNTIPDDDNQVVSLSFGSRVYVLPVPVCEKGTNTYVR 660
Db	622	DHWEKAVITVORPGRIPT	SSRCGNTIPDDDNQVVSLSFGSRVYVLPVPVCEKGTNTYVR 681
Qy	661	LELPQYTSDDSDVSPYTL	IDSLLVMPYCKSLDIFTVGGSGDVVTNSAMETFORYRCLE 720
Db	682	LELPQYTSDDSDVSPYTL	IDSLLVMPYCKSLDIFTVGGSGDVVTNSAMETFORYRCLE 741
Qy	721	NSRSVVKTPMTDVCRNII	FSISALLHQTGLACECDPOGSLSSVCDPNGGQCCQCPNVVGR 780
Db	742	NSRSVVKTPMTDVCRNII	FSISALLHQTGLACECDPOGSLSSVCDPNGGQCCQCPNVVGR 801
Qy	781	ICNRCAPGTFGFGSGCK	PCFCHLQGSVNAFCNPVTGCHCFQGVYARQCDRCCLPGHWGF 840
Db	802	ICNRCAPGTFGFGSGCK	PCFCHLQGSVNAFCNPVTGCHCFQGVYARQCDRCCLPGHWGF 861
Qy	841	PSCQPCQCNHADD	CDPVTGCLNCQDYMTHNCERCLAGYGGDPIIGSGDHCRPCPCPD 900
Db	862	PSCQPCQCNHADD	CDPVTGCLNCQDYMTHNCERCLAGYGGDPIIGSGDHCRPCPCPD 921
Qy	901	GPDSGRQFARSCYQDP	VTLOLACVDCPGYIGSRDCCASGYFGNPFSEVGGSCQPCQCHNN 960
Db	922	GPDSGRQFARSCYQDP	VTLOLACVDCPGYIGSRDCCASGYFGNPFSEVGGSCQPCQCHNN 981
Qy	961	IDTTDPEACDKETGR	CKLCLVHTTEGHCQCFRCFYGDALQDCKKVCNVLGTVOBHCN 1020
Db	982	IDTTDPEACDKETGR	CKLCLVHTTEGHCQCFRCFYGDALQDCKKVCNVLGTVOBHCN 1041

QY	1021	GSDCCDKATGOCCLCLPNVIGONCDRCAPNTWOLASGTGCDPCNCNAHSGFSCNFTG	1080
Db	1042	GSDCCDKATGOCCLCLPNVIGONCDRCAPNTWOLASGTGCDPCNCNAHSGFSCNFTG	1101
QY	1081	QCQCMFGGRTCTCEQCLFWGDPDVECRACDCDPRGTHETPCQDQSTQCQCVGVEGPR	1140
Db	1102	QCQCMFGGRTCTCEQCLFWGDPDVECRACDCDPRGTHETPCQDQSTQCQCVGVEGPR	1161
QY	1141	CDKCTRGYSVPDCTPCHQCFALMDVIIAELTNTRHREKAKALKISGVLPVRETV	1200
Db	1162	CDKCTRGYSVPDCTPCHQCFALMDVIIAELTNTRHREKAKALKISGVLPVRETV	1221
QY	1201	SVYKVKSEIKDILAQSPAAEPKNIGNLFEAEKLIKOVTEMMAQVEVKLSDTTQSNS	1260
Db	1222	SVYKVKSEIKDILAQSPAAEPKNIGNLFEAEKLIKOVTEMMAQVEVKLSDTTQSNS	1281
QY	1261	AKELDSLOTEASLDNTVKELAEOLBPIKNSDIRGALDSITIKYFQMSLEAERVNASTE	1320
Db	1282	AKELDSLOTEASLDNTVKELAEOLBPIKNSDIRGALDSITIKYFQMSLEAERVNASTE	1341
QY	1321	PNSVTEQSAIMDRVEDVMVERESQFKEQEBOEARLLDELAKLQSLDLSAAAEVTCGTP	1380
Db	1342	PNSVTEQSAIMDRVEDVMVERESQFKEQEBOEARLLDELAKLQSLDLSAAAEVTCGTP	1401
QY	1381	PGASCSETCGGPNCTDEGERKCGPGCGGLVTVAHNAWQAMLDQDVLSALAEVQL	1440
Db	1402	PGASCSETCGGPNCTDEGERKCGPGCGGLVTVAHNAWQAMLDQDVLSALAEVQL	1461
QY	1441	SKMVSBAKLADRAKQASDILKTNATKWKDKSNEELNLIKQIRNPLTQDSADLDSI	1500
Db	1462	SKMVSBAKLADRAKQASDILKTNATKWKDKSNEELNLIKQIRNPLTQDSADLDSI	1521
QY	1501	EAVANEVLKWMPESTPQOLNLTEDIRERVELSQVEVILQHSADIAEAEMLLBEAKRA	1560
Db	1522	EAVANEVLKWMPESTPQOLNLTEDIRERVELSQVEVILQHSADIAEAEMLLBEAKRA	1581
QY	1561	SKSATDVKTADVMKALEAEAKQAAKAIQADEDIQGTQNLTLTSESETAASEETL	1620
Db	1582	SKSATDVKTADVMKALEAEAKQAAKAIQADEDIQGTQNLTLTSESETAASEETL	1641
QY	1621	FNASQRISELERNVBELKRAAQSAGEAEYIEKVYTVTKQSAEDVKKTLGDLDSKYKV	1680
Db	1642	FNASQRISELERNVBELKRAAQSAGEAEYIEKVYTVTKQSAEDVKKTLGDLDSKYKV	1701
QY	1681	ENLIATKTEESADARRKAEMLQNEAKTLAQANSKLQLLKDLEKRYEDNORYLEDAQEL	1740
Db	1702	ENLIATKTEESADARRKAEMLQNEAKTLAQANSKLQLLKDLEKRYEDNORYLEDAQEL	1761
QY	1741	ARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKAVYSTCL	1786
RESULT 7			
AA	48448	standard; protein; 1786 AA.	
XX	AA	48448	
XX	AC	48448	
XX	DT	02-MAR-2001 (first entry)	
XX	DE	Human laminin 8 polypeptide, SEQ ID NO: 14.	
XX	KW	Human; laminin 8; neuroprotective; angiogenic; osteopathic;	
XX	KW	arteriosclerotic; glycoprotein; mesenchymal tissue injury;	
XX	OS	vascular tissue injury; neural injury; angiogenesis regulation.	
XX	OS	Homo sapiens.	
XX	PN	W0200066732-A2.	
XX	XX	09-NOV-2000.	
XX	XX	09-NOV-2000.	

XX	28-APR-2000;	2000WO-US011543.	
XX	30-APR-1999;	99US-0131720P.	
PR	21-AUG-1999;	99US-0149738P.	
PR	24-SEP-1999;	99US-0155945P.	
XX	11-FEB-2000;	2000US-0182012P.	
PA	(BIOS-)	BIOSTRATUM INC.	
XX	Kortessmaa J,	Tryggvason K;	
XX	WPI;	2000-687539/67.	
DR	N-PSDB;	AAC83709.	
PT	Purified laminin 8 protein, useful for research and therapeutic purposes		
PT	including peripheral nerve regeneration, treatment of degenerative muscle		
PT	disorders, angiogenesis regulation, and ex vivo cell therapy.		
XX	Claim 5;	Page 150-155; 245pp; English.	
XX	The present sequence is a laminin 8 polypeptide chain. Laminins are a		
CC	family of heterotrimeric glycoproteins that function via binding		
CC	interactions with neighbouring cell receptors and by forming laminin		
CC	networks. They are signalling molecules which influence cellular		
CC	function. Laminin 8 is useful for treating injuries to tissue of		
CC	mesenchymal origin, such as bone, cartilage, tendon, and ligament.		
CC	treating injuries to vascular tissue, promoting cell attachment and		
CC	migration, ex vivo cell therapy, improving the biocompatibility of		
CC	medical devices, and preparing improved cell culture devices and media.		
CC	Laminin 8 is also useful for promoting re-endothelialisation at the site		
CC	of vascular injuries, improving the take of grafts, improving the		
CC	biocompatibility of medical devices, treating neural injuries (neural		
CC	regeneration), regulating angiogenesis, and promoting cell attachment and		
CC	migration		
XX	Sequence	1786 AA;	
SQ	Query Match	100.0%; Score 9654; DB 3; Length 1786;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1765; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	QEPFSGCAGSGCYPATGDLIGRAOKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	60
Db	22	QEPFSGCAGSGCYPATGDLIGRAOKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS	81
QY	61	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQDLAEAFHFLHINTFK	120
Db	82	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQDLAEAFHFLHINTFK	141
QY	121	TFRPAAMLIERSSDFGKTGWYRYFAYDCBASPPGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSSDFGKTGWYRYFAYDCBASPPGISTGPMKKVDDIICDSRYSDIEPST	201
QY	181	EGEVIFRALDPAPFKIEDPYSPRIQNLKLTNLRKFVKLHTGLDNLDSMEIREKYYA	240
Db	202	EGEVIFRALDPAPFKIEDPYSPRIQNLKLTNLRKFVKLHTGLDNLDSMEIREKYYA	261
QY	241	YDVMVVRGNCFCYGHASECAPVDGFEVEVGVHGHCMCRHNTKGLNCELCMPDYHDLWP	300
Db	262	YDVMVVRGNCFCYGHASECAPVDGFEVEVGVHGHCMCRHNTKGLNCELCMPDYHDLWP	321
QY	301	RPAGGRNSACKKCNCHHSISCHFDNAVYLATGNVSGGVCDCCOHNMTGRNCEQCKPFY	360
Db	322	RPAGGRNSACKKCNCHHSISCHFDNAVYLATGNVSGGVCDCCOHNMTGRNCEQCKPFY	381
QY	361	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFTSTGLIAGQCRKLVNVEGHCDCVK	420
Db	382	YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFTSTGLIAGQCRKLVNVEGHCDCVK	441
QY	421	EGFYDLSSDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCQCLPEHGLS	480
Db	442	EGFYDLSSDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCQCLPEHGLS	501

QY 481 NDLGCRPCDCLGALNNSCFABSGQSCSRPHMIGRCNEVEBPGYYFATLDHYLAEAE 540  
Db 502 NDLGCRPCDCLGALNNSCFABSGQSCSRPHMIGRCNEVEBPGYYFATLDHYLAEAE 561  
QY 541 ANLPGVSIIVERQYIQRIPSWTGAGVRUPPEGAYLEFFIDNIPYSMEYDILIRYBOLP 600  
Db 562 ANLPGVSIIVERQYIQRIPSWTGAGVRUPPEGAYLEFFIDNIPYSMEYDILIRYBOLP 621  
QY 601 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPFVCFEKGNTYTVR 660  
Db 622 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPFVCFEKGNTYTVR 681  
QY 661 LELPQYTSDDVSPTLIDSLVIMPYCKSLDIFTVGGSGDGVVWNSAWETTORVRCLE 720  
Db 682 LELPQYTSDDVSPTLIDSLVIMPYCKSLDIFTVGGSGDGVVWNSAWETTORVRCLE 741  
QY 721 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDPOGSLSSVCDPNGGQCCQCRPNVVG 780  
Db 742 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDPOGSLSSVCDPNGGQCCQCRPNVVG 801  
QY 781 TCNRCAPGTGFGSGCKPCBCHLOGSVNAPCNVPTGQCHCFQGVYARQDCRCLPGHWGP 840  
Db 802 TCNRCAPGTGFGSGCKPCBCHLOGSVNAPCNVPTGQCHCFQGVYARQDCRCLPGHWGP 861  
QY 841 PSCQPCOAGHADDPCVTGECINCDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPD 900  
Db 862 PSCQPCOAGHADDPCVTGECINCDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPD 921  
QY 901 GPDGSRQPARSCYQDPVTLQIACVDPYIGSRCDDCASGYFGNPSVEVSGSCQPCQCHNN 960  
Db 922 GPDGSRQPARSCYQDPVTLQIACVDPYIGSRCDDCASGYFGNPSVEVSGSCQPCQCHNN 981  
QY 961 IDTTDPEACDKETGRCLKCLVHTEGHCOCFRGYGDALRODCRCKVCNVLGTVOEHCN 1020  
Db 982 IDTTDPEACDKETGRCLKCLVHTEGHCOCFRGYGDALRODCRCKVCNVLGTVOEHCN 1041  
QY 1021 GSDQCDKATGQCLCLPNVIGQNDRCAPNTWQIASGTGCDPCNCAAHSGFSCNEFTG 1080  
Db 1042 GSDQCDKATGQCLCLPNVIGQNDRCAPNTWQIASGTGCDPCNCAAHSGFSCNEFTG 1101  
QY 1081 QCQCPGFGGRTCECQBLFGDPPVECRACDPCPRGIEPQCDQSTQCVCVEGEGPR 1140  
Db 1102 QCQCPGFGGRTCECQBLFGDPPVECRACDPCPRGIEPQCDQSTQCVCVEGEGPR 1161  
QY 1141 CDKCTRGSGVFPDCTPCHQCFALWDVTIABLNTNRHFRLEKAKALXISGVIQPYRETVD 1200  
Db 1162 CDKCTRGSGVFPDCTPCHQCFALWDVTIABLNTNRHFRLEKAKALXISGVIQPYRETVD 1221  
QY 1201 SVRKVSSEIKDILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVVKLSDDTSSQNST 1260  
Db 1222 SVRKVSSEIKDILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVVKLSDDTSSQNST 1281  
QY 1261 AKELDSLQTEAESLQNTVKEAEOLEFKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1320  
Db 1282 AKELDSLQTEAESLQNTVKEAEOLEFKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1341  
QY 1321 PNSTVEQSALMRDVEDVMMERESQFKEQEQARLLDELQKLSQSLDLSAAAEWTCGTP 1380  
Db 1342 PNSTVEQSALMRDVEDVMMERESQFKEQEQARLLDELQKLSQSLDLSAAAEWTCGTP 1401  
QY 1381 PGASCSETECGGPNCRDTEGSKCGGCGGLVTVVANNKQKAMDLDODVLSALAEVQL 1440  
Db 1402 PGASCSETECGGPNCRDTEGSKCGGCGGGLVTVVANNKQKAMDLDODVLSALAEVQL 1461  
QY 1441 SKWSEAKLRADEAKQSAEDILLKTNAKTEKWDKSNBEELRNLIKQIRNFLTQDSADLDSI 1500  
Db 1462 SKWSEAKLRADEAKQSAEDILLKTNAKTEKWDKSNBEELRNLIKQIRNFLTQDSADLDSI 1521  
QY 1501 EAVANEVLKMEPSTPOOLQNTEDIRERVESLSQVEVILQHSADITARAEMILLEAKRA 1560  
Db 1522 EAVANEVLKMEPSTPOOLQNTEDIRERVESLSQVEVILQHSADITARAEMILLEAKRA 1581

QY 1561 SKSATDVKVTADVMYKEALEEAEKAAQAAEKAIKQADEDIQGTQNTLLTSISETAASEETL 1620  
Db 1582 SKSATDVKVTADVMYKEALEEAEKAAQAAEKAIKQADEDIQGTQNTLLTSISETAASEETL 1641  
QY 1621 FNASORISELERNVZELKRAAONSGBAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1680  
Db 1642 FNASORISELERNVZELKRAAONSGBAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1701  
QY 1681 ENLIAKTEESADARAKEMLQNEAKTLAQAANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740  
Db 1702 ENLIAKTEESADARAKEMLQNEAKTLAQAANSKLQLLKDLERKYEDNQRYLEDKAQEL 1761  
QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765  
Db 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786  
RESULT 8  
AAB90788  
ID AAB90788 standard; protein; 1786 AA.  
XX AAB90788;  
AC AAB90788;  
XX XX  
DT 15-JUN-2001 (first entry)  
XX XX  
DE Human shear stress-response protein SEQ ID NO: 76.  
XX Human; shear stress-response protein; vascular disease; arteriosclerosis.  
XX Homo sapiens.  
OS Homo sapiens.  
XX XX  
PN WO200125427-A1.  
XX XX  
PD 12-APR-2001.  
XX XX  
PF 02-OCT-2000; 2000WO-JP006840.  
XX XX  
PR 01-OCT-1999; 95JP-00280976.  
XX XX  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (NOJI/) NOJIMA H.  
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;  
PI Kuga T, Sekine S, Nakamura Y, Sugano S;  
XX WPI; 2001-266308/27.  
DR N-PSDB; AAH02911.  
XX XX  
PT DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis.  
XX XX  
PS Claim 60; Page 440-449; 678pp; Japanese.  
XX XX  
CC The present invention provides the protein and coding sequences of a  
CC number of human shear stress response proteins. These are useful in the  
CC diagnosis, treatment and screening of vascular diseases caused by  
CC arteriosclerosis, including heart failure, post-PICA restenosis and  
CC hypertension  
XX XX  
SQ Sequence 1786 AA;  
Query Match 100.0%; Score 9654; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QPPEFSYCAEGSCVPATGDLIGRAQKLSVTSTGLHKHPYCIIVSHLQEDKKCFICNS 60  
Db 22 QPPEFSYCAEGSCVPATGDLIGRAQKLSVTSTGLHKHPYCIIVSHLQEDKKCFICNS 81  
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFHFLHMTFK 120  
Db 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVENVTIQLDLEAFHFLHMTFK 141

QY 121 TFRPAAMLIERSDFGKTVGVRYFAYDCEAFPGISTGPMKKVDDIIICDSRYSDIBPST 180  
 Db 142 TFRPAAMLIERSDFGKTVGVRYFAYDCEAFPGISTGPMKKVDDIIICDSRYSDIBPST 201  
 QY 181 EGEVIFRALDPAFKIEDPYSRIQNLKITNRIKFKVLHTGLDNLDSRMEIRKYYA 240  
 Db 202 EGEVIFRALDPAFKIEDPYSRIQNLKITNRIKFKVLHTGLDNLDSRMEIRKYYA 261  
 QY 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVHGHCMCRHNTKGLNCELMDWFYHDLPW 300  
 Db 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVHGHCMCRHNTKGLNCELMDWFYHDLPW 321  
 QY 301 RAEGNSNACKKCNKNEHISICHFPMAYLATGNVSGVCDCCOHNMTGRNCEOCKPFY 360  
 Db 322 RAEGNSNACKKCNKNEHISICHFPMAYLATGNVSGVCDCCOHNMTGRNCEOCKPFY 381  
 QY 361 YQHPERDIDRPNFCERCTCDPASGNEGICDSYDFSTGLIAGQCRCKLNVEGEHCDVCK 420  
 Db 382 YQHPERDIDRPNFCERCTCDPASGNEGICDSYDFSTGLIAGQCRCKLNVEGEHCDVCK 441  
 QY 421 EGYDLSSEDDPFCCKACNPLGTIPGPNPCDSETHCYCKRLVTHQCHDCQCLPHEWGLS 480  
 Db 442 EGYDLSSEDDPFCCKACNPLGTIPGPNPCDSETHCYCKRLVTHQCHDCQCLPHEWGLS 501  
 QY 481 NDLDGCRPCDCLGGALNNSCPAESGCSCRPMMIGRQCNEVEPGYFATLDHLYEABE 540  
 Db 502 NDLDGCRPCDCLGGALNNSCPAESGCSCRPMMIGRQCNEVEPGYFATLDHLYEABE 561  
 QY 541 ANLPGVSVIVERQYIQRIPSWTGAQFVRPEGAYLEFFIDNIPYSMEYDIIIRIEPQLP 600  
 Db 562 ANLPGVSVIVERQYIQRIPSWTGAQFVRPEGAYLEFFIDNIPYSMEYDIIIRIEPQLP 621  
 QY 601 DHWEKAVITVORGRIPTSRRCNTIPDDNQVVSLSPGSRVYVLPVPFCFEKGTNYTVR 660  
 Db 622 DHWEKAVITVORGRIPTSRRCNTIPDDNQVVSLSPGSRVYVLPVPFCFEKGTNYTVR 681  
 QY 661 LELPQYTSDDSVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVWVNSAWETFORVRCLE 720  
 Db 682 LELPQYTSDDSVESPYTLIDSLVLMPCYKSLDIFTVGGSGDGVWVNSAWETFORVRCLE 741  
 QY 721 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDPOGSLSSVCDPNNGGOCQCRPNVGR 780  
 Db 742 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACEDPOGSLSSVCDPNNGGOCQCRPNVGR 801  
 QY 781 TCNRCAPGTGFGPGCKPCECHLQGSVNAFCNPVTGQCHFCQGVYARQCDRCLPGHWGF 840  
 Db 802 TCNRCAPGTGFGPGCKPCECHLQGSVNAFCNPVTGQCHFCQGVYARQCDRCLPGHWGF 861  
 QY 841 PSCQPCQCNHADDPCDVTGECLNCDYTWGHCERCLAGYGDPIIGSDGHCRCPCPD 900  
 Db 862 PSCQPCQCNHADDPCDVTGECLNCDYTWGHCERCLAGYGDPIIGSDGHCRCPCPD 921  
 QY 901 GPDGROFARSCYQDPVTLQACVCDPQYIGSRCDCCASGYFNGNPSVGGSCQPCQCHNN 960  
 Db 922 GPDGROFARSCYQDPVTLQACVCDPQYIGSRCDCCASGYFNGNPSVGGSCQPCQCHNN 981  
 QY 961 IDTTDPEACDKETGRCLKCLYHTGEHCQCRFGYGDALRQDRCKVCNLYGTVOEHCN 1020  
 Db 982 IDTTDPEACDKETGRCLKCLYHTGEHCQCRFGYGDALRQDRCKVCNLYGTVOEHCN 1041  
 QY 1021 GSDCQCKATGQCLCLFNVIQONCDRCAPNTWQASGTGCDPCNCAHAFSGPSCNEFTG 1080  
 Db 1042 GSDCQCKATGQCLCLFNVIQONCDRCAPNTWQASGTGCDPCNCAHAFSGPSCNEFTG 1101  
 QY 1081 QCQCMFPGGRTCECQELFWGDPDVECRACDCCDPRGIETPQDQSTGQCVVEGEGPR 1140  
 Db 1102 QCQCMFPGGRTCECQELFWGDPDVECRACDCCDPRGIETPQDQSTGQCVVEGEGPR 1161  
 QY 1141 CDKCTRGSYGVFPCTPCHQCFALWDVITIAELTNRTHRFLEKAKALISGVIQYRETVD 1200  
 Db 1162 CDKCTRGSYGVFPCTPCHQCFALWDVITIAELTNRTHRFLEKAKALISGVIQYRETVD 1221

QY 1201 SVBRKVEIKDIIAQPAAEPLKNIQNLGFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1260  
 Db 1222 SVBRKVEIKDIIAQPAAEPLKNIQNLGFEAEKLIKDVTEMAQVEVKLSDTTSQSNST 1281  
 QY 1261 AKELDSIQTAESLDNTVVELAQELPFIKNSDIRGALDSITKYPQMSLEAEERUNASTTE 1320  
 Db 1282 AKELDSIQTAESLDNTVVELAQELPFIKNSDIRGALDSITKYPQMSLEAEERUNASTTE 1341  
 QY 1321 PNSTVEQSALMRVEDVMMERESQFKEQEBQARLIDELAGKLSLDLSAAAEEMTCGTP 1380  
 Db 1342 PNSTVEQSALMRVEDVMMERESQFKEQEBQARLIDELAGKLSLDLSAAAEEMTCGTP 1401  
 QY 1381 PGASCSSTEGGPNCRTRDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLALAEVEQL 1440  
 Db 1402 PGASCSSTEGGPNCRTRDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLALAEVEQL 1461  
 QY 1441 SKMYSSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELNLIKQIRNFLTQDSADLDSI 1500  
 Db 1462 SKMYSSEAKLRADAEAKQSAEDILLKTNATKEKMDKSNELNLIKQIRNFLTQDSADLDSI 1521  
 QY 1501 EAVANEVLKXEMPTPQQLQNLTEDIRERVESLSQVEVILQHSAAIDARAEMLLEBAKRA 1560  
 Db 1522 EAVANEVLKXEMPTPQQLQNLTEDIRERVESLSQVEVILQHSAAIDARAEMLLEBAKRA 1581  
 QY 1561 SKSATDVKTADVMYKEALEBAEKAQVAEKAQADEIDIOGTQNLTSISETAASSETL 1620  
 Db 1582 SKSATDVKTADVMYKEALEBAEKAQVAEKAQADEIDIOGTQNLTSISETAASSETL 1641  
 QY 1621 FNASQRISELERNVVEELKRAAQNSGEAEYIEKVYTVTKQSAEDVKKTLQDELDEKVKV 1680  
 Db 1642 FNASQRISELERNVVEELKRAAQNSGEAEYIEKVYTVTKQSAEDVKKTLQDELDEKVKV 1701  
 QY 1681 ENLIAKTEESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKEDNORYLEDKAQEL 1740  
 Db 1702 ENLIAKTEESADARRKAEMLONEAKTLLAQANSKLOLLKDLERKEDNORYLEDKAQEL 1761  
 QY 1741 ARLEGEVRSILKDISQKAVVYSTCL 1765  
 Db 1762 ARLEGEVRSILKDISQKAVVYSTCL 1786

RESULT 9  
 AB81590  
 ID AB81590 standard; protein; 1786 AA.  
 XX AB81590;  
 XX DT 19-SEP-2002 (first entry)  
 XX DE Human laminin 10 second chain protein sequence SEQ ID NO:6.  
 XX KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
 KW tissue repair development; laminin; healing; vascular tissue;  
 KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
 XX proliferation; migration.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..21  
 FT /label= signal  
 FT Protein 22..1786  
 FT /label= laminin\_10\_second\_chain  
 XX WO200250111-A2.  
 XX PD 27-JUN-2002.  
 XX PF 21-DEC-2001; 2001WO-US051035.  
 XX PR 21-DEC-2000; 2000US-0257449P.  
 PR 28-MAR-2001; 2001US-0279282P.  
 PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
XX WPI; 2002-557650/59.  
XX N-PSDB; ABQ72908.  
XX New human laminin-10 proteins, useful for accelerating the healing of  
XX vascular tissue, improving the biocompatibility of grafts, or for  
XX promoting re-endothelialization at the site of vascular injuries.  
XX Claim 9; Page 113-119; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
XX an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are  
XX useful in maintaining cell/tissue phenotype as well as promoting cell  
XX growth and differentiation in tissue repair development. Specifically,  
XX laminin 10 can be used for accelerating the healing injuries of vascular  
XX tissue, improving the biocompatibility of grafts useful for treating such  
XX injuries, for promoting re-endothelialization at the site of vascular  
XX injuries, and promote cell attachment and subsequent cell stasis,  
XX proliferation, differentiation, and/or migration. The present sequence  
XX represents a second chain protein of laminin 10, from the present  
XX invention  
SQ Sequence 1786 AA;  
Query Match 100.0%; Score 9654; DB 5; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QEPFSGYCAEGSCYPATGDLIIIRAQKLSVTSCGLHKPEPYCIVSHLOEDKKCFICNS 60  
DB 22 QEPFSGYCAEGSCYPATGDLIIIRAQKLSVTSCGLHKPEPYCIVSHLOEDKKCFICNS 81  
QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQDLDEAEFHTHLIMTFK 120  
DB 82 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQDLDEAEFHTHLIMTFK 141  
QY 121 TFRPAAMLIERSDFGKTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180  
DB 142 TFRPAAMLIERSDFGKTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201  
QY 181 EGEVIFRALDPAFKIEDYSPRIQNLKLTNLRKFVKLHTLGNLDSRWEIREKYIYA 240  
DB 202 EGEVIFRALDPAFKIEDYSPRIQNLKLTNLRKFVKLHTLGNLDSRWEIREKYIYA 261  
QY 241 VYDMVVRGNCFCYGHASCAPVDGFNEVEGVMVGHGCMCRHNTKGLNCELMDPYHDLPW 300  
DB 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVMVGHGCMCRHNTKGLNCELMDPYHDLPW 321  
QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDDCOHNTMGRCNCEQCKPFY 360  
DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCDDCOHNTMGRCNCEQCKPFY 381  
QY 361 YOHPERDTRDPNFCERCTCDPAGSNEGICDSYTDFTSTGLIAGOCRCKLNVEGSHCDVCK 420  
DB 382 YOHPERDTRDPNFCERCTCDPAGSNEGICDSYTDFTSTGLIAGOCRCKLNVEGSHCDVCK 441  
QY 421 EGFYDLSSDDPFGCKSCACNPLGTIPGNCPCDSETHCYCHRLVTGQHCOCCLPEHWGLS 480  
DB 442 EGFYDLSSDDPFGCKSCACNPLGTIPGNCPCDSETHCYCHRLVTGQHCOCCLPEHWGLS 501  
QY 481 NDLDGCRPCDDGLGALNNSCFABSGQSCSRPHMIGRCNEVEPGYFATLDHYLYEABE 540  
DB 502 NDLDGCRPCDDGLGALNNSCFABSGQSCSRPHMIGRCNEVEPGYFATLDHYLYEABE 561  
QY 541 ANLPGGVSIYERQYIQDRIPSWTGAAGVVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600  
DB 562 ANLPGGVSIYERQYIQDRIPSWTGAAGVVRPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621  
QY 601 DHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVVSLSFGSRVYVLPVPRVCFEKGNTYTVR 660

DB 622 DHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVVSLSFGSRVYVLPVPRVCFEKGNTYTVR 681  
QY 661 LELPOYTSSDSDESPTLIDSLVLMYPYCKSLDIFTVGGSGDGVVWVNSAWETFORYRCLE 720  
DB 682 LELPOYTSSDSDESPTLIDSLVLMYPYCKSLDIFTVGGSGDGVVWVNSAWETFORYRCLE 741  
QY 721 NSRSVVKTPMTDVCNRIIFISALIHQTLGACEDCPQGSLSVCDPNPGQCCQCRPNVYGR 780  
DB 742 NSRSVVKTPMTDVCNRIIFISALIHQTLGACEDCPQGSLSVCDPNPGQCCQCRPNVYGR 801  
QY 781 TCNRCAPGTGFGPSGCKPCCHLOGSVNAPCNVTCGCHCFQGVYARQCDRCLPGHWGF 840  
DB 802 TCNRCAPGTGFGPSGCKPCCHLOGSVNAPCNVTCGCHCFQGVYARQCDRCLPGHWGF 861  
QY 841 PSCQPCQCNHADDCCDPTVTECLNCQDVTMGHCERCLAGYIGDPIIGSDHCRPCPCPD 900  
DB 862 PSCQPCQCNHADDCCDPTVTECLNCQDVTMGHCERCLAGYIGDPIIGSDHCRPCPCPD 921  
QY 901 GPDGRQFARSCYQDPVTLOACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN 960  
DB 922 GPDGRQFARSCYQDPVTLOACVCDPGYIGSRDDCASGYFGNPSVGGSCQPCQCHNN 981  
QY 961 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFYGYGDALRQDCRCKVCNVLGTVQEHCHN 1020  
DB 982 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFYGYGDALRQDCRCKVCNVLGTVQEHCHN 1041  
QY 1021 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCNAAHSFGPSCNBTG 1080  
DB 1042 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCNAAHSFGPSCNBTG 1101  
QY 1081 QCCQMPFGGRTCSQCLFWGDDPVECRACDPRGIEETPCQDOSTGQCVCVEGVEGR 1140  
DB 1102 QCCQMPFGGRTCSQCLFWGDDPVECRACDPRGIEETPCQDOSTGQCVCVEGVEGR 1161  
QY 1141 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNTRHFLKAKAKITSGVIGPYRETVD 1200  
DB 1162 CDKCTRGYSGVFPDCTPCHQCFALWDVIAELTNTRHFLKAKAKITSGVIGPYRETVD 1221  
QY 1201 SYERKVSIEKTLAQSAPAEPLKNTGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNS 1260  
DB 1222 SYERKVSIEKTLAQSAPAEPLKNTGNLFEAEKLIKDVTEMAQVEVKLSDTTSQSNS 1281  
QY 1261 AKELDSLOTAEBSLONTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1320  
DB 1282 AKELDSLOTAEBSLONTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERNVASTTE 1341  
QY 1321 PNSTVEQSMALDRVEDVMMERESQFKQBQAEPLDELAKLOSLOLSAAAEWTCGTP 1380  
DB 1342 PNSTVEQSMALDRVEDVMMERESQFKQBQAEPLDELAKLOSLOLSAAAEWTCGTP 1401  
QY 1381 PGASCSETCGGPNCKRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSEAEVEQL 1440  
DB 1402 PGASCSETCGGPNCKRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSEAEVEQL 1461  
QY 1441 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMKDKNEELNLIKQIRNPLTODSADLDSI 1500  
DB 1462 SKWVSEAKLRADAEAKQSAEDILLKTNATKEMKDKNEELNLIKQIRNPLTODSADLDSI 1521  
QY 1501 EAVANEVLKWEPSPTPOQLONLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLBEAKKA 1560  
DB 1522 EAVANEVLKWEPSPTPOQLONLTEDIRERVESLSQVEVILQHSAAADIAEAEMLLBEAKKA 1581  
QY 1561 SKSATDVKVTADMKVEALEEAEKAQVAEAKAKQADEDIQGTQNLTTSESATASEETL 1620  
DB 1582 SKSATDVKVTADMKVEALEEAEKAQVAEAKAKQADEDIQGTQNLTTSESATASEETL 1641  
QY 1621 FNASQRISELERNEVELKKAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKVV 1680  
DB 1642 FNASQRISELERNEVELKKAQNSGEAEYIEKVYTVKQSAEDVKKTLDGELDEKYKVV 1701  
QY 1681 ENLIAKTTESADARRKAEMLQNEAKTLAQANSKLQLLKOLERYEDNQRYLEKQAEEL 1740

Db	1702	ENLIAKTBESADARRKAEMLQNEAKTLAQAASKLQLLKDLERKYEDNQRYLEDKAQEL	1761
Qy	1741	ARLEGEVRSLLKDISQKAVYSTCL	1765
Db	1762	ARLEGEVRSLLKDISQKAVYSTCL	1786
RESULT 10			
Id	AA048896		
XX	AA048896 standard; protein; 1786 AA.		
XX	AA048896;		
DT	04-APR-2002 (first entry)		
DE	Laminin protein.		
XX	Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;		
KW	psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;		
KW	arthritis; wound healing; Helicobacter pylori; peptic ulcer;		
KW	gene therapy; angiostatin antagonist; endostatin antagonist;		
KW	antiangiogenic; cyclostatic; antiarthritic; antiinflammatory;		
KW	cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;		
XX	gynaecological; cat scratch fever.		
OS	Unidentified.		
XX	WO200193897-A2.		
PN	13-DEC-2001.		
XX	04-JUN-2001; 2001WO-US017947.		
PR	02-JUN-2000; 2000US-0209065P.		
PR	08-MAY-2001; 2001US-0289387P.		
XX	(ENTR-) ENTREMED INC.		
PI	Sim KL, Macdonald NJ;		
XX	WPI; 2002-130569/17.		
DR	N-PSDB; ABA97525.		
XX	Regulating angiogenesis and treatment of angiogenesis-mediated diseases,		
PT	e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding		
PT	compound or actin disrupting compound.		
XX	Example 11; Fig 6A; 95pp; English.		
XX	The present invention relates to methods of regulating angiogenesis in an		
CC	individual by administering an angiogenesis regulating composition		
CC	comprising a tropomyosin binding compound or an actin disrupting		
CC	compound. The compositions are useful for treating diseases and processes		
CC	mediated by angiogenesis including haemangioma, solid tumours, blood		
CC	borne tumours leukaemia, metastasis, Crohn's disease, coronary or		
CC	cerebral collaterals, arthritis, diabetic neovascularisation, macular		
CC	degeneration, wound healing, Helicobacter related diseases, ovulation,		
CC	menstruation, and cat scratch fever. The present sequence is a protein		
CC	described in the exemplification of the invention		
XX	Sequence 1786 AA;		
SQ	Query Match 99.8%; Score 9638; DB 5; Length 1786;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 1763; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	1	QEPFSGYGAEGSCYPATGDLIGRAQLSVTSTGLHKHPYICVSHLQEDKKFCFICNS	60
Db	22	QEPFSGYGAEGSCYPATGDLIGRAQLSVTSTGLHKHPYICVSHLQEDKKFCFICNS	81
Qy	61	QDPYHTINPDSHLIENVTTTAPNRLKIWQSENGVENVTIQLDEAFHETHLIMTFK	120
Db	82	QDPYHTINPDSHLIENVTTTAPNRLKIWQSENGVENVTIQLDEAFHETHLIMTFK	141

Qy	121	TFRPAAMLIERSSDFGTWGVYRYFAYDCBASFFGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSSDFGTWGVYRYFAYDCBASFFGISTGPMKKVDDIICDSRYSDIEPST	201
Qy	181	BGEVIFRALDPARKIEDPPSPRIQNLKLTNLRKFKVKLHTGLNLDLSRMEIREKYYA	240
Db	202	BGEVIFRALDPARKIEDPPSPRIQNLKLTNLRKFKVKLHTGLNLDLSRMEIREKYYA	261
Qy	241	YDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCVRHNTKGLNCELMDYFHLDPW	300
Db	262	YDMVVRGNCFYGHASECAPVDGFNEEVEGMVHGHCVRHNTKGLNCELMDYFHLDPW	321
Qy	301	RPAGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTGNRCQCKPFY	360
Db	322	RPAGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTGNRCQCKPFY	381
Qy	361	YQHERDIRDPNFCERCTCPAGSQNEGICDSYTFDFTSTGLIAGCRCKLVNVEGHCDCVK	420
Db	382	YQHERDIRDPNFCERCTCPAGSQNEGICDSYTFDFTSTGLIAGCRCKLVNVEGHCDCVK	441
Qy	421	BGFYDLSEDPFGCKSCACNPLGTIPGNCPCDSTGHYCKRLVTGHCDCCLPEHGWLS	480
Db	442	BGFYDLSEDPFGCKSCACNPLGTIPGNCPCDSTGHYCKRLVTGHCDCCLPEHGWLS	501
Qy	481	NLDGCRPCDCLGALNNSCFABSGQSCRPBMIGRCQNEVEPGYFATLDHYLYEAE	540
Db	502	NLDGCRPCDCLGALNNSCFABSGQSCRPBMIGRCQNEVEPGYFATLDHYLYEAE	561
Qy	541	ANLGFVSIIVERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	600
Db	562	ANLGFVSIIVERQYIQRIPSWTGAQFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP	621
Qy	601	DHWEKAVITVQRPGRIPTSRRCNGTIPDDNNOVVSLSPGSRVYVLPVPCFEKGTNTVR	660
Db	622	DHWEKAVITVQRPGRIPTSRRCNGTIPDDNNOVVSLSPGSRVYVLPVPCFEKGTNTVR	681
Qy	661	LELPQYSSDSDESPTLLDLSVLMFYKSLDIFTVGGSGDGVVTNSAWETFORYKCLE	720
Db	682	LELPQYSSDSDESPTLLDLSVLMFYKSLDIFTVGGSGDGVVTNSAWETFORYKCLE	741
Qy	721	NSRSVVKTPMTDVCNRIIFISALLHQTGLACEDPQGSLSVCDPNGGOCQCRPNVVR	780
Db	742	NSRSVVKTPMTDVCNRIIFISALLHQTGLACEDPQGSLSVCDPNGGOCQCRPNVVR	801
Qy	781	TCNRCAPTGFGPSGCKPCBCHLQGSVNAFCNPVTGQCHFCQGVYARQCDCLPGHWGF	840
Db	802	TCNRCAPTGFGPSGCKPCBCHLQGSVNAFCNPVTGQCHFCQGVYARQCDCLPGHWGF	861
Qy	841	PSQPCQCNHADDPCDPTGECNLCQDYTMGNCRCLAGYGDPIIGSGDHCRPCPCPD	900
Db	862	PSQPCQCNHADDPCDPTGECNLCQDYTMGNCRCLAGYGDPIIGSGDHCRPCPCPD	921
Qy	901	GPDSGRQFARSCYQDPVTQLQACVCDPGYIGSRCDCCASGYFGNPSVGGSCQPCQCHN	960
Db	922	GPDSGRQFARSCYQDPVTQLQACVCDPGYIGSRCDCCASGYFGNPSVGGSCQPCQCHN	981
Qy	961	IDTTDPEACDKETGRCLKLYHTEGHCQFCRFYGYGDALRQDKCRKVCNVLGTVQSHCN	1020
Db	982	IDTTDPEACDKETGRCLKLYHTEGHCQFCRFYGYGDALRQDKCRKVCNVLGTVQSHCN	1041
Qy	1021	GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGDCPCNCAAHFSGSCNEFTG	1080
Db	1042	GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGDCPCNCAAHFSGSCNEFTG	1101
Qy	1081	QCQCMFGGRTCSBCEQLEFWGDPVECRACDPRGIETPQCDQSTGQCVCEGVGEGPR	1140
Db	1102	QCQCMFGGRTCSBCEQLEFWGDPVECRACDPRGIETPQCDQSTGQCVCEGVGEGPR	1161
Qy	1141	CDKCTRYSGVFPDCTFCHQCFALMDVITABLNTNRHFRLEKAKALKISGVIPYRETVD	1200
Db	1162	CDKCTRYSGVFPDCTFCHQCFALMDVITABLNTNRHFRLEKAKALKISGVIPYRETVD	1221



QY 1201 SVERKVEIKDILAQSPAAPLKNIGNLPFAEKLKDVTEMMAQVEVKLSDTTSQNST 1260  
 DB 1222 SVERKVEIKDILAQSPAAPLKNIGNLPFAEKLKDVTEMMAQVEVKLSDTTSQNST 1281  
 QY 1261 AKELDSIQTEAESLDNTVKELAELEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320  
 DB 1282 AKELDSIQTEAESLDNTVKELAELEFIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341  
 QY 1321 PNSTVQSALMRDVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380  
 DB 1342 PNSTVQSALMRDVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401  
 QY 1381 PGASCSTECGPNCRDTEGERKCGPGCGGLVTVAHNAQKAMDLDODVLSALAEVOL 1440  
 DB 1402 PGASCSTECGPNCRDTEGERKCGPGCGGLVTVAHNAQKAMDLDODVLSALAEVOL 1461  
 QY 1441 SKMVSEAKLRADEAKQSAEDILLKTNATKRMKSKNEELRNLIKQIRNFLTQDSADLDSI 1500  
 DB 1462 SKMVSEAKLRADEAKQSAEDILLKTNATKRMKSKNEELRNLIKQIRNFLTQDSADLDSI 1521  
 QY 1501 EAVANEVLKMEPSTPOOLQNLTEDIRERVESLSQVEVILQHGAADIARAEMLLEAKRA 1560  
 DB 1522 EAVANEVLKMEPSTPOOLQNLTEDIRERVESLSQVEVILQHGAADIARAEMLLEAKRA 1581  
 QY 1561 SKSATDVKVTADMVKEALEAEAKQAQAAKAQKQADEDIQGTQNLITSIESETAASEETL 1620  
 DB 1582 SKSATDVKVTADMVKEALEAEAKQAQAAKAQKQADEDIQGTQNLITSIESETAASEETL 1641  
 QY 1621 FNACRISSELRNVEELKRAQAQNGEAEYIEKVVTYVTKQSAEDVKTGDELDEKVKY 1680  
 DB 1642 FNACRISSELRNVEELKRAQAQNGEAEYIEKVVTYVTKQSAEDVKTGDELDEKVKY 1701  
 QY 1681 ENLJAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1740  
 DB 1702 ENLJAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAQEL 1761  
 QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765  
 DB 1762 ARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 11  
 AAY15461  
 ID AAY15461 standard; protein; 1785 AA.  
 AC AAY15461;  
 XX  
 DT 26-JUL-1999 (first entry)  
 XX Human laminin beta 1 subunit.  
 DE  
 XX Laminin 12; alpha 2; beta 1; gamma 3; subunit; nerve regeneration;  
 KW connective tissue adhesion; tissue repair; wound; nerve growth;  
 KW laminin beta 1 subunit.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9919348-A1.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 08-OCT-1998; 98WO-US021391.  
 XX  
 PR 10-OCT-1997; 97US-0061609P.  
 XX  
 XX (GEHO) GEN HOSPITAL CORP.  
 XX  
 PI Burgeson RE, Champilaud M, Olson P, Koch M, Brunken W;  
 XX  
 DR WPI; 1999-326542/27.  
 DR N-PSDB; AAX59769.  
 XX  
 PT Purified laminin 12 useful for promoting tissue repair and promoting

PT nerve growth.  
 XX Disclosure; Fig 4; 86pp; English.  
 XX The specification describes laminin 12 which includes an alpha 2, beta 1 and gamma 3 subunit. Laminin is a connective tissue adhesion molecule. Laminin is useful for promoting tissue repair due to wounds and to promote nerve growth or regeneration. The present sequence represents human laminin beta 1 subunit  
 XX  
 SQ Sequence 1785 AA;  
 Query Match 99.6%; Score 9618.5; DB 2; Length 1785;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1762; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 QEPFESYCAAGSCYCATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQDKKQFCFICNS 60  
 DB 22 QEPFESYCAAGSCYCATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQDKKQFCFICNS 81  
 QY 61 QDPYHETINPDSHLIENVVTFAPNRLKIWMQSENGVENVTIQLDLAEFFHTLIMTFK 120  
 DB 82 QDPYHETINPDSHLIENVVTFAPNRLKIWMQSENGVENVTIQLDLAEFFHTLIMTFK 141  
 QY 121 TFRPAAMLIERSSDPGKTGWVRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180  
 DB 142 TFRPAAMLIERSSDPGKTGWVRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201  
 QY 181 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNRLKFVKLHTLGNLDSRMEIREKYVA 240  
 DB 202 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNRLKFVKLHTLGNLDSRMEIREKYVA 261  
 QY 241 VYDMVVRGNCFCYGHASCAPVDGFEVEGMVHGHCNCRHTKGLNCELQMDYHDLPW 300  
 DB 262 VYDMVVRGNCFCYGHASCAPVDGFEVEGMVHGHCNCRHTKGLNCELQMDYHDLPW 321  
 QY 301 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCCDQOHTWGRNCQCKPFY 360  
 DB 322 RPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGVCCDQOHTWGRNCQCKPFY 381  
 QY 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDTDFSTGLIAGQCRCKLNTVEGHCYDCK 420  
 DB 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDTDFSTGLIAGQCRCKLNTVEGHCYDCK 441  
 QY 421 EGFYDLSSDEDPGCKSCACNPLGITPGNPNCDSETHCYCKRLVTGQCDQCLPEHWGLS 480  
 DB 442 EGFYDLSSDEDPGCKSCACNPLGITPGNPNCDSETHCYCKRLVTGQCDQCLPEHWGLS 501  
 QY 481 NDLDCRCPCDDLGALNNSCFAESGQSCSRPHMIGROQNEVEPGYYFATLDHYLYEAE 540  
 DB 502 NDLDCRCPCDDLGALNNSCFAESGQSCSRPHMIGROQNEVEPGYYFATLDHYLYEAE 561  
 QY 541 ANLGPVSIVEROYIQDRIPSWTGAGFYRVEGAYLEEFIDNIPYSMEYDILIRVEPOLP 600  
 DB 562 ANLGPVSIVEROYIQDRIPSWTGAGFYRVEGAYLEEFIDNIPYSMEYDILIRVEPOLP 621  
 QY 601 DHWEKAVITVQPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPFVPCFEGKNTYVR 660  
 DB 622 DHWEKAVITVQPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPFVPCFEGKNTYVR 681  
 QY 661 LELPQYTSDDSDVESPYTLIDSLVLMPCYKSLDITFTVGGSGDVVWTSNFWTQRYRCL 720  
 DB 682 LELPQYTSDDSDVESPYTLIDSLVLMPCYKSLDITFTVGGSGDVVWTSNFWTQRYRCL 741  
 QY 721 NSRSVVKTPMTDVCNIIIFSIALLHQTLGACEDCPQGSLSVCDPNNGCQCCRPNVVGR 780  
 DB 742 NSRSVVKTPMTDVCNIIIFSIALLHQTLGACEDCPQGSLSVCDPNNGCQCCRPNVVGR 801  
 QY 781 TCNRCAPGTFFGPGCKPCCECHLQGSVNAFCNPVTGQCHQFGVYARQCDRCCLPGHWGF 840  
 DB 802 TCNRCAPGTFFGPGCKPCCECHLQGSVNAFCNPVTGQCHQFGVYARQCDRCCLPGHWGF 861  
 QY 841 PSCQPCQCNHADDCCDPTVTECLNCQDVTWGHNCERCLAGYVGPDIIGSGDHCRPCPCPD 900



Db 202 EGEVIFRALDPAFIEDPYSPRQNLKILNIRKFKVKLHTLGDNLDSRMEIREKYYIA 261  
Qy 241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGHCNRHNTKGLNCELCHMDFYHDLPW 300  
Db 262 VYDMVVRGNCFCYGHASECAPVDGVNEVEGMVHGHCNRHNTKGLNCELCHMDFYHDLPW 321  
Qy 301 RPAEGRNSACKKCNKNEHSISCHFDMVAVLATGNTSGVYCDQCHNTWGRNCEQCKPFY 360  
Db 322 RPAEGRNSACKKCNKNEHSISCHFDMVAVLATGNTSGVYCDQCHNTWGRNCEQCKPFY 381  
Qy 361 YQHPERDIRPNFCERCTCDPAGSQNEGICDSTDFSTGLIAGQCRCKLVNVEGHECHDVCK 420  
Db 382 FQHPERDIRPNLCEPCTCDPAGSENGGICDGYTDFSVGLIAGQCRCKLVNVEGHECHDVCK 441  
Qy 421 EGFYDLSSDPFGKSCACNPLGTIPGNCPCDSETHCYCKRLVGTQHOCHDQCLPEHWGLS 480  
Db 442 EGFYDLSSDPFGKSCACNPLGTIPGNCPCDSETHCYCKRLVGTQHOCHDQCLPEHWGLS 501  
Qy 481 NDLGCRPCDCLGGLNNSCFABSGQSCSRPHMIGRQCNEVEPGYFYFATLDHYLAEAE 540  
Db 502 NDLGCRPCDCLGGLNNSCFABSGQSCSRPHMIGRQCNEVEPGYFYFATLDHYLAEAE 561  
Qy 541 ANLPGVSVIVERQYIQDIRIPSWTGAQFVRPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 600  
Db 562 ANLPGVSVIVERQYIQDIRIPSWTGAQFVRPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 621  
Qy 601 DHWEKAVITVORPGRIPTSRSCGNTIPDDNQVVSLSFGSRVYVLPVPVCFEKGNTVTVR 660  
Db 622 DHWEKAVITVORPGRIPTSRSCGNTIPDDNQVVSLSFGSRVYVLPVPVCFEKGNTVTVR 681  
Qy 661 LELPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETTQRYRCLE 720  
Db 682 LELPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETTQRYRCLE 741  
Qy 721 NSRSVVKTPMTDVCNRNIIFSLIHLHTGLACEDPOGSLSSVCDPNGGOCQCRPNVVG 780  
Db 742 NSRSVVKTPMTDVCNRNIIFSLIHLHTGLACEDPOGSLSSVCDPNGGOCQCRPNVVG 801  
Qy 781 TCNRCAPGTGFGPGCKPCCHIQGSVNAFCNPVTGQCHCFQGVYARQCDRCPLGHWGF 840  
Db 802 TCNRCAPGTGFGPGCKPCCHIQGSVNAFCNPVTGQCHCFQGVYARQCDRCPLGHWGF 861  
Qy 841 PSCQPCQNGHADDPCVTCNQCQDYTMHCNRCERCLAGYGDPIIGSDGHCPCPCPD 900  
Db 862 PSCQPCQNGHADDPCVTCNQCQDYTMHCNRCERCLAGYGDPIIGSDGHCPCPCPD 921  
Qy 901 GPDGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSBVGSCQPCQCHN 960  
Db 922 GPDGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASGYFGNPSBVGSCQPCQCHN 981  
Qy 961 IDTTDPEACDXTGRCLKCLYHTEGHEHCFQCFRFGYGDALRQDCRCKVCNVLGTVOEHCH 1020  
Db 982 IDTTDPEACDXTGRCLKCLYHTEGHEHCFQCFRFGYGDALRQDCRCKVCNVLGTVOEHCH 1041  
Qy 1021 GSDCCDCKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFPGSCNFTG 1080  
Db 1042 GSDCCDCKATGQCLCLPNVIGONCDRCAPNTWQLASGTGCDPCNCAHSGFPGSCNFTG 1101  
Qy 1081 QCCMPFGGRTSCQCLFNGDPDVECRACDPCPRGIETPCDQOSTQOCVCVEGVGPR 1140  
Db 1102 QCCMPFGGRTSCQCLFNGDPDVECRACDPCPRGIETPCDQOSTQOCVCVEGVGPR 1161  
Qy 1141 CDKCTRGVGVFPDCTPCHQCPALMDVIIAELTNTRTHFLEKAKALISGVIPIRYETVD 1200  
Db 1162 CDKCTRGVGVFPDCTPCHQCPALMDVIIAELTNTRTHFLEKAKALISGVIPIRYETVD 1221  
Qy 1201 SYERKVSIEIKDILASPAAPLKNIGNLFEBAKLIKDVTEMAQVEVKLSDDTQSQNST 1260  
Db 1222 SYERKVSIEIKDILASPAAPLKNIGNLFEBAKLIKDVTEMAQVEVKLSDDTQSQNST 1281  
Qy 1261 AKELSLQTEAESLNTWKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVASTTE 1320

Db 1282 AGELGALQAEASLDKTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVASTTE 1341  
Qy 1321 PNSTVEQALMRDRVEDVMMERESQFKQKQBEQARLLDELQAGKLSQSLDLSAAAEWTCGTP 1380  
Db 1342 PNSTVEQALMRDRVEDVMMERESQFKQKQBEQARLLDELQAGKLSQSLDLSAAAEWTCGTP 1401  
Qy 1381 PGASCSECCGPNCRDTEGERKCGGPGCGGLVTVVAVNAWOKAMDLDQDVLASALAEVEOL 1440  
Db 1402 PGASCSECCGPNCRDTEGERKCGGPGCGGLVTVVAVNAWOKAMDLDQDVLASALAEVEOL 1461  
Qy 1441 SKWSEAKLRADAKQSAEDILLKTNATKQKQKSNELNLIKQIRNFLTQDSADLDSI 1500  
Db 1462 SKWSEAKLRADAKQSAEDILLKTNATKQKQKSNELNLIKQIRNFLTQDSADLDSI 1521  
Qy 1501 EAVANEVLKMPSTPQOLQNLTDIERVESLSQVEVILQHSAADTARAEMLLEAKRA 1560  
Db 1522 EAVANEVLKMPSTPQOLQNLTDIERVESLSQVEVILQHSAADTARAEMLLEAKRA 1581  
Qy 1561 SKSATDVKTADWKEALEEAKQAQVAAKAIKQADEDIQCTQNLTLTISEETAASETL 1620  
Db 1582 SKSATDVKTADWKEALEEAKQAQVAAKAIKQADEDIQCTQNLTLTISEETAASETL 1641  
Qy 1621 FNASORISELEENVELKRAQKAAQNSGEAEYIEKVYVTVKQSAEDVYKTLDGELDEKYKV 1680  
Db 1642 FNASORISELEENVELKRAQKAAQNSGEAEYIEKVYVTVKQSAEDVYKTLDGELDEKYKV 1701  
Qy 1681 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLLKOLEKXYEDNQVLEDAQEL 1740  
Db 1702 ENLIAKTTESADARRKAEMLQNEAKTLLAQANSKQLLKOLEKXYEDNQVLEDAQEL 1761  
Qy 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765  
Db 1762 VRLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 13  
AAB48450  
ID AAB48450 standard; protein; 1786 AA.  
XX  
AC AAB48450;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX  
OS Mus musculus.  
XX  
PN W0200066732-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX  
PR 30-APR-1999; 99US-0131720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX  
PA (BIOS-) BIOSTRATUM INC.  
XX  
PI Kortessmaa J, Tryggvason K;  
XX  
DR WPI; 2000-687539/67.  
DR N-PSDB; AAC83711.  
XX  
PT Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX



ID	ABB81592 standard; protein; 1786 AA.
XX	
AC	ABB81592;
XX	
DT	19-SEP-2002 (first entry)
XX	
DE	Mouse laminin 10 second chain protein sequence SEQ ID NO:10.
XX	
KW	Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;
KW	tissue repair development; laminin; healing; vascular tissue;
KW	re-endothelialisation; vascular injury; cell attachment; cell stasis;
KW	proliferation; migration.
XX	
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..21
FT	Protein /label= signal
FT	22..1786
FT	/label= laminin_10_second_chain
XX	
FN	WO200250111-A2.
XX	
PD	27-JUN-2002.
XX	
PF	21-DEC-2001; 2001WO-US051035.
XX	
PR	21-DEC-2000; 2000US-0257449P.
PR	28-MAR-2001; 2001US-0279282P.
PR	13-NOV-2001; 2001US-00279282.
XX	
PA	(BIOS-) BIOSTRATUM INC.
XX	
PI	Tryggvason K, Doi M, Thyboll J;
PI	WPI; 2002-557650/59.
DR	N-PSDB; ABQ72910.
XX	
PT	New human laminin-10 proteins, useful for accelerating the healing of
PT	vascular tissue, improving the biocompatibility of grafts, or for
PT	promoting re-endothelialization at the site of vascular injuries.
XX	
PS	Claim 9; Page 140-145; 231pp; English.
XX	
CC	The present invention describes human laminin alpha 5. Also described is
CC	an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are
CC	useful in maintaining cell/tissue phenotype as well as promoting cell
CC	growth and differentiation in tissue repair development. Specifically,
CC	laminin 10 can be used for accelerating the healing injuries of vascular
CC	tissue, improving the biocompatibility of grafts useful for treating such
CC	injuries, for promoting re-endothelialisation at the site of vascular
CC	injuries, and promote cell attachment and subsequent cell stasis.
CC	proliferation, differentiation, and/or migration. The present sequence
CC	encodes a second chain protein of laminin 10, from the present invention
XX	
SQ	Sequence 1786 AA;
	Query Match 94.2%; Score 9092; DB 5; Length 1786;
	Best Local Similarity 93.0%; Pred No. 0;
	Matches 164; Conservative 71; Mismatches 52; Indels 0; Gaps 0;
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Qy	61 QDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEPHFTHLIMTFK 120
Db	82 RDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEPHFTHLIMTFK 141
Qy	121 TFPAAWLIERSDFGKTGWVTRYFAYDCEASFPFGISTGPMKKVDDIIICDSRYSDIEPST 180
Db	142 TFPAAWLIERSDFGKTGWVTRYFAYDCEASFPFGISTGPMKKVDDIIICDSRYSDIEPST 201



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DB 502 NDLGCRPCDCLGALNNSCSEDSGQSCCLPHMIGQCNVEPQYFATLDHYLYEAE 561  
QY 541 ANLPGVSIVEROYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 600  
DB 562 ANLPGVVVVEROYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 621  
QY 601 DHWEKAVITVORPGRIPSSSCGNTIIPDDNOVUSLSFGSRVYVLPVPVCFEKGNTYVR 660  
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QY 661 LELPQYSSSDVESPYTLIDSLVMPYCKSLDFTVGGSDGVVVTNSAMETFORVRCLE 720  
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QY 721 NSRSVVKTPMTDVCRNIIIFSALLHQTGLACEDPOGSSVSCDPPNGGOCQCPNVVGR 780  
DB 742 NSRSVVKTPMTDVCRNIIIFSALLHQTGLACEDPOGSSVSCDPPNGGOCQCPNVVGR 801  
QY 781 TCNRCAPGTGFGPGCKPCCHLQGSVNAPCNVPGCHFCQGVYARQCDRCLPGHWGF 840  
DB 802 TCNRCAPGTGFGPGCKPCCHLQGSASAFCDAITGCHCFQGIYARQCDRCLPGHWGF 861  
QY 841 PSCQPCQCNHADDPCDVTGECINACQDYTMGNHCERCLAGYIGDPIIGSGDHCRCPCPCPD 900  
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DB 1698 ENLIAKTEESADARRKAEMLQNEAKTLLAQANSKIQLLKDLERKYEDNQYLEDKAQEL 1757  
QY 1741 ARLEGEVRSLLKDIQSKVA 1759  
DB 1758 VRLEGEVRSLLKDIQSKVA 1776

Search completed: May 18, 2004, 14:41:59  
Job time : 53.9797 secs



Sequence 28, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 8, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 16, Appl  
Sequence 12, Appl  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 5, Appl  
Sequence 10, Appl

28 1673 17.3 1584 4 US-09-562-702A-28  
29 1667 17.3 278 2 US-08-460-309-13  
30 1667 17.3 278 2 US-08-125-077-13  
31 1605 16.6 3635 4 US-09-845-583A-2  
32 1565 16.2 3111 2 US-08-460-309-4  
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34 1559.5 16.2 3088 4 US-09-562-702A-8  
35 1559.5 16.2 3089 4 US-09-562-702A-4  
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45 1515.5 15.7 1587 4 US-09-845-583A-10

ALIGNMENTS

RESULT 1  
US-09-562-702A-16  
; Sequence 16, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-16

Query Match 100.0%; Score 9654; DB 4; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model  
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Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9654	100.0	1765	4	US-09-562-702A-16
2	9654	100.0	1765	4	US-09-561-818A-16
3	9654	100.0	1786	4	US-09-562-702A-14
4	9654	100.0	1786	4	US-09-561-818A-14
5	9654	100.0	1786	4	US-09-561-709B-9
6	9092	94.2	1786	4	US-09-562-702A-18
7	9092	94.2	1786	4	US-09-561-818A-18
8	8873	91.9	1725	4	US-09-562-702A-20
9	8873	91.9	1725	4	US-09-561-818A-20
10	6051.5	62.7	1196	1	US-08-144-121-4
11	6051.5	62.7	1196	2	US-08-785-893-4
12	5046	52.3	1799	4	US-09-845-583A-6
13	4923	51.0	1798	4	US-09-561-709B-11
14	4918	50.9	1798	4	US-09-845-583A-8
15	3832.5	39.7	1761	4	US-09-561-709B-1
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RESULT 2  
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; Sequence 16, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortsema, Jarrko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-16

Query Match 100.0%; Score 9654; DB 4; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 241 VYDMVVRNCFYGHASECAPDVGNEVGMVHGMCHRNKGLNCELMDPYHDLPW 300  
DB 241 VYDMVVRNCFYGHASECAPDVGNEVGMVHGMCHRNKGLNCELMDPYHDLPW 300  
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361 YCHPERDIRDNFNCERCTCDPAGSNEGICDSYDTFSTGLIAGQCRCKLVNVEGHSDVCK 420  
361 YCHPERDIRDNFNCERCTCDPAGSNEGICDSYDTFSTGLIAGQCRCKLVNVEGHSDVCK 420  
421 EGFYDLSSDDPGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCDCDCLPEHWGLS 480  
421 EGFYDLSSDDPGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCDCDCLPEHWGLS 480  
481 NDLDCRCPCDCLGALNNSCFASGQSCSRPHMIGRQCNVEPGYYPATLDHYLYABE 540  
481 NDLDCRCPCDCLGALNNSCFASGQSCSRPHMIGRQCNVEPGYYPATLDHYLYABE 540  
541 ANLGPVSIVERQYIQRIPSWTGAQVVRPGAVLEFIDNI PYSMEYDILIRYEPOLP 600  
541 ANLGPVSIVERQYIQRIPSWTGAQVVRPGAVLEFIDNI PYSMEYDILIRYEPOLP 600  
601 DHWEKAVITVQRPGRIPSSRCNTIPDDNDQVWSLSPGSRVYVLPREVCFEKGNTYVR 660  
601 DHWEKAVITVQRPGRIPSSRCNTIPDDNDQVWSLSPGSRVYVLPREVCFEKGNTYVR 660  
661 LELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVNTSAWETFORYRCL 720  
661 LELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVNTSAWETFORYRCL 720  
721 NSRSVVKTPMTDVCNRIIPSIALLHQTLGACEDPQGLSSVCDPNGGQCCQCRNVVGR 780  
721 NSRSVVKTPMTDVCNRIIPSIALLHQTLGACEDPQGLSSVCDPNGGQCCQCRNVVGR 780  
781 TCNRCAPGTFGPGSKCKPCBCHLQGSVNAFONPVYTGQCHQCGVYARQCDRCLPHWGF 840  
781 TCNRCAPGTFGPGSKCKPCBCHLQGSVNAFONPVYTGQCHQCGVYARQCDRCLPHWGF 840  
841 PSCQPCQNGHADDPCDVTGECNCDYTMGNHCERCLAGYGDPIIGSGDHCRCPD 900  
841 PSCQPCQNGHADDPCDVTGECNCDYTMGNHCERCLAGYGDPIIGSGDHCRCPD 900  
901 GPDGSRQFARSCYQDPVTLOLACVCDPVGIVGRDCCASGYFNGSEVGGSCQPCQCHN 960  
901 GPDGSRQFARSCYQDPVTLOLACVCDPVGIVGRDCCASGYFNGSEVGGSCQPCQCHN 960  
961 IDTTDEACDKETGRCLKCLYHTEGHCOCFRFGYVGDALRODCRKCYNVLTGVQEH 1020  
961 IDTTDEACDKETGRCLKCLYHTEGHCOCFRFGYVGDALRODCRKCYNVLTGVQEH 1020  
1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFTG 1080  
1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFTG 1080  
1081 QCCMPFGGRTSCQCLFWGDPDVECRACDPRGIEPTQDOSTGQCVVEGVGPR 1140  
1081 QCCMPFGGRTSCQCLFWGDPDVECRACDPRGIEPTQDOSTGQCVVEGVGPR 1140  
1141 CDKCTRGYSVPDCTPCHQCFALMDVITAEITNRTHREKAKALKISGVIGPYRETV 1200  
1141 CDKCTRGYSVPDCTPCHQCFALMDVITAEITNRTHREKAKALKISGVIGPYRETV 1200  
1201 SVERKVSIEKIDILAQSPAAEPLKNI ONLFEAEKLI KOVTEMAQVEVKLSDTTQSNS 1260  
1201 SVERKVSIEKIDILAQSPAAEPLKNI ONLFEAEKLI KOVTEMAQVEVKLSDTTQSNS 1260  
1261 AKELDSLOTEAESLNTVKELEAELEFIKNSDIRGALDSITKYFQNSLEAEERVNASTE 1320  
1261 AKELDSLOTEAESLNTVKELEAELEFIKNSDIRGALDSITKYFQNSLEAEERVNASTE 1320  
1321 PNSTVQSALMRDRVEDVMRESQFKEQBEQARLLDELAGKLSLDLSAAAEWTCGTP 1380  
1321 PNSTVQSALMRDRVEDVMRESQFKEQBEQARLLDELAGKLSLDLSAAAEWTCGTP 1380  
1381 PGASCSETCCGNCRTDEGERKCGGPGCGGLVTVAHNAQWAMLDQDVLGALAEVEQL 1440  
1381 PGASCSETCCGNCRTDEGERKCGGPGCGGLVTVAHNAQWAMLDQDVLGALAEVEQL 1440

1441 SKMWSEAKLRADAEAKOSAEEDILLKTNAKEMDKNEELRNLIKOIRNFLTQDSADLDSI 1500  
1441 SKMWSEAKLRADAEAKOSAEEDILLKTNAKEMDKNEELRNLIKOIRNFLTQDSADLDSI 1500  
1501 EAVANVILKXEMPSTPQQLONTEDIRERVESLSQVEVILQHSADIAEAEMLEBEAKA 1560  
1501 EAVANVILKXEMPSTPQQLONTEDIRERVESLSQVEVILQHSADIAEAEMLEBEAKA 1560  
1561 SKSATDVKTADVMKALEAEAKAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA 1620  
1561 SKSATDVKTADVMKALEAEAKAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA 1620  
1621 FNASQRISELERNVEELKKAQA 1680  
1621 FNASQRISELERNVEELKKAQA 1680  
1681 ENLIAKTTESADARPAEMLQNEAKTLAQANSKLQLLKDLERKYEDNORYLEDKAQEL 1740  
1681 ENLIAKTTESADARPAEMLQNEAKTLAQANSKLQLLKDLERKYEDNORYLEDKAQEL 1740  
1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765  
1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765

## RESULT 3

US-09-562-702A-14  
; Sequence 14, Application US/09562702A

; Patent No. 6632790

; GENERAL INFORMATION:

; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use

; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-562-702A-14

Query Match 100.0%; Score 9654; DB 4; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCFICNS 60  
DB 22 QEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKCFICNS 81  
QY 61 QDPYHETLNPDASHLIENVTTFAPNRLKIWKQSENGVENVTIQLDLAEPEHFTLIMTEK 120  
DB 82 QDPYHETLNPDASHLIENVTTFAPNRLKIWKQSENGVENVTIQLDLAEPEHFTLIMTEK 141  
QY 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCASFPGISGPMKKVDDIICDSRYSDIEPST 180  
DB 142 TFRPAAMLIERSSDFGKTGWYRYFAYDCASFPGISGPMKKVDDIICDSRYSDIEPST 201  
QY 181 EGEVIFRALDPAPFKIEPYPSPRIQNLKIITNLRKFVKLHTLGNLDLSRWEIREKYYA 240  
DB 202 EGEVIFRALDPAPFKIEPYPSPRIQNLKIITNLRKFVKLHTLGNLDLSRWEIREKYYA 261  
QY 241 VYDMVVRGNCFCYGHASECAPVDGFEVEGVHCHMCRCRHNKXGLNCELMDPFDHLPW 300

Db 262 VYDMVVRGNCFCYGHASECAPVDGFEVGMVHGHCMCRHNTKGLNCELCDMPYHDLPW 321  
Qy 301 RPAEGRNSACKKNCNHSISCHFDMAVYLATGNVGGVCDCHQHTMGRNCEQCKPFY 360  
Db 322 RPAEGRNSACKKNCNHSISCHFDMAVYLATGNVGGVCDCHQHTMGRNCEQCKPFY 381  
Qy 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLVNVEGHCDCVK 420  
Db 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRCKLVNVEGHCDCVK 441  
Qy 421 EGFYDLSSDFGCKSCACNPLGTIPGNPCDSTGHCHYCKRLVTGQHCQCLPEHNGLS 480  
Db 442 EGFYDLSSDFGCKSCACNPLGTIPGNPCDSTGHCHYCKRLVTGQHCQCLPEHNGLS 501  
Qy 481 NDLGCRPCDDCLGGALNNSCFASGQSCSRPHMIGRQCNVEPGYYFATLDHYLYEABE 540  
Db 502 NDLGCRPCDDCLGGALNNSCFASGQSCSRPHMIGRQCNVEPGYYFATLDHYLYEABE 561  
Qy 541 ANLGGVSIQVROYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 600  
Db 562 ANLGGVSIQVROYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQLP 621  
Qy 601 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSGSRVYVLPVPVCFEKGNTYVR 660  
Db 622 DHWEKAVITVQRPGRIPTRSSRCGNTIPDDNQVVSLSGSRVYVLPVPVCFEKGNTYVR 681  
Qy 661 LELPYTSSDSVESPYTLIDSLVMPYCKSLDFTVGGSGDGVWTSNASETFORYECLE 720  
Db 682 LELPYTSSDSVESPYTLIDSLVMPYCKSLDFTVGGSGDGVWTSNASETFORYECLE 741  
Qy 721 NSRSVVKTPMTDVCNRIIPFSALLHQTGLACEDDPQSLSSVCDPNNGGOCQCRPNVVGR 780  
Db 742 NSRSVVKTPMTDVCNRIIPFSALLHQTGLACEDDPQSLSSVCDPNNGGOCQCRPNVVGR 801  
Qy 781 TCNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 840  
Db 802 TCNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 861  
Qy 841 PSCQPCQNGHADDCCDPTVTECLNCDYTMGHNCERCLAGYGPPIIGSDHCHCEPCPD 900  
Db 862 PSCQPCQNGHADDCCDPTVTECLNCDYTMGHNCERCLAGYGPPIIGSDHCHCEPCPD 921  
Qy 901 GPDGQRFARSQYQDPVTLLQACVCDPGYIGSRDCCASGYFGNPSVGGSCQPCQCHNN 960  
Db 922 GPDGQRFARSQYQDPVTLLQACVCDPGYIGSRDCCASGYFGNPSVGGSCQPCQCHNN 981  
Qy 961 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYGGDALRQDCRCKVCNVLGTVQHCN 1020  
Db 982 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYGGDALRQDCRCKVCNVLGTVQHCN 1041  
Qy 1021 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNNAHSFGPSCNFTG 1080  
Db 1042 GSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNNAHSFGPSCNFTG 1101  
Qy 1081 QCCMPGFGGRTCSQBELFWGDDPVECRACDPRGIETPCQDOSTQCCVCVCEGVGPR 1140  
Db 1102 QCCMPGFGGRTCSQBELFWGDDPVECRACDPRGIETPCQDOSTQCCVCVCEGVGPR 1161  
Qy 1141 CDKCTRGVGVPCDTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIQYRETV 1200  
Db 1162 CDKCTRGVGVPCDTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIQYRETV 1221  
Qy 1201 SYERKVSEIKDIAQSPAAPLKNIGNLFEEAKLIDKVTENMAQVEVKLSDTTSQSNST 1260  
Db 1222 SYERKVSEIKDIAQSPAAPLKNIGNLFEEAKLIDKVTENMAQVEVKLSDTTSQSNST 1281  
Qy 1261 AKELDSLQTEASLQNTVKELAELEFIKNSDIRGALDSITKYFOMSELEAERVNASTTE 1320  
Db 1282 AKELDSLQTEASLQNTVKELAELEFIKNSDIRGALDSITKYFOMSELEAERVNASTTE 1341  
Qy 1321 PNSTVQSALMDRVEDVNMERESQFKQBQEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380

Db 1342 PNSTVQSALMDRVEDVNMERESQFKQBQEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401  
Qy 1381 PGASCSETCEGPGNCRCTDEGERKCGPGCGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1440  
Db 1402 PGASCSETCEGPGNCRCTDEGERKCGPGCGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1461  
Qy 1441 SKMWSEAKLRADAEAKQSAEDILLKTNAKEMKMDKNEELRNLIKQIRNFLTQDSADLDSI 1500  
Db 1462 SKMWSEAKLRADAEAKQSAEDILLKTNAKEMKMDKNEELRNLIKQIRNFLTQDSADLDSI 1521  
Qy 1501 EAVANEVLKXWMPSTPQOLNLTEDIRVERVESLSQVEVILQHSAAADIAAEMLLEAKRA 1560  
Db 1522 EAVANEVLKXWMPSTPQOLNLTEDIRVERVESLSQVEVILQHSAAADIAAEMLLEAKRA 1581  
Qy 1561 SKSATDVKTADMKVEALEEAKQAQVAEAKATQKQADEDIQGTQNLTTSESSTAASETL 1620  
Db 1582 SKSATDVKTADMKVEALEEAKQAQVAEAKATQKQADEDIQGTQNLTTSESSTAASETL 1641  
Qy 1621 FNASQRISELRNVEBELKFKAAQNSGEAEYIEKVYTVVKQSAEDVKKTLDGELDEKYYKV 1680  
Db 1642 FNASQRISELRNVEBELKFKAAQNSGEAEYIEKVYTVVKQSAEDVKKTLDGELDEKYYKV 1701  
Qy 1681 ENLIAKTTESADARAKAEMLQNEAKTLLAQAQSKLQLLKDLERKYEDNORVLEDKAQEL 1740  
Db 1702 ENLIAKTTESADARAKAEMLQNEAKTLLAQAQSKLQLLKDLERKYEDNORVLEDKAQEL 1761  
Qy 1741 ARLEGVRSLLKXDISQKAVYSTCL 1765  
Db 1762 ARLEGVRSLLKXDISQKAVYSTCL 1786

## RESULT 4

US-09-561-818A-14  
; Sequence 14, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortsemaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-14

Query Match 100.0%; Score 9654; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QEPERSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYVSHLQEDKKCFICNS 60  
Db 22 QEPERSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYVSHLQEDKKCFICNS 81  
Qy 61 QDPYHETLNPDSHLIENVVTTAPNRLKIWQSGENVNTIQLDLAEAFHFTHLIMTFK 120  
Db 82 QDPYHETLNPDSHLIENVVTTAPNRLKIWQSGENVNTIQLDLAEAFHFTHLIMTFK 141  
Qy 121 TFPAPAWLIERSDFGKTGWVRYPAYDCEAFPGIGSTGPMKKVDDIICDSRYSDIEPST 180  
Db 142 TFPAPAWLIERSDFGKTGWVRYPAYDCEAFPGIGSTGPMKKVDDIICDSRYSDIEPST 201  
Qy 181 EGEVIFRALDPAPKIEDPYSPIQNLLKITNRIKPVKLTGDNLLDSRMEIREKYYTA 240  
Db 202 EGEVIFRALDPAPKIEDPYSPIQNLLKITNRIKPVKLTGDNLLDSRMEIREKYYTA 261  
Qy 241 VYDMVVRGNCFCYGHASECAPVDGFEVGMVHGHCMCRHNTKGLNCELCDMPYHDLPW 300  
Db 262 VYDMVVRGNCFCYGHASECAPVDGFEVGMVHGHCMCRHNTKGLNCELCDMPYHDLPW 321

301 QY RAEGNSNACKKCNKCNHNSISCHFDMAVYLATGNVSGVCDCCOHTNMGRCNCEOCKP 360  
322 Db RAEGNSNACKKCNKCNHNSISCHFDMAVYLATGNVSGVCDCCOHTNMGRCNCEOCKP 381  
361 QY YQHPERDIRDPNFCERCTCDPAGSNEGICDSYTFSTGLIAGQCRCKLNVEGECDVCK 420  
382 Db YQHPERDIRDPNFCERCTCDPAGSNEGICDSYTFSTGLIAGQCRCKLNVEGECDVCK 441  
421 QY EGFYDLSSDDPFGCKSCACNPLGTTIPGNNPCDSETHGYCKKLVGQCHDQCLPHHWGLS 480  
442 Db EGFYDLSSDDPFGCKSCACNPLGTTIPGNNPCDSETHGYCKKLVGQCHDQCLPHHWGLS 501  
481 QY NLDGCRPCDCLGGALNNSCFAESQCSRCRPHMIGRQCNEVEPGVYFATLDHLYEABE 540  
502 Db NLDGCRPCDCLGGALNNSCFAESQCSRCRPHMIGRQCNEVEPGVYFATLDHLYEABE 561  
541 QY ANLPGVSIYERQYIQRIPSWTGAQVVRPGAVLEFFIDNIPYSMEYDILIRYEPOLP 600  
562 Db ANLPGVSIYERQYIQRIPSWTGAQVVRPGAVLEFFIDNIPYSMEYDILIRYEPOLP 621  
601 QY DHWEKAVITVQRPGRIPTSRRCNTIPDDNOVWSLSPGSRVVLPRPVCPKGNVTVR 660  
622 Db DHWEKAVITVQRPGRIPTSRRCNTIPDDNOVWSLSPGSRVVLPRPVCPKGNVTVR 681  
661 QY LELPQYTSDDSDVESPYTLLDLSVLMPCYKSLDIFTVGGSGDVVTNSAWETFORYRCL 720  
682 Db LELPQYTSDDSDVESPYTLLDLSVLMPCYKSLDIFTVGGSGDVVTNSAWETFORYRCL 741  
721 QY NRSVYKTPMTDVCNRIIFSIISALHOTGLACECPQGSLSVCDPBGQCCOCRNNVGR 780  
742 Db NRSVYKTPMTDVCNRIIFSIISALHOTGLACECPQGSLSVCDPBGQCCOCRNNVGR 801  
781 QY TNCRCAPGTFGPGSPCKCECHLQGSVNAFCNPNVTGQCHFCQGVYARQDCRLPGHWGF 840  
802 Db TNCRCAPGTFGPGSPCKCECHLQGSVNAFCNPNVTGQCHFCQGVYARQDCRLPGHWGF 861  
841 QY PSQPCQCNHADDPCDPTVTECLNCDYTMGNHCERCLAGYGDPIIGSGDHCRCPD 900  
862 Db PSQPCQCNHADDPCDPTVTECLNCDYTMGNHCERCLAGYGDPIIGSGDHCRCPD 921  
901 QY GPDGSRQFARSCYQDPVTLLQACVCPGVIYGRCDCCASGYFNGPSEVGGSCQPCQCHNN 960  
922 Db GPDGSRQFARSCYQDPVTLLQACVCPGVIYGRCDCCASGYFNGPSEVGGSCQPCQCHNN 981  
961 QY IDTTDEACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLGTVOEHCN 1020  
982 Db IDTTDEACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLGTVOEHCN 1041  
1021 QY GSDCCQDKATGQCLCLPNVIGQNCRCAPNTWOLASGTGCDPCNCAHSGFSPSCNEFTG 1080  
1042 Db GSDCCQDKATGQCLCLPNVIGQNCRCAPNTWOLASGTGCDPCNCAHSGFSPSCNEFTG 1101  
1081 QY QCQCMFPGGRTCSCEQELFWGDDPVECRACDPRGIETPQCDQSTGQCVGVEGPR 1140  
1102 Db QCQCMFPGGRTCSCEQELFWGDDPVECRACDPRGIETPQCDQSTGQCVGVEGPR 1161  
1141 QY CDKCTRGYSGVFPDCTPCHQCQFALWDVITAEITNRTHRELEKAKLKISGVIGPYRETVD 1200  
1162 Db CDKCTRGYSGVFPDCTPCHQCQFALWDVITAEITNRTHRELEKAKLKISGVIGPYRETVD 1221  
1201 QY SVERKVSIEKIDILAQSPAAEPLKNIENLFEAEKLIKQVTEMMAQVEVKLSDTTSQSNS 1260  
1222 Db SVERKVSIEKIDILAQSPAAEPLKNIENLFEAEKLIKQVTEMMAQVEVKLSDTTSQSNS 1281  
1261 QY AKELDSLQTEAESLDNTVLEABQLFEIKNSDIRGALDSITKYFQMSLEABERNVASTE 1320  
1282 Db AKELDSLQTEAESLDNTVLEABQLFEIKNSDIRGALDSITKYFQMSLEABERNVASTE 1341  
1321 QY PNSTVQSALMRDRVEDVMMERESQFKEQEQEARLLDELAKQLQSLDLSAAAEATCGTP 1380  
1342 Db PNSTVQSALMRDRVEDVMMERESQFKEQEQEARLLDELAKQLQSLDLSAAAEATCGTP 1401

1381 QY PGASCSETECGPNCRTEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLSALAEVEQL 1440  
1402 Db PGASCSETECGPNCRTEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLSALAEVEQL 1461  
1441 QY SKMWSEAKLRADBAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFJTQDSADLDSI 1500  
1462 Db SKMWSEAKLRADBAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFJTQDSADLDSI 1521  
1501 QY EAVANEVLKMEPSTPOOLQNLTERIRVESLSQVEVILQHSAAADIARAEMLLEAKRA 1560  
1522 Db EAVANEVLKMEPSTPOOLQNLTERIRVESLSQVEVILQHSAAADIARAEMLLEAKRA 1581  
1561 QY SKSATDVKVTADVMVKEALEEAEAKQAUAHKAIAQADEDIQGTQNLTSISETAAABETL 1620  
1582 Db SKSATDVKVTADVMVKEALEEAEAKQAUAHKAIAQADEDIQGTQNLTSISETAAABETL 1641  
1621 QY FNASQRISELERNVUELKRKAQNSGEAEVIEKVVTVKQSAEDVKTLDELDEKVKY 1680  
1642 Db FNASQRISELERNVUELKRKAQNSGEAEVIEKVVTVKQSAEDVKTLDELDEKVKY 1701  
1681 QY ENLIJAKTSEBSADARRKAEMLQNEAKTLLAQANSKQLQLKDLERKYEDNQRYLEDKAQEL 1740  
1702 Db ENLIJAKTSEBSADARRKAEMLQNEAKTLLAQANSKQLQLKDLERKYEDNQRYLEDKAQEL 1761  
1741 QY ARLEGEVRSLLKDISQKAVVYSTCL 1765  
1762 Db ARLEGEVRSLLKDISQKAVVYSTCL 1786

RESULT 5  
US-09-561-709B-9  
; Sequence 9, Application US/09561709B  
; Patent No. 682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champilaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-9

Query Match 100.0%; Score 9654; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QEPFSGCAEGSCYPATGDLITGRAQKLSVTSTCGLHKPEPYCIYSHLOEDKCKFCNS 60  
Db 22 QEPFSGCAEGSCYPATGDLITGRAQKLSVTSTCGLHKPEPYCIYSHLOEDKCKFCNS 81  
QY 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEAFHFTLIMTFK 120  
Db 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENVTIQLDLAEAFHFTLIMTFK 141  
QY 121 TFRPAAMLIERSDFGTGWYRYFAYDCASPGISTGPMKKVDDIICDSRYSDIEPST 180  
Db 142 TFRPAAMLIERSDFGTGWYRYFAYDCASPGISTGPMKKVDDIICDSRYSDIEPST 201  
QY 181 EGEVIFRALDPAPKIEDPYSPRIQNLKLTNRLIKFVKLHTLGDNLDSRMEIREKYYA 240

Db 202 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRIFVKLHTLGLDNLDSRMEIREKYYA 261  
QY 241 VYDMVVRGNCFCYGHASECAPVDFNEVEGVHGHCMCRHNTKGLNCELQWDFVHDLPW 300  
Db 262 VYDMVVRGNCFCYGHASECAPVDFNEVEGVHGHCMCRHNTKGLNCELQWDFVHDLPW 321  
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Db 322 RPAEGRNSACKKNCNEHSISCHFDMAVYLAGNVSGVCDCHQNTWGRNCCEQCKPFY 381  
QY 361 YQHPERDIRPNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGQCRCKLVNVEGHCDCVCK 420  
Db 382 YQHPERDIRPNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGQCRCKLVNVEGHCDCVCK 441  
QY 421 EGYDLSSEDPCKKSCACNPLGTPGGNPPCSETHCYCKRLVTHQCHDCQCLPEHWGLS 480  
Db 442 EGYDLSSEDPCKKSCACNPLGTPGGNPPCSETHCYCKRLVTHQCHDCQCLPEHWGLS 501  
QY 481 NDLGCRPCDCLDGGALNNSCFAESQCSQCRPHMIGRCQNEVEPGYFATLDHYLYEAE 540  
Db 502 NDLGCRPCDCLDGGALNNSCFAESQCSQCRPHMIGRCQNEVEPGYFATLDHYLYEAE 561  
QY 541 ANLPGVSVVEROYIQRIPSWTAGFVRVPGAYLEFPDINIPYSMEYDILIRYBOLP 600  
Db 562 ANLPGVSVVEROYIQRIPSWTAGFVRVPGAYLEFPDINIPYSMEYDILIRYBOLP 621  
QY 601 DHWEKAVITVORPGRIPTSRCNTIPDDDNQVSLSPGRVYVLPVPCPEKGTNTYR 660  
Db 622 DHWEKAVITVORPGRIPTSRCNTIPDDDNQVSLSPGRVYVLPVPCPEKGTNTYR 681  
QY 661 LELPQVTSDDSVESYTTILDSLVLMPYCKSLDITVGGSGDGVVWNSAWETPQRYCLE 720  
Db 682 LELPQVTSDDSVESYTTILDSLVLMPYCKSLDITVGGSGDGVVWNSAWETPQRYCLE 741  
QY 721 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACECPDQSSLSVCDPNQCGQCCQCPNVVGR 780  
Db 742 NSRSVVKTPMTDVCNRIIFSIALLHOTGLACECPDQSSLSVCDPNQCGQCCQCPNVVGR 801  
QY 781 TCRNCAPTGFGPSPCKCECHLOGSVNAFNPVVTGQCHCFQGVYARQCDRCPLGHWGF 840  
Db 802 TCRNCAPTGFGPSPCKCECHLOGSVNAFNPVVTGQCHCFQGVYARQCDRCPLGHWGF 861  
QY 841 PSQPCQCNHADDCTPVTGECNLCQDVTMGHNCERCLAGYVGPPIIGSGDHCRPCPCPD 900  
Db 862 PSQPCQCNHADDCTPVTGECNLCQDVTMGHNCERCLAGYVGPPIIGSGDHCRPCPCPD 921  
QY 901 GPDGSGQFARSCYQDPVTQLQACVCDPGVIGSRCDCCASGYFGNPSFVGGSCQPCQCHNN 960  
Db 922 GPDGSGQFARSCYQDPVTQLQACVCDPGVIGSRCDCCASGYFGNPSFVGGSCQPCQCHNN 981  
QY 961 IDTTDPEACDKETGRCLKCLYHTEGHEQCFRFGYVGDALQDQCRKVCNVLGTQVQHCN 1020  
Db 982 IDTTDPEACDKETGRCLKCLYHTEGHEQCFRFGYVGDALQDQCRKVCNVLGTQVQHCN 1041  
QY 1021 GSDQCCKATGQCLCLPNVIGONCDRCAPNTWOLASGTGCDPCNCAHSPGSCNFTG 1080  
Db 1042 GSDQCCKATGQCLCLPNVIGONCDRCAPNTWOLASGTGCDPCNCAHSPGSCNFTG 1101  
QY 1081 QOCQMGFGGRTCSCEQLFWGDQDVECRACDPCDPRGLETQCDQSTGQCVCVGVGEGPR 1140  
Db 1102 QOCQMGFGGRTCSCEQLFWGDQDVECRACDPCDPRGLETQCDQSTGQCVCVGVGEGPR 1161  
QY 1141 CDKCTRGYSVPDCTPCHQCFALNDVIAELTNTRHFLKAKALISGVIQYRRTVD 1200  
Db 1162 CDKCTRGYSVPDCTPCHQCFALNDVIAELTNTRHFLKAKALISGVIQYRRTVD 1221  
QY 1201 SVERKVSSEIKDILASPAEAPLKNIGLFEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1260  
Db 1222 SVERKVSSEIKDILASPAEAPLKNIGLFEAEKLIKDVTEMAQVEVKLSDDTTSQSNST 1281  
QY 1261 AKELDSLQTEARSLDNTVKELAEQLEFKNDSIRGALDSITKYQMSLEAEERVNASTTE 1320  
Db 1282 AKELDSLQTEARSLDNTVKELAEQLEFKNDSIRGALDSITKYQMSLEAEERVNASTTE 1341

QY 1321 PNSTVQSALMRDVEDVWMBRESQFKEQBEQARLIDELAGKLOSLDLSAAAEWTCGTP 1380  
Db 1342 PNSTVQSALMRDVEDVWMBRESQFKEQBEQARLIDELAGKLOSLDLSAAAEWTCGTP 1401  
QY 1381 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNANWQKAMDLDODVLSALAEVEQL 1440  
Db 1402 PGASCSETECGGPNCRCTDEGERKCGGPGCGGLVTVAHNANWQKAMDLDODVLSALAEVEQL 1461  
QY 1441 SKWVSEAKLRADAQKQSAEDILLKTNATKEKMDKSNBELNLIKQIRNFLTQDSADLDSI 1500  
Db 1462 SKWVSEAKLRADAQKQSAEDILLKTNATKEKMDKSNBELNLIKQIRNFLTQDSADLDSI 1521  
QY 1501 EAVANEVLKMEMSPPOQLQNLTEDIRREVESLSQVEVILQHSAAADTARAEMMLEEAKRA 1560  
Db 1522 EAVANEVLKMEMSPPOQLQNLTEDIRREVESLSQVEVILQHSAAADTARAEMMLEEAKRA 1581  
QY 1561 SKSATDVKTADWKEALEEAEKQAAEKAKIQAEDDIQGTQNLNLTISSEETAASSETL 1620  
Db 1582 SKSATDVKTADWKEALEEAEKQAAEKAKIQAEDDIQGTQNLNLTISSEETAASSETL 1641  
QY 1621 FNASQRISELEARNVELKRAKAAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1680  
Db 1642 FNASQRISELEARNVELKRAKAAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYYKV 1701  
QY 1681 ENLIAKTTESADARKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLSDKAQEL 1740  
Db 1702 ENLIAKTTESADARKAEMLQNEAKTLLAQANSKLOLLKDLERKYEDNORYLSDKAQEL 1761  
QY 1741 ARLEGEVRSLLKDISQKAVVYSTCL 1765  
Db 1762 ARLEGEVRSLLKDISQKAVVYSTCL 1786

## RESULT 6

US-09-562-702A-18  
; Sequence 18 Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-18

Query Match 94.2%; Score 9092; DB 4; Length 1786;  
Best Local Similarity 93.0%; Pred. No. 0;  
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYVSHLOEDKKCFICNS 60  
Db 22 QEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYCIYVSHLOEDKKCFICNS 81  
QY 61 QDPVHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLEAEFPHFLHMTFK 120  
Db 82 RDPVHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDLEAEFPHFLHMTFK 141  
QY 121 TFRPAAMLIERSDFGKTGWGYRYFAYDCEASFGISGPMKKVDDIICDSRYSDIEPST 180

1222 SVEKKVNEIKDILLAQSPAAEPKNIIGILFEEAEKLTQDVTEKMAQVEVKLTDTASQSNST 1281  
1261 AKELDSLOTAEISDINTVKELEAOLFIKNSDIRGALDSITKYFQMSLEAEERVNASTTIE 1320  
1282 AGELGALOAAEASLUKTVKELAEOLFIKNSDIRGALDSITKYFQMSLEAEERVNASTTIE 1341  
1321 PNSTVEQSALMRVEDVMMERESQFKEQOEQARLLDELAKLQSLDLSALAEVEQL 1380  
1342 PNSTVEQSALMRVEDVMMERESQFKEQOEQARLLDELAKLQSLDLSALAEVEQL 1401  
1381 PGASCSSECGGPNCRTRDEGERKCGGPGCGGLVTVAHNAKQMDLDDQDVLALAEVEQL 1440  
1402 PGASCSSECGGPNCRTRDEGERKCGGPGCGGLVTVAHNAKQMDLDDQDVLALAEVEQL 1461  
1441 SKMVSSEAKLRADEAKQSAEDILLKTNATKEMKDSNBEELANLIKQIRNFUTQDSADLDSI 1500  
1462 SKMVSSEAKLRADEAKQSAEDILLKTNATKEMKDSNBEELANLIKQIRNFUTQDSADLDSI 1521  
1501 BAVANEVLKXEMPTPOOLNLTEDIRERVESISOVEVILQHSAADTARAEMLLEAKRA 1560  
1522 BAVANEVLKXEMPTPOOLNLTEDIRERVESISOVEVILQHSAADTARAEMLLEAKRA 1581  
1561 SKSATDVKTADMYKEALEAEAKQAAKQADEDIQGTQNLTSISEETAASBETL 1620  
1582 SKSATDVKTADMYKEALEAEAKQAAKQADEDIQGTQNLTSISEETAASBETL 1641  
1621 FNASORISELERNVEELKRAAQSNGEAEYIEKVVTVKQSAEDVKKTLDELDEKYYKV 1680  
1642 TNASORISELERNVEELKRAAQSNGEAEYIEKVVTVKQSAEDVKKTLDELDEKYYKV 1701  
1681 ENLAKTTEESADARRKAEMLONEAKTLLAQANSKLQLLKDLERKEDNORYLEDKQAE 1740  
1702 ENLAKTTEESADARRKAEMLONEAKTLLAQANSKLQLLKDLERKEDNORYLEDKQAE 1761  
1741 ARLEGEVRSLLKDISQKVVAVYSTCL 1765  
1762 VALLEGEVRSLLKDISQKVVAVYSTCL 1786

RESULT 7  
US-09-561-818A-18  
; Sequence 18, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561.818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-18

Query Match 94.2%; Score 9092; DB 4; Length 1786;  
Best Local Similarity 93.0%; Pred No. 0;  
Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QPEFESYGCABGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQDKKCFICNS 60  
DB 22 QPEFESYGCABGSCYPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLQDKKCFICNS 81  
QY 61 QDPYHETLNPDHSLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFHTLIMTFK 120  
DB 82 RDPYHETLNPDHSLIENVTTFAPNRLKIWQSENGVENVTIQLDLAEFHTLIMTFK 141  
QY 121 TPRPAMLIERSSDPGKWTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180  
DB 142 TPRPAMLIERSSDPGKWTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201

142 TPRPAMLIERSSDPGKWTGWYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201  
181 EGEVIFRALDPAPKIEDPSPRIQNLKITNRIKFIKVLITGLDNLDSRMEIREKYIYA 240  
202 EGEVIFRALDPAPKIEDPSPRIQNLKITNRIKFIKVLITGLDNLDSRMEIREKYIYA 261  
241 VYDMVVRGNCFCYGHASECAPVDGFEYVGHGCMCRHNTKGLNCELMDFFVHDLPW 300  
262 VYDMVVRGNCFCYGHASECAPVDGFEYVGHGCMCRHNTKGLNCELMDFFVHDLPW 321  
301 RPAEGNSNACKKNCNEHSISCHPDMVFLATGNVSGVCDCCQHTNMGRCCEQKPPY 360  
322 RPAEGNSNACKKNCNEHSISCHPDMVFLATGNVSGVCDCCQHTNMGRCCEQKPPY 381  
361 YQHPERDIRPNCERCTCDPAGSNEGICDSYTFSTGLIAGOCCKLNVGEHCDVCK 420  
382 YQHPERDIRPNCERCTCDPAGSNEGICDSYTFSTGLIAGOCCKLNVGEHCDVCK 441  
421 EGYDLSSEDPFCKSCACNPLGTIPGGNCPDSETHCYCKRLVTQHCDCQCLPQHGLS 480  
442 EGYDLSSEDPFCKSCACNPLGTIPGGNCPDSETHCYCKRLVTQHCDCQCLPQHGLS 501  
481 NDLGCRPCDCLGGALNNSCFABSGOCSPHMIQRCNEVEPGYVYFATLHLYEABE 540  
502 NDLGCRPCDCLGGALNNSCFABSGOCSPHMIQRCNEVEPGYVYFATLHLYEABE 561  
541 ANLPGVSVVEROYIQRIPSWTGAQVRVPEGAYLEEFTDIPYSMEYDILIRYEPQLP 600  
562 ANLPGVSVVEROYIQRIPSWTGAQVRVPEGAYLEEFTDIPYSMEYDILIRYEPQLP 621  
601 DHWEKAVITVQRPERIPTSRGCTIPDDNQVSVLSPGSRVYVLPVPCFKGTNYTVR 660  
622 DHWEKAVITVQRPERIPTSRGCTIPDDNQVSVLSPGSRVYVLPVPCFKGTNYTVR 681  
661 LELPQYTSAGSDVESPTLIDSLVMPYCKSLDFTVGGSGDGVNTSNWETFORVCL 720  
682 LELPQYTSAGSDVESPTLIDSLVMPYCKSLDFTVGGSGDGVNTSNWETFORVCL 741  
721 NSRSVVKPTMTDVCNRIIFISALHQTGLACEDCPQGSLSVCDPNQGCQCPNPNVGR 780  
742 NSRSVVKPTMTDVCNRIIFISALHQTGLACEDCPQGSLSVCDPNQGCQCPNPNVGR 801  
781 TCRNCAPEGTGFGSGCKPECHLQSVNACFNPVTQCHCFQGVVARQCDRLCPHWF 840  
802 TCRNCAPEGTGFGSGCKPECHLQSVNACFNPVTQCHCFQGVVARQCDRLCPHWF 861  
841 PSCQPCOCHGALDCTVTGECISCDYTTGHCNCRCLAGYVGPDIIGSDHCRPCPCPD 900  
862 PSCQPCOCHGALDCTVTGECISCDYTTGHCNCRCLAGYVGPDIIGSDHCRPCPCPD 921  
901 GPDGSRGFARSCYQDPVTLQACVDPGYIGSRCDCCASGYFGNPSVGVSCPCOCHN 960  
922 GPDGSRGFARSCYQDPVTLQACVDPGYIGSRCDCCASGYFGNPSVGVSCPCOCHN 981  
961 IDTTDPACXKETGRCLKLYHTEGECQCFYGYGDLRQCRKVCNLYGTQVHECN 1020  
982 IDTTDPACXKETGRCLKLYHTEGECQCFYGYGDLRQCRKVCNLYGTQVHECN 1041  
1021 GSDCCDKATQCCCLPNVIGQNCDCRCAPTNWLASGTCDPCNCAHSGFSGSNEFTG 1080  
1042 GSDCCDKATQCCCLPNVIGQNCDCRCAPTNWLASGTCDPCNCAHSGFSGSNEFTG 1101  
1081 QCQMPFGGRTCSCEQELFWGDDPVECRACDCCDPRGIEPQDQSTGQCVGVGEGPR 1140  
1102 QCQMPFGGRTCSCEQELFWGDDPVECRACDCCDPRGIEPQDQSTGQCVGVGEGPR 1161  
1141 CDKCTRGSYGVFPDCTPCHQCFALWDVIAELNTRHFRLEKAKALISGVIQYRETVD 1200  
1162 CDKCTRGSYGVFPDCTPCHQCFALWDVIAELNTRHFRLEKAKALISGVIQYRETVD 1221  
1201 SVEKKVNEIKDILLAQSPAAEPKNIIGILFEEAEKLTQDVTEKMAQVEVKLTDTASQSNST 1260



Qy	181	EGEVITRALDPARKIEDPYSRIQNLKJITNLRIRKFKVCLHTLGDNLDSRMIRKYYIA	240
Db	202	EGEVITRALDPARKIEDPYSRIQNLKJITNLRIRKFKVCLHTLGDNLDSRMIRKYYIA	261
Qy	241	YVDMVVRGNCFCYGHASECAPVDGFNEBEGMVHGHCMCRHNTKGLNCLZCMTDFVHDLPW	300
Db	262	YVDMVVRGNCFCYGHASECAPVDGFNEBEGMVHGHCMCRHNTKGLNCLZCMTDFVHDLPW	321
Qy	301	RAEAGNSNACKKCNKCNHSISCHFDMAVLATGNTVSGVCGDDCOHNTMGRNCEOCKEFPY	360
Db	322	RAEAGNSNACKKCNKCNHSISCHFDMAVLATGNTVSGVCGDDCOHNTMGRNCEOCKEFPY	381
Qy	361	YQHPERDIRDPNFCBRCTCDPAGSONEGICDSYDTFSTGLIAQCRCKLVNVEGEHCYCK	420
Db	382	FQHPERDIRDPNLCEPCTCDPAGSENGGICDGYTFDSVGLIAQCRCKLVNVEGEHCYCK	441
Qy	421	EGFYDLSBDDPGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTOGHQDCQCLPHEWGLS	480
Db	442	EGFYDLSAEDPYGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTOGHQDCQCLPHEWGLS	501
Qy	481	NLDLDCRCPCCDLGGALNNSCFASGQSCRPHMIGRQCNVEBPGYYPATLDHYLYEABE	540
Db	502	NLDLDCRCPCCDLGGALNNSCERSGQSCLPHMIGRQCNVEBPGYYPATLDHYLYEABE	561
Qy	541	ANLPGCVSIVERQYIQDRIPSWTGAGFVRVPBGAYLEFFIDNIPKSMYEDILIRYEPOLP	600
Db	562	ANLPGCVVVERQYIQDRIPSWTGPGFVRVPBGAYLEFFIDNIPKSMYEDILIRYEPOLP	621
Qy	601	DHWEKAVITVQBPGRIPTSRSCGNITIPDDNQVUSLSPGSRVYVLPVRPVCBEKGNITVVR	660
Db	622	DHWEKAVITVQBPGRIPASSRCGNITVDDNQVUSLSPGSRVYVLPVRPVCBEKGNITVVR	681
Qy	661	LLEPQYTSDSDESFPYLIQSLVLMFYCKSLDIFTVGGSGDGVNTSAMETFORYRCLE	720
Db	682	LLEPQYTAGSDSVESPYTFIDSLVLMFYCKSLDIFTVGGSGDGVNTSAMETFORYRCLE	741
Qy	721	NSRSVVVKTPTMTDVCENITIFSALIHOTGLACSDPQGLSSVCDPBGQCCOCHRNVTGR	780
Db	742	NSRSVVVKTPTMTDVCENITIFSALIHOTGLACSDPQGLSSVCDPBGQCCOCHRNVTGR	801
Qy	781	TNCRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLCPGHMGF	840
Db	802	TNCRCAPGTGFGPSGCKPCBCHLQGSASAFCDAITGQCHCFQGIYARQCDRLCPGYMGF	861
Qy	841	PSCQPCQCNHADDPCDPTVTECLNCDQYTWGHCNCRCLAGYGDPIITGSGDHCRPCPCPD	900
Db	862	PSCQPCQCNHADDPCDPTVTECLNCDQYTWGHCNCRCLAGYGDPIITGSGDHCRPCPCPD	921
Qy	901	GPDSGRQFARSCYQDPVTTLQACVCDPGYITGSRCDPCASGYFNTSEVGGSCQPCQCHNN	960
Db	922	GPDSGRQFARSCYQDPVTTLQACVCDPGYITGSRCDPCASGYFNTSEVGGSCQPCQCHNN	981
Qy	961	IDTTDPEACDKETGRCLKCLVHTBEGHCQPCRGYGYGDALRODCRCKCVNYLGTVOEHON	1020
Db	982	IDTTDPEACDKXTGRCLKCLVHTBEGHQCQLCOYGYGYGDALRODCRCKCVNYLGTVEHON	1041
Qy	1021	GSDDCQDKATGGCLCPNVITQONCDRCAPNTWOLASGTGDCPCNCAHSPGSCNBEFTG	1080
Db	1042	GSDDCQDKATGGCLCPNVITQONCDRCAPNTWOLASGTGDCPCNCAHSPGSCNBEFTG	1101
Qy	1081	QCCCMFPGFGRATCSECQBLFWGDPDVECRACDCCDPRGIETPCQDQSTQCQCVGVEGQPR	1140
Db	1102	QCCCMFPGFGRATCSECQBLFWGDPDVECRACDCCDPRGIETPCQDQSTQCQCVGVEGQPR	1161
Qy	1141	CDKCTRGYSGVFPDCTCHOCFALWDVITIAELNTRHFRLEKAKAKITSGVIGYBRETVD	1200
Db	1162	CDKCTRGYSGVFPDCTCHOCFALWDVITIAELNTRHFRLEKAKAKITSGVIGYBRETVD	1221
Qy	1201	SYERKVSIEKQILAQSPAABEPLKNIQNLFFEAELKIKOVTEMAQVEVKLSDTTSQSNST	1260
Db	1222	SYEKVNIQILAQSPAABEPLKNIQNLFFEAELKIKOVTEMAQVEVKLSDTTSQSNST	1281

Qy	1261	AKELDSLOTEAESLDNVTYKELAEQLEBFINKSDIRGALDSITIKYFQMSLEABERVNASTTE	1320
Db	1282	AGELGALQAEBSLDXTYKELAEQLEFINKSDIQGALDSITIKYFQMSLEAEKVNASTTD	1341
Qy	1321	PNSTVEOSALMRORVEDVMNERESQPKQEBOEARLLDELAKLQSLDLSAAAEMTCGTP	1380
Db	1342	PNSTVQSGALTRDRVEDLMLERESPFKEQOEBOARLLDELAKLQSLDLSAAQMTCTGP	1401
Qy	1381	PGASCSBTECGGPNCRDTDBGERKCGPGCGGLVTVAHNAWQKAMDLDQDVL SALAEVQL	1440
Db	1402	PGADCSEBCEGPNCRDTDBGERKCGPGCGGLVTVAHSAWQKAMDPRDVL SALAEVQL	1461
Qy	1441	SKWVSSAKLRADAEKQSAEDILLKTNAWKMDKSNEELRNLIKQIRNFLTODSADLDSI	1500
Db	1462	SKWVSEAKVRADAEKQNAQDVLKTNATEKVKDSNEDJRNLIKQIRNFLTEDSADLDSI	1521
Qy	1501	EAVANEVILKWEPMSTPQQQLONTEDIRREVSLQSQVEVILQHSADIAEAEMLEEKAKA	1560
Db	1522	EAVANEYLKSGNASTPQQQLONTEDIRREVLTLSQVEVILQOOSADIAEAELLEEAKKA	1581
Qy	1561	SKSATDVKTADVMVKALAEAEKAAQVAABKAIKQADEDIQGTQNLTLTSESETAAEETL	1620
Db	1582	SKSATDVKTADVMVKALAEAEKAAQVAABKAIKQADEDIQGTQNLTLTSESETAAEETL	1641
Qy	1621	FNASQRISELERNVZELKRAAONGSEABYIEKVVYTVKQSAEDVVKTL DGBLDEKVKV	1680
Db	1642	TNASQRIKSLERNVZELKRAAONGSEABYIEKVVYSVKQNAADVVKTL DGBLDEKVKV	1701
Qy	1681	ENLIAKTTESADARKEMLQNEAKTLQAQNSKLOLLKDLKERYEDNORYLEDKQAEQ	1740
Db	1702	ESLIAKTTESADARKEMLQNEAKTLQAQNSKLOLLEDLERYEDNQKLYEDKQAEQ	1761
Qy	1741	ARLEGEVRSLKDIOSKVAVYSTCL	1765
Db	1762	VRLEGEVRSLKDIOSKVAVYSTCL	1786

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RESULT 8
US-09-562-702A-20
; Sequence 20, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-562-702A-20

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Query Match      91.9%; Score 8873; DB 4; Length 1725;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY      41 EPYCIVSHLQDKKCFICNSQDPHYETLPDPSHLIENVVTFAPNRLKIWQSENGYEV 100
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Db       1 EPYCIVSHLQDKKCFICDSRDPHYETLPDPSHLIENVVTFAPNRLKIWQSENGYEV 60

QY     101 TQLDLAEFFHTHLINFTFKTPAAMLIERSDDSGKTGWVRYRAYDCASFPGISGTP 160
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Db 61 TIQLDLAEAFHFTLHIMTFKTRPAAMLIERSDFGKTGWYRYFAYDCESFPFGISTGP 120  
QY 161 MKKYDDIICDSRYSDIEPTEGEVIFRALDPARKIEDPYSRIQNLKITNLRIKFKVLH 220  
Db 121 MKKYDDIICDSRYSDIEPTEGEVIFRALDPARKIEDPYSRIQNLKITNLRIKFKVLH 180  
QY 221 TLGDNLLDSRMREIREKYYIYAVDMVVRGNCFCYGHASECAPDVGNEVEGMVGHCMCR 280  
Db 181 TLGDNLLDSRMREIREKYYIYAVDMVVRGNCFCYGHASECAPDVGNEVEGMVGHCMCR 240  
QY 281 HNTKGLNCEL CMDFYHDLRWRPABGNSNACKKNCNEHSISCHPDMAYLATGNVSGV 340  
Db 241 HNTKGLNCEL CMDFYHDLRWRPABGNSNACKKNCNEHSISCHPDMAYLATGNVSGV 300  
QY 341 CDDCQNTWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 400  
Db 301 CDDCQNTWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGL 360  
QY 401 IAGQCRKLVNVEGHECHDVCKEGYDLSDBDPGCKSCACNPLGTIPGPNCPDSETHCYC 460  
Db 361 IAGQCRKLVNVEGHECHDVCKEGYDLSDBDPGCKSCACNPLGTIPGPNCPDSETHCYC 420  
QY 461 KRLVTCQHCDCQCLPEHWSLNDLDGCRPCDCDLGGALNNSCFABESQCCSCRPHMIGRCN 520  
Db 421 KRLVTCQHCDCQCLPEHWSLNDLDGCRPCDCDLGGALNNSCFABESQCCSCRPHMIGRCN 480  
QY 521 EVBPGYFATLDHYLYEABEANLPGVSVIVEROYIQDRIPSWTGAQFVRVPEGAYLEPFI 580  
Db 481 EVBPGYFATLDHYLYEABEANLPGVSVIVEROYIQDRIPSWTGAQFVRVPEGAYLEPFI 540  
QY 581 DNTPYSMEXDILRYEPQLPDHWEKAVITVQRGRIPTSRGNTTIPDDDNQVVSLSGCS 640  
Db 541 DNTPYSMEXDILRYEPQLPDHWEKAVITVQRGRIPTSRGNTTIPDDDNQVVSLSGCS 600  
QY 641 RYVVLPRPVCFEKGTNYTVLELIPQYTSDSVSVESPYTLDLSLVLMYCKSLDIFTVGS 700  
Db 601 RYVVLPRPVCFEKGTNYTVLELIPQYTSDSVSVESPYTLDLSLVLMYCKSLDIFTVGS 660  
QY 701 GDGVNTNSAETQRYKCLNSVSVKMTMTDVCNIIIPSIALLHOTGLACECPQGS 760  
Db 661 GDGVNTNSAETQRYKCLNSVSVKMTMTDVCNIIIPSIALLHOTGLACECPQGS 720  
QY 761 SSVCDPNGGQCCRPNVVGRNCRAPGTGFGPSPGCKPCCECHQSGVNAFCNVPVGGCH 820  
Db 721 SSVCDPNGGQCCRPNVVGRNCRAPGTGFGPSPGCKPCCECHQSGVNAFCNVPVGGCH 780  
QY 821 CFQGYARQCDRLPHWGPSPQPCQCNHADDPTVTECLNCDYTWGHCERCLAG 880  
Db 781 CFQGYARQCDRLPHWGPSPQPCQCNHADDPTVTECLNCDYTWGHCERCLAG 840  
QY 881 YGDPITIGSDHCRPCPCPDGSPGSRQFARSCYQDPVTQLACVCDPFGYIGSRCDPCASG 940  
Db 841 YGDPITIGSDHCRPCPCPDGSPGSRQFARSCYQDPVTQLACVCDPFGYIGSRCDPCASG 900  
QY 941 YFGNPSVGGSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGHCQFCRPGYGDAL 1000  
Db 901 YFGNPSVGGSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGHCQFCRPGYGDAL 960  
QY 1001 RQDRCKVCNVLGTQVQHCNMGSDCCDKATGQCLCLPNVIGQNCDCRPAWTWOLASGTGC 1060  
Db 961 RQDRCKVCNVLGTQVQHCNMGSDCCDKATGQCLCLPNVIGQNCDCRPAWTWOLASGTGC 1020  
QY 1061 DPCNCAAHFGSPSCNFTGQCCMPFGGRTCSBCEQLFWGDPDVECRACDCDPRGIET 1120  
Db 1021 DPCNCAAHFGSPSCNFTGQCCMPFGGRTCSBCEQLFWGDPDVECRACDCDPRGIET 1080  
QY 1121 PQCDQSTGQCVGVGVRGPRCDKTRGYSVFPDCTPCHOCFALWVIAELNTRHREL 1180  
Db 1081 PQCDQSTGQCVGVGVRGPRCDKTRGYSVFPDCTPCHOCFALWVIAELNTRHREL 1140  
QY 1181 EKAKALISGIVGYPRETVDSEKVESEIKDIIAQSPAABPLXVIGNLFEAEKLIKDV 1240  
Db 1141 EKAKALISGIVGYPRETVDSEKVESEIKDIIAQSPAABPLXVIGNLFEAEKLIKDV 1200

QY 1241 EMMAQVVKLSDDTTSQSNSTAKELDSLOTEABESLDNVTVKELAEQLBFIKNSDIRGALDSI 1300  
Db 1201 EMMAQVVKLSDDTTSQSNSTAKELDSLOTEABESLDNVTVKELAEQLBFIKNSDIRGALDSI 1260  
QY 1301 TKYFQMSLEAEERVNASTTTPNSPNSVQESALMRDRVEDVMMERESQPKKEQEOQARLDEL 1360  
Db 1261 TKYFQMSLEAEERVNASTTTPNSPNSVQESALMRDRVEDVMMERESQPKKEQEOQARLDEL 1320  
QY 1361 AGKLSQSLDLGAAAEAMTCGTPPGASCSETECGGPNCRDEGERKGGPGCGGLVTVANAW 1420  
Db 1321 AGKLSQSLDLGAAAEAMTCGTPPGASCSETECGGPNCRDEGERKGGPGCGGLVTVANAW 1380  
QY 1421 QKAMLDQDVLSALAEVQOLSKMVSEAKLRADAKQSAEDILLKTNATKEKMDKSNEELR 1480  
Db 1381 QKAMLDQDVLSALAEVQOLSKMVSEAKLRADAKQSAEDILLKTNATKEKMDKSNEELR 1440  
QY 1481 NLIKOIRNFITQDSADLDSIEAVANEVLKMEMPESTPOQLQNLTEIDIRERVESLSQVEVIL 1540  
Db 1441 NLIKOIRNFITQDSADLDSIEAVANEVLKMEMPESTPOQLQNLTEIDIRERVESLSQVEVIL 1500  
QY 1541 QHSAADTARAEMLLEAEAKRASKSATDVKTADVMYKEALEBAEKAQVAEKAIKOADEDIQ 1600  
Db 1501 QHSAADTARAEMLLEAEAKRASKSATDVKTADVMYKEALEBAEKAQVAEKAIKOADEDIQ 1560  
QY 1601 GTONLLTSIESETAASEBETLNFNASORISELERNVVEELKRAAQAQNSGEAEYIEKVYTVKQ 1660  
Db 1561 GTONLLTSIESETAASEBETLNFNASORISELERNVVEELKRAAQAQNSGEAEYIEKVYTVKQ 1620  
QY 1661 SAEDVKTLDGELDEKVKVKNENLAKITTESADARRKAEMLONEAKTLLAQANSKLOLLK 1720  
Db 1621 NADDVKTLDGELDEKVKVKNENLAKITTESADARRKAEMLONEAKTLLAQANSKLOLLK 1680  
QY 1721 DLERYEDNQRYLDEKAEQELARLEGEVRSLLKDI:SQKAVVYSTCL 1765  
Db 1681 DLERYEDNQRYLDEKAEQELARLEGEVRSLLKDI:SEKAVVYSTCL 1725

## RESULT 9

US-09-561-818A-20  
; Sequence 20, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-20

Query Match 91.9%; Score 9873; DB 4; Length 1725;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 41 EPCYIVSHLQDKKCFICNSQDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 100  
Db 1 EPCYIVSHLQDKKCFICNSQDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGVENV 60  
QY 101 TIQLDLAEAFHFTLHIMTFKTRPAAMLIERSDFGKTGWYRYFAYDCESFPFGISTGP 160  
Db 61 TIQLDLAEAFHFTLHIMTFKTRPAAMLIERSDFGKTGWYRYFAYDCESFPFGISTGP 120  
QY 161 MKKYDDIICDSRYSDIEPTEGEVIFRALDPARKIEDPYSRIQNLKITNLRIKFKVLH 220  
Db 121 MKKYDDIICDSRYSDIEPTEGEVIFRALDPARKIEDPYSRIQNLKITNLRIKFKVLH 180

QY 221 TLGDNLLSRMBIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHQWCR 280  
DB 181 TLGDNLLSRMBIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHQWCR 240  
QY 281 HNTKGLNCLCMLDFHDLFWRPABGRNSNACKKNCNNEHSISCHFDMAVYLATGNVSGV 340  
DB 241 HNTKGLNCLCMLDFHDLFWRPABGRNSNACKKNCNNEHSISCHFDMAVYLATGNVSGV 300  
QY 341 CDDCHNTMGRNCECKPYYQHPERD.RDPNFCBCTCDPAGSONEGICDSYDFSTGL 400  
DB 301 CDDCHNTMGRNCECKPYYQHPERD.RDPNFCBCTCDPAGSONEGICDSYDFSTGL 360  
QY 401 IAGQCRKLNVEGHCDCVCKEYFDLSAEDPYGCKSCACNPLGTTIPGNGPCDSETGYCYC 460  
DB 361 IAGQCRKLNVEGHCDCVCKEYFDLSAEDPYGCKSCACNPLGTTIPGNGPCDSETGYCYC 420  
QY 461 KRLVTGQRCDQCLPWHGLSNDLDCRCDLGLALNNSCFABSGQCSCLPHMIGROCN 520  
DB 421 KRLVTGQRCDQCLPWHGLSNDLDCRCDLGLALNNSCFABSGQCSCLPHMIGROCN 480  
QY 521 EYEGPYFATLHYLYEABEANLPGVSIYERQYIOTDRIPSWTGAQFVRVPEGAYLEFFI 580  
DB 481 EYEGPYFATLHYLYEABEANLPGVSIYERQYIOTDRIPSWTGAQFVRVPEGAYLEFFI 540  
QY 581 DNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRGNTIPDDNQVLSLSPGS 640  
DB 541 DNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRGNTIPDDNQVLSLSPGS 600  
QY 641 RYVVLPRPVCFEKGMNVTYRLLEPQYTSDSVSPYTLIDSLVMPYCKSLDIFTVGG 700  
DB 601 RYVVLPRPVCFEKGMNVTYRLLEPQYTSDSVSPYTLIDSLVMPYCKSLDIFTVGG 660  
QY 701 GOGVNTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALHQTGLACECDPQSL 760  
DB 661 GOGVNTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALHQTGLACECDPQSL 720  
QY 761 SSVCDPNGCQCRPNVVRGRTNRCAPGTFGFGSPGCKPCBCHLQGSVNAFCNPVTGQCH 820  
DB 721 SSVCDPNGCQCRPNVVRGRTNRCAPGTFGFGSPGCKPCBCHLQGSVNAFCNPVTGQCH 780  
QY 821 CFQGVVARQCDRLPHWGFPGSQPCQNGHADDCTPVTGECINCDYTMGHNCERCLAG 880  
DB 781 CFQGVVARQCDRLPHWGFPGSQPCQNGHADDCTPVTGECINCDYTMGHNCERCLAG 840  
QY 881 YGDPPIIGSDHCRPCPCPDGSPGROPARSYQBPVTLQACVCDPGVIGSRCDDCASG 940  
DB 841 YGDPPIIGSDHCRPCPCPDGSPGROPARSYQBPVTLQACVCDPGVIGSRCDDCASG 900  
QY 941 YFNPSEVGSGCQPCQCHNNDITDPEACDKEGTGRLKCLYHTEGHCQFCRFGYGDAL 1000  
DB 901 YFNPSEVGSGCQPCQCHNNDITDPEACDKEGTGRLKCLYHTEGHCQFCRFGYGDAL 960  
QY 1001 RQDRCVCNLYGTQVCEHNGSDCCDKATGQCLCPNVIGQNCRCAPNTWQLASGTGC 1060  
DB 961 RQDRCVCNLYGTQVCEHNGSDCCDKATGQCLCPNVIGQNCRCAPNTWQLASGTGC 1020  
QY 1061 DPCNNAHSGFSGCNEFTGQCCMPFGGRTCSCEQLFWGDPDVECRACDPRGIET 1120  
DB 1021 DPCNNAHSGFSGCNEFTGQCCMPFGGRTCSCEQLFWGDPDVECRACDPRGIET 1080  
QY 1121 PQCDQSTGQCVCEGVEGPRCDKCTGYSGVPPDCTPCHQCFALMDVIIAELTNRHFL 1180  
DB 1081 PQCDQSTGQCVCEGVEGPRCDKCTGYSGVPPDCTPCHQCFALMDVIIAELTNRHFL 1140  
QY 1181 EKAKALKISGIVGYRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNLFFEEAEKLIKQVT 1240  
DB 1141 EKAKALKISGIVGYRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNLFFEEAEKLIKQVT 1200  
QY 1241 EMMAQVEVKLSDTTSOSNSTAKELDSLOTEAESLNTVKELABOLEFFIKNSIRGALDSI 1300  
DB 1201 EMMAQVEVKLSDTTSOSNSTAKELDSLOTEAESLNTVKELABOLEFFIKNSIRGALDSI 1260  
QY 1301 TKYFQMSLEAEKRVNASTTDPNSTVQESALTRDRVEDLMLERESPFFKEQOEQARLLDEL 1360

DB 1261 TKYFQMSLEAEKRVNASTTDPNSTVQESALTRDRVEDLMLERESPFFKEQOEQARLLDEL 1320  
QY 1361 AGKQLSLDLISAAAEVMTGTPPGASCSETCCGPGNCRKTDEGKRCGCGGGLVTVAHNAW 1420  
DB 1321 AGKQLSLDLISAAAEVMTGTPPGASCSETCCGPGNCRKTDEGKRCGCGGGLVTVAHNAW 1380  
QY 1421 QKAMDLDQDVLGALAEVQLSKMWSEAKRABEAKQSAEDILLKTNATKEKMDKNEELR 1480  
DB 1381 QKAMDLDQDVLGALAEVQLSKMWSEAKRABEAKQSAEDILLKTNATKEKMDKNEELR 1440  
QY 1481 NLKIQJRNFTLTDSDADLSIEAVANVLKWMPESTPQQLNLTEDIRERVESLSQVEVIL 1540  
DB 1441 NLKIQJRNFTLTDSDADLSIEAVANVLKWMPESTPQQLNLTEDIRERVESLSQVEVIL 1500  
QY 1541 QHSAADIAEAEMLLEAKSASKSATDVKTADVMVKEALBEAKQAQVAEAKIKQADEDIQ 1600  
DB 1501 QHSAADIAEAEMLLEAKSASKSATDVKTADVMVKEALBEAKQAQVAEAKIKQADEDIQ 1560  
QY 1601 GTQNLTSISETAASEETLFPASORISELERNVEELKEKAAQNSGEAEVIEKVVTVKQ 1660  
DB 1561 GTQNLTSISETAASEETLFPASORISELERNVEELKEKAAQNSGEAEVIEKVVTVKQ 1620  
QY 1661 SAEVDKTKLDGELDEKXKVENLIAKTTESADARRKAEMLQNEAKTLAQAQNSKLOLLK 1720  
DB 1621 SAEVDKTKLDGELDEKXKVENLIAKTTESADARRKAEMLQNEAKTLAQAQNSKLOLLK 1680  
QY 1721 DLERKVEDNORYLEDQAOLARLEGEVRSLLKDISOKVAVYSTCL 1765  
DB 1681 DLERKVEDNORYLEDQAOLARLEGEVRSLLKDISOKVAVYSTCL 1725

## RESULT 10

US-08-144-121-4  
; Sequence 4, Application US/08144121  
; Patent No. 5610031  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagan, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/144,121  
; FILING DATE: 27-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Domain

LOCATION: 1..250  
FEATURE: 62.7%; Score 6051.5; DB 1; Length 1196;  
NAME/KEY: Domain Best Local Similarity 67.7%; Pred. No. 0;  
LOCATION: 251..437 Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;  
FEATURE: 438  
NAME/KEY: Domain  
LOCATION: 808..840  
FEATURE: 841..1196  
US-08-144-121-4

Query Match 62.7%; Score 6051.5; DB 1; Length 1196;

Best Local Similarity 67.7%; Pred. No. 0;

Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;

QY 1 QEFYSYGCAGSCYPATGDLGCGAQLSVTS-TGGLHKPEPYCIVSHLQEDKKCFICN 59  
DB 1 QEFYSYGCAGSCYPATGDLGCGAQLSVTS-TGGLHKPEPYCIVSHLQEDKKCFICN 60  
QY 60 SQDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENVTIQLDLEAFHFTLIMTF 119  
DB 61 SQDPYHETLNPDSHLIENVVTTTAPNRLKIWQSENGVENVTIQLDLEAFHFTLIMTF 120  
QY 120 KTRPAAWLIERSDFGKTVGVRYFAYDCEASFPGLISTGPMKKVDDIICDSYSIDIEPS 179  
DB 121 KTRPAAWLIERSDFGKTVGVRYFAYDCEASFPGLISTGPMKKVDDIICDSYSIDIEPS 180  
QY 180 TEGEVIERALDPAFKIEDPSPRIQNLKITNRIKFKVLTGLDNLDSRMEIREKYYV 239  
DB 181 TEGEVIERALDPAFKIEDPSPRIQNLKITNRIKFKVLTGLDNLDSRMEIREKYYV 240  
QY 240 AVYDMVVRGNCFCYGHASECAPVDGFEVEGVMVHGCMCRHNTKGINLCELMDFVHDL 299  
DB 241 AVYDMVVRGNCFCYGHASECAPVDGFEVEGVMVHGCMCRHNTKGINLCELMDFVHDL 300  
QY 300 WRPAEGRNSACKKNCNEHSISCHFDMAVYLTATGNVSGGVCDCCOHNWGRNCECKPF 359  
DB 301 WRPAEGRNSACKKNCNEHSISCHFDMAVYLTATGNVSGGVCDCCOHNWGRNCECKPF 360  
QY 360 YYQHPERDIRPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRKLNVEGEHCDVC 419  
DB 361 YYQHPERDIRPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRKLNVEGEHCDVC 420  
QY 420 KEGFYDLSSDDPPCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQCLPEHWGL 479  
DB 421 KEGFYDLSSDDPPCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCDCQCLPEHWGL 437  
QY 480 SNLDGCRPCDCLGGLALNNSCFAESQSCSRPHMIGRCQNEVEPGYFATLDHYLYEAE 539  
DB 438  
QY 540 EANLPGVSIIVERQYIQDRIPSWTGAFTVRVPEGAYLEFFIDNIPYSMEYDILIRYEPQL 599  
DB 438  
QY 600 PDHWEKAVITVQRPGRIPTSRCGNTIPDDNQVWSLSPGSRVWLPVRPVEKGTNYTV 659  
DB 438  
QY 660 RLELPQYTSDDSDVESPYTLIDSLVLMFYCKSLDIFTVGGSGDGVWVNSAWETFORVRL 719  
DB 438  
QY 720 ENSRSVVKTPMTDYCRNIIFISALLHOTGLACECDPQGSLSVYCDPNNGCQCRPNVWG 779  
DB 438  
QY 780 RTCNRCAFGTFGFGSGCKPCCECHLQGSVNACNPVVTGQCHCFQGVYARQCRCRLPGHWG 839

RESULT 11

US-08-735-893-4

; Sequence 4, Application US/08735893

; Patent No. 5914317

; GENERAL INFORMATION:

; APPLICANT: Burgeson, Robert E.

APPLICANT: Wagman, David W.  
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: BOSTON  
STATE: Massachusetts  
COUNTRY: United States  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/735,893  
FILING DATE: 18-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/144,121  
FILING DATE: 27-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1196 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1..250  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 251..437  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 438..807  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 808..840  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 841..1196  
US-08-735-893-4

Query Match 52.7%; Score 6051.5; DB 2; Length 1196;  
Best Local Similarity 67.7%; Pred. No. 0;  
Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;

Qy 1 QEPFSGYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPPYCIIVSHLQEDKKCFICN 59  
Db 1 QEPFSGYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPPYCIIVSHLQEDKKCFICN 60  
Qy 60 SQDPYHETLNPDSHLIENVVTPAPNRLKIWQSENGVENVTIQLDLAEAFHFLIMTF 119  
Db 61 SQDPYHETLNPDSHLIENVVTPAPNRLKIWQSENGVENVTIQLDLAEAFHFLIMTF 120  
Qy 120 KTRFPAAMLIERSDFGKTWGVRYFAYDCEASFGISTGPMKKYDDIICDSRYSDIEPS 179  
Db 121 KTRFPAAMLIERSDFGKTWGVRYFAYDCEASFGISTGPMKKYDDIICDSRYSDIEPS 180  
Qy 180 TEGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYYY 239  
Db 181 TEGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYYY 240

240 AVYDMVVRGNCFCYGHASECAPVDGNEVEGVHCHCMCRHNTKGLNCELMDYHDL 299  
241 AVYDMVVRGNCFCYGHASECAPVDGNEVEGVHCHCMCRHNTKGLNCELMDYHDL 300  
300 WRPAEGRNSNACKKCNNEHSISCHPDMAYLATGNVSGVCDCCOHNMTGRNCEQCKPF 359  
301 WRPAEGRNSNACKKCNNEHSISCHPDMAYLATGNVSGVCDCCOHNMTGRNCEQCKPF 360  
360 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRKLNVEGSHCDVC 419  
361 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRKLNVEGSHCDVC 420  
420 KEGFYDLSSDDPFGCKSCACNPLGTIPGNGPCDSSTGHYCKRLVTGHCDCOCLBEHWGL 479  
421 KEGFYDLSSDDPFGCKS----- 437  
480 SNDLDGCRPCDCLGGALNNSCFABSGQSCSRPHMIGRCNEVEPGYFATLDHYLBAE 539  
438 ----- 437  
540 EANLPGVSIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFDINIPYSMEYDILIRYQL 599  
438 ----- 437  
600 PDHWEKAVITVORPGRIPTSSRCGNTIPDDNQVSVLSPGSRVYVLPVPCFEKGTNTV 659  
438 ----- 437  
660 RLELPQYTSDDSDVESPYTLIDSLVLMFYCKSLDIFTVGGSGDGVVWTSANETQRICL 719  
438 ----- 437  
720 ENSRSVVKTEMTDVCNRIIFSISALLHQTGLACECDPQGSLSVCDPNPGQCCQCRPNVVG 779  
438 ----- 437  
780 RTCNRCAPGTGFGSPGCKPCCHLOGSVNAPCNPTQCHCFQGVYARQCDRLCPHWG 839  
438 ----- 437  
840 FPSCQPCQCNHADDPCDPTVTECLNCQDVTMHNCRCLAGYVGPPIIGSDHCRPCPCP 899  
438 ----- 437  
900 DGPDSGRQFARCYQDPVTLQLACVDFGYIGSRCDCCASGYFGNPSEVGGSCQPCQCHN 959  
438 ----- 437  
960 NIDTTPDEACDKETGKCLKLYHTEGHCQFCRFGYGDALRQCRKVCNLYLGTVOEHC 1019  
438 -----CVCNLYLGTVOEHC 450  
1020 NGSDDCCDKATQCLCLPNVIGQNCDCRCAPTWOLASGTGCDPCNCAHSHFGSPSCNEFT 1079  
451 NGSDDCCDKATQCLCLPNVIGQNCDCRCAPTWOLASGTGCDPCNCAHSHFGSPSCNEFT 510  
1080 GOCQCMFPGGRTCSCEQLFWGDPDVECRACDCCDPRGIEPQCDQSTGQCVCVEGVEGP 1139  
511 GOCQCMFPGGRTCSCEQLFWGDPDVECRACDCCDPRGIEPQCDQSTGQCVCVEGVEGP 570  
1140 RCDKTRGSGVFPDCTPCHQCQFALWDVIIAELNTRHFRLEKAKALKISGVIQPYRETV 1199  
571 RCDKTRGSGVFPDCTPCHQCQFALWDVIIAELNTRHFRLEKAKALKISGVIQPYRETV 630  
1200 DSVERKVSIEIKDILAQSPAAPLKNIGNLFEAEKLIKDVTEMAAQVEVKLSDTTSQSN 1259  
631 DSVERKVSIEIKDILAQSPAAPLKNIGNLFEAEKLIKDVTEMAAQVEVKLSDTTSQSN 690  
1260 TAKELDSLOTEASLDNTVKELAQLEPIKNSDITRGALDSITKYFQMSLEAEERVNASTT 1319  
691 TAKELDSLOTEASLDNTVKELAQLEPIKNSDITRGALDSITKYFQMSLEAEERVNASTT 750

QY 1320 EPNSTVEQSALMRDRVEDVMMERESQFKEKQEQARLLDELAKGLQSLDLSAAAEWTCGT 1379  
DB 751 EPNSTVEQSALMRDRVEDVMMERESQFKEKQEQARLLDELAKGLQSLDLSAAAEWTCGT 810  
QY 1380 PGCASCSETECGPNCRTDEGERKCGCGCGGLVTVAHNAWOKAMDLDQDVLSALAEVEQ 1439  
DB 811 PGCASCSETECGPNCRTDEGERKCGCGCGGLVTVAHNAWOKAMDLDQDVLSALAEVEQ 870  
QY 1440 LSKMWSEAKLRADAEAKQSAEDILLKTNAKEMKDKSNEELRNLIQIRNFLTQDSADLDS 1499  
DB 871 LSKMWSEAKLRADAEAKQSAEDILLKTNAKEMKDKSNEELRNLIQIRNFLTQDSADLDS 930  
QY 1500 IEAVANEVLKMBPSPPOOLNLTEDIRERVSLSQVEVILQHSAADTARAEMLLEAKR 1559  
DB 931 IEAVANEVLKMBPSPPOOLNLTEDIRERVSLSQVEVILQHSAADTARAEMLLEAKR 990  
QY 1560 ASKSATDVKVTVADMVKEALEEAEKAQAAEKAQADEDIQGTQNLNLTSEISETAASET 1619  
DB 991 ASKSATDVKVTVADMVKEALEEAEKAQAAEKAQADEDIQGTQNLNLTSEISETAASET 1050  
QY 1620 LFNASQRISELERNVBELRKAQNSGEABYTEKVYTVKQSAEDVKKTLDELDEKYYK 1679  
DB 1051 LFNASQRISELERNVBELRKAQNSGEABYTEKVYTVKQSAEDVKKTLDELDEKYYK 1110  
QY 1680 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAE 1739  
DB 1111 VENLIAKTEESADARRKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNQRYLEDKAE 1170  
QY 1740 LARLEGEVRSLLKDISQKAVYSTCL 1765  
DB 1171 LARLEGEVRSLLKDISQKAVYSTCL 1196

RESULT 12  
US-09-845-583A-6  
; Sequence 6, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845, 583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1799  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-6

Query Match 52.38; Score 5046; DB 4; Length 1799;  
Best Local Similarity 51.18; Pred. No. 8.1e-285;  
Matches 901; Conservative 304; Mismatches 544; Indels 14; Gaps 7;  
QY 8 GCAGGCVPATGDLIGRAOKLSVTSCTGLHKPEPYCIVSHLQEDKKCFICNSQDPYHET 67  
DB 44 GCSRGSCYPATGDLVGRADLTASSCTGLHSQPICYIVSHLQEDKKCFICNSRRFPFSAR 103  
QY 68 LNPDSHLEIENVVTFAPNRLKIKWQSENGVENTIQLDLEAEFHTLIMTKTFRPAAM 127  
DB 104 DNPNSHRIQNVVTSFAPQRTAWQSENGVPMVTIQLDLEAEFHTLIMTKTFRPAAM 163  
QY 128 LIERSSDFGTWGVYRFAVDCASPPGISTGPMKVDVDDIICDSRYSDIEPSPTEGEVIFR 187  
DB 164 LVESADFGTWHVYRFSYDCADDFGIPLAPRWDVDCSRSEIEPSTEGEVIFR 223  
QY 188 ALDPAPKIEDPSPRIQNLKILNRIKFKVLKTLGDNLLDSRMEIREKYYAVYDMVVR 247

DB 224 VLDPATIPDPYASRQNLKILNRLVNLTRLHTLGNLLDPRREIREKYYALYELVIR 283  
QY 248 GNCFCYGHASECAPVDGFNEEVGMVGHGCMCHNTKGLNCELQMDPYHDLPHRPAEGRN 307  
DB 284 GNCFCYGHASQCAPAPGAPAHABGMVHGACICKHNTGLNCEQCDPFYQDLPHRPAEDGH 343  
QY 308 SNACKKCNCKNEHSISCHFDMAVYLATGNVSGVYCDQCHNTMGRNCEQCKFFYYQPERD 367  
DB 344 THACRCKECNGHSHCHFDMAVYASGNVSGVYCDQCHNTAGRHCEFCFFPYRPTKD 403  
QY 368 IRDPNFCERCTCDPAGSQNEGICDSTYDFSTGJLAGCRCKLVNVEGSHDVCKEGFFVDS 427  
DB 404 MEDFAVCRPCDDPMSQDGRCDSDHDPVLGLVSGQCRCKEHVGTTRCQCCQDFGLS 463  
QY 428 SEDPFGKSCACNPLGTIPGNCPCDSETHCYCKRLVTGOHCDQCLPEHNGLSNDLDGCR 487  
DB 464 ASDPRGQRCOCNRSRGTVPGSSPCDSSGTCFCKRLVTGHCDCRCLPCHWGLSHDLDGCR 523  
QY 488 PCDCDLGALNNSCFABSGQCSRPHMIGRCQNEVEPYFYFATLDHLYLVAEAEANLGPV 547  
DB 524 PCDCDVGGALDPQCDDEATGQCPCRQHMIGRRCBQVQGYPRPFLDHLTWEAAQAQ-QQVL 582  
QY 548 SIVERQYIQDRIPSWTGAGFVRPEGAYLEFFIDNTPYSNEYDILIRYEPQLPDHNEKAV 607  
DB 583 EVVERLVNRETSPWTFGVRLREGQEVFLVTSPLRAMDYDILLURKEVQVPEQMAELE 642  
QY 608 ITVORPKRIPTSSRCGNTIPDDNQVVSLSPGSRYVVLPRPVCPEKGTNTYVLELEPYT 667  
DB 643 LMVQRPVPSNAHSPCGHVLPKDDRIQGLMHNTRVLVPRPVCLEPGISYKLLKLTG-T 701  
QY 668 SSDSDVESPYT--LIDSLVLMYPYCKSLDITFTVGGSGDGVVTNSAWETFORYLENSRSV 725  
DB 702 GGRAQPTSYSGLLIDSLVLPVLEMP---SGDAAALERRTTTFEYRCHBEGLMP 757  
QY 726 VKTPMTVDCRNLIPIISALLHQTGLACECDPQGSLSVCDPNGGQCCOCRRNVVGRTCNRC 785  
DB 758 SKAPLSETCAPLLISVSALYNGALPCCDPQGSLSSECSFPHGQCRCKEGVVGRRCDVC 817  
QY 786 APGTGFGPSCGKPCCECHLQGSVNAFCNVPVTGQCHQCGVYARQCDRLCGHWGFPSCQP 845  
DB 818 ATGYVGFPGAGCAQCQCSPDGALSALCEGTSQCPRCRPAFGALRCDCRCQCGWGFPCR 877  
QY 846 CQCNHADDQDPVTGECINODYTMGNHCRCLAGYVGDPIIGSGDHCRCPCPCPDGDSG 905  
DB 878 CVCNGRADECOTHTGACLGCKNDYTGGEHCERCIAFGHDPALPYGGQCRCPCEPGEQSG 937  
QY 906 RQFARSCYQDDEVTLQLACVCDPQGYIGSRCDDCASGYFNGPSEVSGSCQPCQCHNNDITD 965  
DB 938 RHFATSCHRDGYSQIVCHCSEAGYTLRCBACAPGFPDPSKPGRCQLCECSGNDPMD 997  
QY 966 PEACDKETGRCLKLYHTEGHCQFCRFGYVGDALRODCRCKVCNYLGTVQEHNGSD-C 1024  
DB 998 PDACDPHTGQCLRLHNTEGPHCGYCKPGFPHGQAARQSCHRCTCNLLGTDPRRCPSDILC 1057  
QY 1025 QCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGCDPCNCAHSPGSCNEFTGQCC 1084  
DB 1058 HCDSTGQCLCLPHVQGLNCDCHCAPNFTNSGRGQCPACHPRSARGPTCNEFTGQCHC 1117  
QY 1085 MPFGGRTCSQBELFWGDDPVECRACDCDPRGRIETPCQDOSTGQCVVEGVEGPRCDKC 1144  
DB 1118 HAGFGRTCSQBELFWGDDPGLQCRACDCDPRGIDKPKQCHRSTGHCSCRPVSGVRCDCQ 1177  
QY 1145 TRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHELEKAKALKISGIVGYPVRETVDVSVER 1204  
DB 1178 ANGSGVFPACHPCACPGDWDVRVVDLAARTRLEQWAGELQOTGVLAGFESSFLNQ 1237  
QY 1205 KYSEIKDILAQSPAAPLKNIGNIFEEAEKLI---IKQVTEMAQVEVKLSLSTTQCSNSTA 1261  
DB 1238 KLGWVQAIMSNARNAS--AASAKLVEATEGLRHEIGKTERLTQLEAELTAVQDENFAN 1295  
QY 1262 KELDSLQTEASLQNTVKELAEQLEFKNSDIRGALDSITKYFQMSLEAEERVAASSTPEP 1321

Db 1296 HALSGLERDGFALNLTQLRDLHLEILKHSNFIKAYDSIRHAKSQTSEARRANASTFAY 1355  
Qy 1322 NSTVEQSALMRDRVEDVWMERESQFKQEQARLDLDELAKGLQSLDLGSAABMTCTGTPP 1381  
Db 1356 PSPVNSADTTRRTVELMGAKENFNHRLANOQALGRLSAHTILSLAGINELVCGAPG 1415  
Qy 1382 GASQSETECGGPNCRITDEGRKCGGPGCGGLVTVAHNAWKAMDLODDVLALAEVQLS 1441  
Db 1416 DAPCATSPCGAGCRDEBDGQPCGGGLGCSGAAPADLALGRAHRSQAEIQRALVEGGIL 1475  
Qy 1442 KMUSEAKLRADEAKQSAEDILLKTNATKEMDKSNELNMLKIQIRNFITQDSALDSTE 1501  
Db 1476 SRVSETRQAEAAQRAALDKANASRGQVQANQELRELQNVDFLSQSGADPDSIE 1535  
Qy 1502 AVANEVLKEMPSPPQOLNLTDIRVERBSLQSEVILQHSAAIDARAEMLEBAKXAS 1561  
Db 1536 MVATRVLDISIPASPEQIQRALAEIARVSLADVTILAHMTGQVRRAEQLQDAHAR 1595  
Qy 1562 KSATDVVTADMKALEEAEKQVAEAKAKQADEDIQGTQNLTSISETAASBETLF 1621  
Db 1596 SRABERQKATVQALAEARAGAGAAQGAIRAVVDTQNTBOTQORVORWAGAKSLN 1655  
Qy 1622 NASQRISELERNVEELKRAQNSGEAEYIEKVYVTVKQSAEDVKKTLDELDEKXKVE 1681  
Db 1656 SAGERARQLDALLEALKKRAAGNSLAASATAETAGSAQSRAREAEKQLEQVGDQYQTVR 1715  
Qy 1682 NLIAKTEESADARKAEMLQNEAKTLLAQANSKLQLLKDLERKYEDNORYLEDQAELA 1741  
Db 1716 ALAEKAGVLAQARABQURDEARDLQAOQKLQRLQELBGTVEENERALEGKAQLD 1775  
Qy 1742 RLEGEVRLKDISQKAVYSTC 1764  
Db 1776 GLEARMESVLQAINLQVQIYNTC 1798

RESULT 13  
US-09-561-709B-11  
; Sequence 11, Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champliand, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; CURRENT FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-11

Query Match 51.0%; Score 4923; DB 4; Length 1798;  
Best Local Similarity 49.9%; Pred. No. 1.1e-277;  
Matches 880; Conservative 307; Mismatches 564; Indels 12; Gaps 6;  
Qy 8 GCAEGSCYPATGDLILGKAKLSVTSTCGLHKPEPVCIVSHLOEDKKCFICNSODPYHET 67  
Db 41 GCSRGSCYPATADLLVGRADRITASTGCLNGRQYCIIVSHLOEDKKCFICNSRRPFSAR 100  
Qy 68 LNPDSHLIENVVTFAPNRLKIWQSENGENVVITQDLAEAFHFTLIMTKTFRPAAM 127  
Db 101 DNPHTHRIQNVVTSFAPQRAAWQSQNGIPAVTITQDLAEAFHFTLIMTKTFRPAAM 160

Qy 128 LIRSSDFGTWGVYFYFAYDCEASPPGISTGPMKKVDDIICDSRYSIEPSTEGEVIPIR 187  
Db 161 LVRSADAFGRTHVYFYFSDGADFPVPLAPFRHWDVWCESRYSEIETPSTEGEVIYR 220  
Qy 188 ALDPAFKIEDPYSPRIQNLKLTNLRIKFKVLHTLGDNLDSRMEIRKYYVAVYDMVVR 247  
Db 221 VLDPALPIPDPIYSRLQNLKLTNLRIKFKVLHTLGDNLDSRMEIRKYYVAVYDMVVR 280  
Qy 248 GNCFCYGHASECAPVDGFNEVEGVMHGMCHRNKTKGLNCELMDFFHDLRWRPAEGRN 307  
Db 281 GNCFCYGHASECAPAPAPAHAEAGMVGACICKENTRGLNCEQCCQDFYDLRWRPAEAGH 340  
Qy 308 SNACKCKNCNHSISCHFDMAVYLATGNVSGVDCDCHQNTMGRNCECKPFPYOHBERD 367  
Db 341 SHACRCDRHRGTHSCHFDMAVYLGSEVSGVDCGCHQNTAYRHCELCRFFEDPTKD 400  
Qy 368 IRDPNCECTCDPAGSQNEGICDSYTPSTGLIAGQCRCKLVNGBEGCDVCKSGFYDLS 427  
Db 401 LRDPVACRSCDCCDFMGSQDGGRCDSHDDPALGLVSGQCRKEHVVGTCQCCRDGFFGLS 460  
Qy 428 SEDPFCKSCACNPLGTIPGPNPCDSETHCYCKELVTCQHCDCQCLPESHGSLNDDGCR 487  
Db 461 ISDPSCRRCCQCNARGTVPGSTPCDPNSGSCYCKELVTRGCDRCLPGHGLSLDLSGR 520  
Qy 488 PCDCDLGGALNNSCPAESQCSRPHMTGRQCNVEPGYFATLDHYLYEAEANLGPV 547  
Db 521 PCDCDVGGLDPCQDEGTQCHROHMYRRCEQVQPGYFRPFLDHLHWEAENTR-GQVL 579  
Qy 548 SIVEROYIQRIPSWTGAFFVPEGAYLEFPIDNIPYSMEYDILIRYEPOLPHWEKAV 607  
Db 580 DVVERLVTPGETPSMTSGFVLESGQTLFIVASVPNAMDYDLRLLEPQVPSQWAELE 639  
Qy 608 ITVOREGRIPTSSRCGNITPDDNQVNSLPGSRVVTLPVCEKFGKNTYVRLLEQYT 667  
Db 640 LIVQRPGPVPAHSLCGHLVPRDRDITQGLQPHARYLIPFNVCLEPFGISYKHLKULVR-T 698  
Qy 668 SSDSDVSEPYT---LIDSVLMPYCKSLDIFTVGGSGDVVTVNSAWETFORXCLENSR 723  
Db 699 GGSAPQETPYSGPLDLSLVLPVLEMF---SGDAAALERQATPEYQCHEEGL 754  
Qy 724 SVVKPMTDVCENIIFSLHHTGACEDDPOGSLSSVCDPNSGSCQCPNVVGTGN 783  
Db 755 VPSKTSPSACAPLISLTIYNGALPCQNPQGSLSSECNPHGGQCLCKPVGVRD 814  
Qy 784 RCAPGTFGPGSKPCCHLQGVNAPFNVPVTQCHCFQGVYARQCDRCLPGHMGFPSC 843  
Db 815 TCAPGVYFGFTGCQACQCSPRGALLSLCERTSQCLRTGAFGLRCDACQCGQWGFPC 874  
Qy 844 QPCQNGHADDCDPTGCLNCDYTWGNCERCLAGYGDPIIGSGDHCEPCPCPDGPD 903  
Db 875 RVCVNGHADECNTHGACLRDHTGHEHCERCIAGFHGDRPLPYGAQCRPCPCPGPG 934  
Qy 904 SGRQFARSCYQDPVTQLACVCDPQYIGSRDCCASGYFGNPSVGGSCQPCQCHNIDT 963  
Db 935 SQRHFATSCHQDEYSQIVCHCRAGYTLRCEACAPQGFQDPSRPGRCQLCECSGNIDP 994  
Qy 964 TDPEACDKETGRCLKLVHTEGHCQCFRFGYGDALRQDCKVCVNYLGTVOHQHNGSD 1023  
Db 995 MDPDACDPHGGQCLKCLHHTGPHCAHSPKPGHQAARQSHRCTNLLGTNPQCCSPD 1054  
Qy 1024 -CCDKATGQCLCLPNVIGQNCDCAPNTWOLASGTGCDPCNCAHSPGSCNFTGQC 1082  
Db 1055 QCHCDPSSGQCPCLPNVQALAVDRCAPFNWLTSGHCQCPACCLPSPEEGPTCNEFTGQC 1114  
Qy 1083 QCMPCFGGRTCECQELFWGDPDVECRACDCDREGIETPCDDOSTGOCVGVGEGPRCD 1142  
Db 1115 HCLCFGGRTCECQELHWGDPGLQCHACDCDSGIDTPQCHRTGHTCTCRPGSVGRCD 1174  
Qy 1143 KCTRYSYGVFPDCTPCHQCFALMDVIIAELTNTRHFLERAKALKISGVIQVYRETVDSV 1202  
Db 1175 QCARGSGIFPACHPCACFGMDWRVVDLAARTQRLQRAQELQQTGVLGAFESSFWHM 1234  
Qy 1203 ERKVESEIKDIL-AQSPAEPLKNIGNLFEAEKLIKDVTEWMAQVEVKLSDTTSQSNSTA 1261



Db	1235	QKLGIVQIVGARNTSAASTAQLVEATELREIGEATEHLTQLEADITDQDENFNA	1294	Db	101	DNPHTRHIONVTSFAPORRAAWQSONGIPAVTIQDLEAEHFHILIMTFKTRPAA	160
Qy	1262	KELDSIQTEAESLNDNTVKELAQLEFIKNSDIRGALDSTTKYFQMSLEABERVA	1321	Qy	128	LIERSSDFGKTGWYRYFAYDCEASFFGISTGPMKKVDDIICDSRYSDIIPSTEGE	187
Db	1295	HALSGLERDLALNLTROLDQCHLKEHSNFIAYDSIRHSHSQAEEARANT	1354	Db	161	LVERSAFGRTHWYRYFSCGADFGVPLAPRHWDVVCESRYSEIPESTEGEVI	220
Qy	1322	NSTVEOSALMRDVEDVMMERESQKEQBEQARILDELAGKLQSLDLSAAAE	1381	Qy	188	ALDPAFKIEPSPRIQNLKITNLRIKFVKLHTLGNLDSMEIREKYYAYVDMV	247
Db	1355	PSVSNASARHTEALMAQKEDFNSKMANQRALCKLSAHTHTLSLTDINEL	1414	Db	221	VLDPAIPDPYSSRIQNLKITNLRIKLTNLNLTGLNLDLPPREIREKYYAL	280
Qy	1382	GASCFTECGPNCRTDDEBERKCGGPGCGGLVTVAINAWQKAMDLDQDVLS	1441	Qy	248	GNCFYGHASECAPVDGFNEEVGCMVHGHCWCRHNTKGLNCELCDMFYHDL	307
Db	1415	LHHDRTSPCGAGCRDEGPOPCGGLSCNGAATAADLALGRARHTQAELO	1474	Db	281	GNCFYGHASECAPAPGAHAEGMVHGACICKHNTREGLNCEQCDQFYRDL	340
Qy	1442	KWYSEAKLRADEAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFLTQ	1501	Qy	308	SNACKKCNBHSISCHFDMAVYLATGNVSGVCDCCOHNMTGNRCCEQKFF	367
Db	1475	SRVAETRRQASEAQRAQALDKANASRGVQEGANQELQELQSVKDFLNQ	1534	Db	341	SHACKCKDRHGHTSCHFDMAVYLGSGVSGVCDGCOHNTAWRHCELCRCP	400
Qy	1502	AVANEYLKMBEPTPOQLNLTEDIRREVESLSQVEVILQHSAADTARAEM	1561	Qy	368	IRDNFCERCTCDPAGSNEGICDSTYDFSTGLIAGQCRCKLVNVEGSHCD	427
Db	1535	MVATRVLELSIPASAEQIHLGAIABERVSADVAIDAILARTVGDVRRAR	1594	Db	401	LRDPAVRSCTDPMGQDGRCDHDDPALGLVSGQCRKEHVHTRCQOCRCR	460
Qy	1562	KSATDVKTADMYKEALEBAEKAQVAEKAKOADEDIQGTQNLTSIESETA	1621	Qy	428	SEDPFGKSCACNPLGTIPGNCPCDSETHCYCKRLVTGHCDOCLPEHWGL	487
Db	1595	SWAEDEKQKAEVYQAALEEAQRAQAGIAQGAIRGAVADTRDTQTLQ	1654	Db	461	ISDPGCRRCQCNARGTVPSTPCDPSGSCYCKRLVTGRGCDRLPGHWGL	520
Qy	1622	NASORTSELERNVEELKRAAKQNSGEAEYIEKVYTVKQSAEDVKTKDGH	1681	Qy	488	PCDCLGALNNSCFASGQSCPRHMIQRCNEVEPGYFATIDHLYLAEAEAN	547
Db	1655	SAGERARQLDALLEALKLKEAGNSLAETAETAGSAQRAQAEQLLRGP	1714	Db	521	PCDCLGALNNSCFASGQSCPRHMIQRCNEVEPGYFATIDHLYLAEAEAN	579
Qy	1682	NLIAKTESADARRKAEMLONEAKYLLAQANSKIQLLKLEKEDNORYLED	1741	Qy	548	STIVERQITQDRIPSWTGAQGVVPEGAYLEFFIDNIPIYSMEYDILIRY	607
Db	1715	ALAEKQAGVLAQARABQFDEARDLQAAQKQRLQLOELEGTYBENRA	1774	Db	580	DVERLVTPGTPSWTSGFVRLQEGQTLFVAVSNAMDYDILLRLPOVPQ	639
Qy	1742	RLGEVRSLLKDISQKAVVYSTC 1764		Qy	608	ITVQRPGRIPSPSCGNITPDDNQVSVLSPGSVYVLPVPCFEKGTNTVRL	667
Db	1775	GLEARMRSVLQAINLQVQINTC 1797		Db	640	LIVQRPGEVPAHSLCGHLVPRDDRIQGTLOPHARYLIFPNPVCLEPGIS	698
RESULT 14				Qy	668	SSDSVSESPYT---LIDSLVMPYCKSLDIFTVGGSGDGVVTVNSAWETT	723
US-09-845-583A-8				Db	699	GGSAQPETPYSGPGLLIDSLVLRVLVLEMF-----SGDAAALERQAT	754
Sequence 8, Application US/09845583A				Qy	724	SVVKTMTDVCNRTIIFSISALLHOTGLACHCDPQGSLSVCDPNGGQOC	783
Patent No. 6635616				Db	755	VPSKTSPEACAPLLISLTIYNGALPCQCNPGSLSSECNPHGGQCLCKP	814
GENERAL INFORMATION:				Qy	784	RCAPCTEGFSGCKPCBCHLQGSVNAFCNPVTQCHCFQGVVYARQCDRL	843
APPLICANT: Burgeson, Robert				Db	815	TCAPGYIGFTGQACCCSPRGALSSLCERTSQCLCRGAPGLRCDACQ	874
APPLICANT: Brunken, William Joseph				Qy	844	QPCQNGHADDPCVTCBCLNCQDYTMGNHCERCLAGYDPIIGSGDHCR	903
APPLICANT: Champliand, Marie-France				Db	875	RPVCNGHADECNTHGTACGLCRDLTGGEHCERCITAGFHGDPRLPY	934
APPLICANT: Hunter, Dale				Qy	904	SGRQFARSQYODPVTQLQACVCDPGYIGSRCCDCASGVFGNPSVGG	963
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF				Db	935	SQRHFATSCHODEYSQQIVCHCRAGYITGLRCEACAPQGFDPSPRG	994
FILE REFERENCE: 10287-056001				Qy	964	TDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCRCKVCN	1023
CURRENT APPLICATION NUMBER: US/09/845,583A				Db	995	MDPDAADPHPGQCLRLHHTTSGHCAHSKPGFHGQAAARQSCHRCT	1054
CURRENT FILING DATE: 2001-04-30				Qy	1024	CCQDKATGQCLCLPNVIGQNCDCRCPNTWOLASGTCDCPCNCAH	1082
PRIOR APPLICATION NUMBER: US 60/200,863				Db	1055	QCHDPSGQCPCLPNVQALAVDRCAPNFWLTSGHGQCPACLPSP	1114
PRIOR FILING DATE: 2000-05-01				Qy	1083	QCMRFGGRTCEQOEFLWGDPDVECRACDCDPRGIETPQCDQSTG	1142
NUMBER OF SEQ ID NOS: 18				Db	1115	HCLCGFGRTCEQOEFLWGDPDVECRACDCDPRGIETPQCDQSTG	1174
SOFTWARE: FastSeq for Windows Version 4.0				Qy	1143	KTRQYGVFPDCTPCHQCQFALMDVITAEALNTRHFRLEKAKALIS	1202
SEQ ID NO 8				Db	1175	QCARGFSIFPACHPCFACFGDWRVQDLAARTQRLAQRAQELQOT	1234
LENGTH: 1798							
TYPE: PRT							
ORGANISM: Homo sapiens							
US-09-845-583A-8							
Query Match							
Best Local Similarity							
Matches 879; Conservative 307; Mismatches 565; Indels 12; Gaps 6;							
Qy	8	CGAEGCYPATGDLIIQRAOKLSVTSTCGLHKPEPVCIVSHLOEDKKCFIC	67				
Db	41	GCSSRGCYPATADLLVGRADRLTASSTCGLNQRPYCVIVSHLQDEKKCF	100				
Qy	68	LNPDHLIENVVTFAPNRLKIMWQSENGVENTIOLDLEAEHFHILIMTFK	127				



Db 1086 TSQSHCDQLTQGPCCKLGYGKRCSECEYNYGDPGRCIPDCNCRAGTQKICDPDTG 1145  
 QY 1129 QCVVGVGPRCDKXCTRGYSVPDCTPCHQCPCALMDVIIAELTNTRHFLFKAKAKI 1188  
 Db 1146 MCRCEGVGQKCDRCARHSGEPCTCQCHLCPDQDHTISSLSKAVOGLMLAANME - 1204  
 QY 1189 SGVIGPYEETVDSVER-----KVSEIKDILAO--PARAPLANICNLPEEAELIKOV 1239  
 Db 1205 -----DKRETLUPVCADPKLGNVSEIERLKHVPFPGKFLK-----VKDY 1247  
 QY 1240 TEMMAQVEVKLSDTTTSQSNSTAKELDSLOTEAESLDNTVKELAPQLEF---IKNSDIRGA 1296  
 Db 1248 HDSVRQTMQNLNEQLKAVVEFDLKTIERAKNEADLLLEDQBEIDLQSSVLNASTDS 1307  
 QY 1297 LDSITKYPMLEAEERNASTTENSTVEQASALMRDRVEDVMVERESQFKQEQAQL 1356  
 Db 1308 SENIKKYTHISSAEKKIN----ETSSINTSANTRN-----DLITI 1345  
 QY 1357 LDELAK-----LQSL-----DLAAEMTCGTPFGASCSETGCGPNCTRDEGERKCG 1406  
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 QY 1407 PCGGLVTVANAMOKAMDLDQDVLALAEVQLSKMVSEAKLRADAKOSAEEDILLKTN 1466  
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 Db 1644 HA-----VNAKVQAEQAQHA-GSLEKEFVELKKQVAILORTITGTGLTKGVKQ 1695  
 QY 1701 LQNEAKTLAQANSKLQLLKDLERYEDNQRYLEDKAQELARLEGEVYRSLDKDISQKVAV 1760  
 Db 1696 LKDAAEKLAGDTEAKIRITDLERKIQDLNLSRQAKADQLRILEDDQVVAIKNEIVEQEK 1755  
 QY 1761 YSTC 1764  
 Db 1756 YARC 1759

Search completed: May 18, 2004, 15:01:59  
 Job time : 24.3519 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 44.9032 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-8  
Perfect score: 9654  
Sequence: 1 QPEFSYGAEGSCYPATGD.....EVRSLIKDISQKAVYSTCL 1765

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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ALIGNMENTS

RESULT 1  
US-10-037-182-8  
; Sequence 8, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-8

Query Match	100.0%	Score 9654	DB 14	Length 1765
Best Local Similarity	100.0%	Pred. No. 0		
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QY	61	QDPYHETLNPDLSHLLNVVTFAPNRLKIWWQSENGENVITQLDEAFHFTLIMTFK	120	
Db	61	QDPYHETLNPDLSHLLNVVTFAPNRLKIWWQSENGENVITQLDEAFHFTLIMTFK	120	
QY	121	TFRPAAMLIERSDFGKWTGWVRYFAYDCBASFPDGTGPMKKYDDIDICDSYSYDIEST	180	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	9654	100.0	1786	9	US-09-873-676-113
3	9654	100.0	1786	9	US-09-938-275-6
4	9654	100.0	1786	14	US-10-037-182-6
5	9092	94.2	1786	9	US-09-938-275-7
6	9092	94.2	1786	14	US-10-037-182-10
7	8873	91.9	1725	15	US-10-037-182-12
8	6044.5	62.6	1196	16	US-10-443-349-4
9	5084	52.7	1801	9	US-09-938-275-8
10	5048	52.3	1798	9	US-09-938-275-9
11	5046	52.3	1799	9	US-09-845-593-6
12	4918	50.9	1798	9	US-09-845-593-8
13	3765	39.0	1808	15	US-10-369-493-5986
14	3076.5	31.9	1101	12	US-10-387-971-18
15	2348	24.3	527	12	US-09-925-298-703

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Db 181 EGEVIFRALDPAFKIEDPVSPTQNLKLTNRIKFKVLTGLDNLDSRVEIREKYYA 240  
Qy 241 VYDMVVRGNCFCYGHASBAPVDGPNVEVGMVHGMCHRNHTKGLNCELMDPYHDLPW 300  
Db 241 VYDMVVRGNCFCYGHASBAPVDGPNVEVGMVHGMCHRNHTKGLNCELMDPYHDLPW 300  
Qy 301 RPAEGRNSACKKCNCHNSISCHFDMAVYATGNVSGVGDCCQNTWGRNCEOCKEFPY 360  
Db 301 RPAEGRNSACKKCNCHNSISCHFDMAVYATGNVSGVGDCCQNTWGRNCEOCKEFPY 360  
Qy 361 YQHPERDIRPNFCERTCDPAGSQNEGI CDSYTFSTGLIAGQCRKLNVEGEHCDCVCK 420  
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Qy 481 NDLGRCPCDCDILGGALNNSCFABSCQSCRPHMIGROQNEVEPGYFATLDHYLYEABE 540  
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Qy 841 PSCQPCQCNHADDCTPVTGECNLCDQYTMGHNCERCLAGYVGDPIIGSGDHCRPCPCPD 900  
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Qy 901 GPDGSRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASGYFGNPSVGGSCQPCQCHNN 960  
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RESULT 2  
US-09-873-676-113  
; Sequence 113, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: Macdonald, Nicholas J.  
; APPLICANT: Sim Kim L.  
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 113  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-873-676-113

Query Match 100.0%; Score 9654; DB 9; Length 1786;  
Best Local Similarity 100.0%; Pred. NO. 0;  
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QY 241 VYDMVVRGNCFCYGHASECAPVDGPFNEVEGVMVHGMCRHNTKGLNCLMDFVHDLFW 300  
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DB 1042 GSDCQCDKATGQCLCLPNVIGQNCDCAPNTWQLASGTGDCPCNCAHSGFSPCNBEFTG 1101  
QY 1081 QCQCMFPGGRTCSBQELFWGDDPVECRACDPCDPRGIEPTPCDQSTGQCVVEGVEGR 1140  
DB 1102 QCQCMFPGGRTCSBQELFWGDDPVECRACDPCDPRGIEPTPCDQSTGQCVVEGVEGR 1161  
QY 1141 CDKCTRGYSVFPDCTPCHQCFALMDVITIAELTNRTHRELEKAKALKTSGVIGPVRETV 1200  
DB 1162 CDKCTRGYSVFPDCTPCHQCFALMDVITIAELTNRTHRELEKAKALKTSGVIGPVRETV 1221  
QY 1201 SVKRVSEIKDIIAQSPAAPLKNIGNLFEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1260

DB 1222 SVKRVSEIKDIIAQSPAAPLKNIGNLFEAEKLIKDVTEMMAQVEVKLSDTTSQSNST 1281  
QY 1261 AKELDSLQTEAEBSLONTVKELAEQLEFKNSDIRGALDSITKYFQMSLEASERVNASTTE 1320  
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DB 1402 PGASCSETECGGPNCRCTDEGERKCGPGCGGLVTVVAHNAWQKAMDLDQDVLASAEVEQL 1461  
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DB 1642 FNASQRISELERNVBEKXKAAQNSGEAEYIEKVYTVTKQSAEDVYKTLDGELDEKXKVV 1701  
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DB 1702 ENLIAKTTESDARAKBMLQNEAKTLQAQNSKLQLLKOLERYEDNQRYLEDKQAEEL 1761  
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DB 1762 ARLEGEVRSLLKDISOKVAVYSTCL 1786

RESULT 3  
US-938-275-6

; Sequence 6, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P07942  
; DATABASE ENTRY DATE: 1988-08-01  
US-938-275-6

Query Match 100.0%; Score 9654; DB 9; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QBPFSYGCAGSCYPATGDLIIQRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 60  
DB 22 QBPFSYGCAGSCYPATGDLIIQRAQKLSVTSTCGLHKPEPYCIVSHLQEDKKCFICNS 81  
QY 61 QBPYHETLNPDSHLENTVVTTFAPNRLKIWNQSENGVNTIQLDLAEFPHTLIIMTFK 120

Db 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWKQSENGVENVTIQIDLEAEFHFTHLIMTFK 141

Qy 121 TFRPAAMLIERSDFGKTGWYRYPAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST 180

Db 142 TFRPAAMLIERSDFGKTGWYRYPAYDCEASFPGISTGPMKKVDDIIICDSRYSDIEPST 201

Qy 181 EGEVIFRALDPAFKIEDYSPRIQNLKLTNLRKFVKLHTLGNLLDGRMEIREKYVYA 240

Db 202 EGEVIFRALDPAFKIEDYSPRIQNLKLTNLRKFVKLHTLGNLLDGRMEIREKYVYA 261

Qy 241 VYDMVVRGNCFCYGHASCAVDFGNEVEGMVHGHCMCRHNTKGLNCELDMDFYHDLFW 300

Db 262 VYDMVVRGNCFCYGHASCAVDFGNEVEGMVHGHCMCRHNTKGLNCELDMDFYHDLFW 321

Qy 301 RPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGVGGVCDCCQNTWGRNCEQCKPFY 360

Db 322 RPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNVSGVGGVCDCCQNTWGRNCEQCKPFY 381

Qy 361 YQHPREDIRDNFCECTCDPAGSQNEGI CDSYTDFTSTGLIAGOCCKLVNVEGHCDCVCK 420

Db 382 YQHPREDIRDNFCECTCDPAGSQNEGI CDSYTDFTSTGLIAGOCCKLVNVEGHCDCVCK 441

Qy 421 EGFYDLSSEDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTCQHCDCQCLPEHMGLS 480

Db 442 EGFYDLSSEDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTCQHCDCQCLPEHMGLS 501

Qy 481 NDLDCRCDCDGLGALNNSCFASGQSCSCEPHMIGRQNEVEPGYFATLDHYLYEABE 540

Db 502 NDLDCRCDCDGLGALNNSCFASGQSCSCEPHMIGRQNEVEPGYFATLDHYLYEABE 561

Qy 541 ANLPGVSIIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRPEPOLP 600

Db 562 ANLPGVSIIVERQYIQRIPSWTGAGFVRVPEGAYLEFFIDNIPYSMEYDILIRPEPOLP 621

Qy 601 DHEKXAVITVORPBGRIPTSSRCGNTIPDDNQVVSLSGSRVYVTLRPPVCFEKGNTYVR 660

Db 622 DHEKXAVITVORPBGRIPTSSRCGNTIPDDNQVVSLSGSRVYVTLRPPVCFEKGNTYVR 681

Qy 661 LELPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVWNTNSAWETFORYCL 720

Db 682 LELPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVWNTNSAWETFORYCL 741

Qy 721 NRSVSVKTPMTDVCNRIIFSIALLHOTGLACEDCPGSLSSVCDPNGGQCCORPNVGR 780

Db 742 NRSVSVKTPMTDVCNRIIFSIALLHOTGLACEDCPGSLSSVCDPNGGQCCORPNVGR 801

Qy 781 TGNRCAPGTFFGPGSGCKPCBECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 840

Db 802 TGNRCAPGTFFGPGSGCKPCBECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPGHWGF 861

Qy 841 PSCQPCQNGHADDCCPVTGCLNCDYTMGHNCECLAGYGDPIIGSGDHCRCPCPCPD 900

Db 862 PSCQPCQNGHADDCCPVTGCLNCDYTMGHNCECLAGYGDPIIGSGDHCRCPCPCPD 921

Qy 901 GDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCASGYFGNPSVEGSGCQPCQCHNN 960

Db 922 GDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCASGYFGNPSVEGSGCQPCQCHNN 981

Qy 961 IDTTDPEACDXTGRCCLKLYHTEGEHCQFCRFYGYGDALRQDCRCVCNVLGTQVQHCN 1020

Db 982 IDTTDPEACDXTGRCCLKLYHTEGEHCQFCRFYGYGDALRQDCRCVCNVLGTQVQHCN 1041

Qy 1021 GSDCCDCYATGQCLCLPNVIGQNCDCAPNTWOLASGTGDCPCNCAHNSFGPSNFTG 1080

Db 1042 GSDCCDCYATGQCLCLPNVIGQNCDCAPNTWOLASGTGDCPCNCAHNSFGPSNFTG 1101

Qy 1081 QCCCMFPGFGRGTCSECOELFWGDPDVECRACDCDPRGIETPQDQSTGQCVGVGEGFR 1140

Db 1102 QCCCMFPGFGRGTCSECOELFWGDPDVECRACDCDPRGIETPQDQSTGQCVGVGEGFR 1161

Qy 1141 CDKCTRGSGVFPDCTPCHOCFALLMDVITIAELNTRHTRFLERAKALKISGVIGPVRFTVD 1200

Db 1162 CDKCTRGSGVFPDCTPCHOCFALLMDVITIAELNTRHTRFLERAKALKISGVIGPVRFTVD 1221

Qy 1201 SVERKYSEIKDILASPAAPLKNIGNLFBEAEKLIKDVTEMMAQVEVKLSDTTQSNS 1260

Db 1222 SVERKYSEIKDILASPAAPLKNIGNLFBEAEKLIKDVTEMMAQVEVKLSDTTQSNS 1281

Qy 1261 AKELDSLQTEASRLDNTVKELAEQLSEFKNSDIRGALDSITKYFQMSLEAEERVNASATTE 1320

Db 1282 AKELDSLQTEASRLDNTVKELAEQLSEFKNSDIRGALDSITKYFQMSLEAEERVNASATTE 1341

Qy 1321 PNSTVQSALMDRVEDVNMERESQFKQSEARLDELAKGLQSLDLSAAAEAMTCGTP 1380

Db 1342 PNSTVQSALMDRVEDVNMERESQFKQSEARLDELAKGLQSLDLSAAAEAMTCGTP 1401

Qy 1381 PGASCSETCCGPGNCRCTDEGERKCGGPGCGGLVTVAHNAWOKAMDLDQDVL SALAEVEQL 1440

Db 1402 PGASCSETCCGPGNCRCTDEGERKCGGPGCGGLVTVAHNAWOKAMDLDQDVL SALAEVEQL 1461

Qy 1441 SKMVSASAKIRABEAKQSAEDILLKTNATKEMKDKSNBELNLIKQIRNFLTQDSADLDSI 1500

Db 1462 SKMVSASAKIRABEAKQSAEDILLKTNATKEMKDKSNBELNLIKQIRNFLTQDSADLDSI 1521

Qy 1501 EAVANEVLKXWMPSTPQQLQNTEDIRERVESLSQVEVILQHSAAIDARAEMLLEAKRA 1560

Db 1522 EAVANEVLKXWMPSTPQQLQNTEDIRERVESLSQVEVILQHSAAIDARAEMLLEAKRA 1581

Qy 1561 SKSATDVKTADWVKEALEEAEKAAQVAAEKAKQADEDIQGTQNLITTSISSETAASSETL 1620

Db 1582 SKSATDVKTADWVKEALEEAEKAAQVAAEKAKQADEDIQGTQNLITTSISSETAASSETL 1641

Qy 1621 FNASQRISELENNVEELKRAAKAQSSEAEYIEKVYVTVKQSAEDVKKTLDELDEKYYKV 1680

Db 1642 FNASQRISELENNVEELKRAAKAQSSEAEYIEKVYVTVKQSAEDVKKTLDELDEKYYKV 1701

Qy 1681 ENLIATKTEESADARBAEMLQNEAKTLAQAANSKQLLQKDLERKEDNORYLEDKAQEL 1740

Db 1702 ENLIATKTEESADARBAEMLQNEAKTLAQAANSKQLLQKDLERKEDNORYLEDKAQEL 1761

Qy 1741 ARLEGEVRSLLKXDISQKVAVYSTCL 1765

Db 1762 ARLEGEVRSLLKXDISQKVAVYSTCL 1786

RESULT 4

US-10-037-182-6

; Sequence 6, Application US/10037182

; Publication No. US20030044899A1

; GENERAL INFORMATION:

; APPLICANT: Tryggvason, Karl

; APPLICANT: Doi, Masayuki

; APPLICANT: Thyboll, Jill

; TITLE OF INVENTION: Recombinant Laminin 10

; FILE REFERENCE: 99-274-F

; CURRENT APPLICATION NUMBER: US/10/037,182

; CURRENT FILING DATE: 2001-12-21

; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: 60/257,449

; PRIOR FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 6

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-037-182-6

Query Match 100.0%; Score 9654; DB 14; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSPFSGYCAEGSCYCPATGDLIIIGRAOKLSVTSTCGLHKPEPCYIVSHLQEDKCKFCINS 60

Db 22 QSPFSGYCAEGSCYCPATGDLIIIGRAOKLSVTSTCGLHKPEPCYIVSHLQEDKCKFCINS 81



QY 61 QDPYHETLNPDSHLLIENVVTTTAPNRLKIWKQSENGVENVTIQLDLBAEFHFTHLIMTFK 120  
 DB 82 QDPYHETLNPDSHLLIENVVTTTAPNRLKIWKQSENGVENVTIQLDLBAEFHFTHLIMTFK 141  
 QY 121 TTRPAAMLIERSDFGKTVGVRYPAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 180  
 DB 142 TTRPAAMLIERSDFGKTVGVRYPAYDCEASFPFGISTGPMKKVDDIICDSRYSDIEPST 201  
 QY 181 EGEVIFRALDPAFKIEDPYPSPRIQNLKLTNLRKFKVHLHTLGNLLDSRMEIREKYYA 240  
 DB 202 EGEVIFRALDPAFKIEDPYPSPRIQNLKLTNLRKFKVHLHTLGNLLDSRMEIREKYYA 261  
 QY 241 VYDMVVRGNCFCYGHASACAPVDGNBVEGMVHGHCMCRNTKGLNCELCHMDPYHDLPW 300  
 DB 262 VYDMVVRGNCFCYGHASACAPVDGNBVEGMVHGHCMCRNTKGLNCELCHMDPYHDLPW 321  
 QY 301 RPAEGNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGNCRCQCKPFY 360  
 DB 322 RPAEGNSNACKKCNCHNEHSISCHFDMAVYLATGNVSGVCDCCQHNMTGNCRCQCKPFY 381  
 QY 361 YQHPERDIRDPFCERCTCDPAGSQNEGICDSYTPSTGLIAGQCRCKLVNVEGSHCDVCK 420  
 DB 382 YQHPERDIRDPFCERCTCDPAGSQNEGICDSYTPSTGLIAGQCRCKLVNVEGSHCDVCK 441  
 QY 421 EGFYDLSSDDPFGCKSCACNPLGTTIPGPNPCDSETHGHCYCKRLVTGQHCDCQCLPEHWGLS 480  
 DB 442 EGFYDLSSDDPFGCKSCACNPLGTTIPGPNPCDSETHGHCYCKRLVTGQHCDCQCLPEHWGLS 501  
 QY 481 NDLGCRPCDCDLGALANNSCFABSGQSCSRPHMIGROCNVEBPGYFATLIDHYLYEABE 540  
 DB 502 NDLGCRPCDCDLGALANNSCFABSGQSCSRPHMIGROCNVEBPGYFATLIDHYLYEABE 561  
 QY 541 ANLPGVSVIERYQIQRIPSWTGAQFVRVPEGALEFFIDNIPYSMEYDILIRYEPQLP 600  
 DB 562 ANLPGVSVIERYQIQRIPSWTGAQFVRVPEGALEFFIDNIPYSMEYDILIRYEPQLP 621  
 QY 601 DHWEKAVITVQPRGRIPTSSRCNTIPDDNQVNSLSPGSRVYVLPRVCFEKGNTYTVR 660  
 DB 622 DHWEKAVITVQPRGRIPTSSRCNTIPDDNQVNSLSPGSRVYVLPRVCFEKGNTYTVR 681  
 QY 661 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVTVNSAWETFORVRCLE 720  
 DB 682 LELPQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGSGDGVVTVNSAWETFORVRCLE 741  
 QY 721 NSRSVVKTPMTDVCNRNIIIFSIALLHOTGLACECDPQSSLSVCDPNQGQCCRPNVVGR 780  
 DB 742 NSRSVVKTPMTDVCNRNIIIFSIALLHOTGLACECDPQSSLSVCDPNQGQCCRPNVVGR 801  
 QY 781 TCNRCAPGTGFGPSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 840  
 DB 802 TCNRCAPGTGFGPSPGCKPCECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRCCLPGHWGF 861  
 QY 841 PSCQPCQCHGADDCCDPTVTEGLNCODYTMGHNCERCLAGYGGDPIIGSGDHCRPCPCPD 900  
 DB 862 PSCQPCQCHGADDCCDPTVTEGLNCODYTMGHNCERCLAGYGGDPIIGSGDHCRPCPCPD 921  
 QY 901 GPDGRQFARSCVQDPVTLQLACVCDPVGIGSRCDCCASGYFGNPSVGGSCQPCQCHN 960  
 DB 922 GPDGRQFARSCVQDPVTLQLACVCDPVGIGSRCDCCASGYFGNPSVGGSCQPCQCHN 981  
 QY 961 IDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDRLQDCKKVCNVLGTVQBHCN 1020  
 DB 982 IDTTDPEACDKETGRCLKCLYHTEGHCQFCRFGYGGDRLQDCKKVCNVLGTVQBHCN 1041  
 QY 1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAAHSGFSGSCNEFTG 1080  
 DB 1042 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAAHSGFSGSCNEFTG 1101  
 QY 1081 QCQCMGFGGRGTCSECOELFWGDRDVECRACDCDPRGIETPCQDOSTQCVCVVEGGR 1140  
 DB 1102 QCQCMGFGGRGTCSECOELFWGDRDVECRACDCDPRGIETPCQDOSTQCVCVVEGGR 1161

QY 1141 CDKCTRGYGVFPDCTPCHQCFAWDVIIAELTNRTHRFLEKAKALKISGVIQYRETVD 1200  
 DB 1162 CDKCTRGYGVFPDCTPCHQCFAWDVIIAELTNRTHRFLEKAKALKISGVIQYRETVD 1221  
 QY 1201 SVYKVSIIKIDILAQSPAAPLKNIGNLPSEAEKLIKQVTEMMAQVEVKLSDTTSQSNST 1260  
 DB 1222 SVYKVSIIKIDILAQSPAAPLKNIGNLPSEAEKLIKQVTEMMAQVEVKLSDTTSQSNST 1281  
 QY 1261 AKELDSLQTEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNSTTE 1320  
 DB 1282 AKELDSLQTEAESLQNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERVNSTTE 1341  
 QY 1321 PNSTVQSAALMRDRVEDVMMERESQFKQEBOEARLLDELAKGLQSLDLSAAAEVMTGTP 1380  
 DB 1342 PNSTVQSAALMRDRVEDVMMERESQFKQEBOEARLLDELAKGLQSLDLSAAAEVMTGTP 1401  
 QY 1381 PGASCSETECGPNCRDDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASALAEVEQL 1440  
 DB 1402 PGASCSETECGPNCRDDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLASALAEVEQL 1461  
 QY 1441 SKWSEAKLRADAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFUTQDSADLDSI 1500  
 DB 1462 SKWSEAKLRADAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFUTQDSADLDSI 1521  
 QY 1501 EAVANEVLKEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAADITARAEMLLEAKRA 1560  
 DB 1522 EAVANEVLKEMPSTPQOLQNLTEDIRERVESLSQVEVILQHSAADITARAEMLLEAKRA 1581  
 QY 1561 SKSATDVKTADMYKEALEBAEKAQVAEKAIKQADEDIQGTQNLTSISESTAASEETL 1620  
 DB 1582 SKSATDVKTADMYKEALEBAEKAQVAEKAIKQADEDIQGTQNLTSISESTAASEETL 1641  
 QY 1621 FNASQRISELERNEVEELKRAAQNSEAEYIEKVYVTVKQSAEDVKTLDGELDEKYYKV 1680  
 DB 1642 FNASQRISELERNEVEELKRAAQNSEAEYIEKVYVTVKQSAEDVKTLDGELDEKYYKV 1701  
 QY 1681 ENLIAKTTESADARRKAEMLQNEAKTLQAANSKLOLLKDLERKYEDNORYLEDKAAQEL 1740  
 DB 1702 ENLIAKTTESADARRKAEMLQNEAKTLQAANSKLOLLKDLERKYEDNORYLEDKAAQEL 1761  
 QY 1741 ARLEGEVRSLLKDISQKVAVYSTCL 1765  
 DB 1762 ARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 5

US-09-938-275-7  
 ; Sequence 7, Application US/09938275  
 ; Patent No. US20020111305A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerardo Castillo  
 ; APPLICANT: Alan Snow  
 ; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
 ; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
 ; FILE REFERENCE: PROTEO.P03  
 ; CURRENT APPLICATION NUMBER: US/09/938,275  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1786  
 ; TYPE: PRT  
 ; ORGANISM: Mus Musculus  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: Swissprot P02469  
 ; DATABASE ENTRY DATE: 1989-07-01  
 US-09-938-275-7

Query Match 94.2%; Score 9092; DB 9; Length 1786;  
 Best Local Similarity 93.0%; Pred. No. 0;  
 Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;  
 QY 1 QEPFSYGAESGSCYPATGDLIGRAQKLSVTSTCGLHKEPYPYCIVSHLQEDKKCFICNS 60

Db 22 QEPFSGYAGSGCYPATGDLIIAGRAQLSVTSTCGLHKPEPYCIIVSHLQEDKCFIDS 81  
QY 61 QDPVHETINPDSHLENIWVTFAPNRLKIWQSENGVENVTIOLDLEAFPHTHLIMTFK 120  
Db 82 RDPVHETINPDSHLENIWVTFAPNRLKIWQSENGVENVTIOLDLEAFPHTHLIMTFK 141  
QY 121 TFRPAAMLIERSSDFGTWGYRYFYAYDCBASPFGISTGPMKKVDDIIICDSRYSDIERST 180  
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QY 181 EGEVIFRALDPAFAKIEDPYSPRIONLLKINLSIKFVKLHTLGDNLIDSRMEIREKYIYA 240  
Db 202 EGEVIFRALDPAFAKIEDPYSPRIONLLKINLSIKFVKLHTLGDNLIDSRMEIREKYIYA 261  
QY 241 VYDMVVRGNCFYCHASACAPVDGPNFEEVGMVHGHCRCRHNKTGLNCLCMDFYHDLFW 300  
Db 262 VYDMVVRGNCFYCHASACAPVDGPNFEEVGMVHGHCRCRHNKTGLNCLCMDFYHDLFW 321  
QY 301 RPAEGRNSACKNCNEHSISCHFDMAVYLATGNVSGVGVCDCCOHNWGRNCEOCKPY 360  
Db 322 RPAEGRNSACKNCNEHSISCHFDMAVYLATGNVSGVGVCDCCOHNWGRNCEOCKPY 381  
QY 361 YQHPERDIRPNFCERTCDPAGSNEBICDSTYDFSTGLIAGQCRCKLNVEGECDCVCK 420  
Db 382 FOHPERDIRPNFCERTCDPAGSNEBICDSTYDFSTGLIAGQCRCKLNVEGECDCVCK 441  
QY 421 EGFYDLASEDPGCKSCACNPLGTIPGNPCDSETHCYCKRLVTGCHDOCLPBGHGLS 480  
Db 442 EGFYDLASEDPGCKSCACNPLGTIPGNPCDSETHCYCKRLVTGCHDOCLPBGHGLS 501  
QY 481 NDLGCRPCDCDGLGALNNSCFAESQCSRCRPMIGRQCNVEPFGYFATLDHYLYEABE 540  
Db 502 NDLGCRPCDCDGLGALNNSCFAESQCSRCRPMIGRQCNVEPFGYFATLDHYLYEABE 561  
QY 541 ANLPGVSVIYVERQVQIDRIPSWTCAGVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 600  
Db 562 ANLPGVSVIYVERQVQIDRIPSWTCAGVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 621  
QY 601 DHWEKAVITVQRPGRIPSTRSCGNTIPDDDNQVSVLSPGSRVYVLPVPRPCFEKGNITYVR 660  
Db 622 DHWEKAVITVQRPGRIPSTRSCGNTIPDDDNQVSVLSPGSRVYVLPVPRPCFEKGNITYVR 681  
QY 661 LELPYQVTSQSDVESPTLIDSLVLMYPYCKSLDIPVGGSGGVVNTNSAWETFOYVRCLE 720  
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QY 721 NSRSVVKTPMTDVCRNIIFISALLHOTGLACEDCPQGSLSVCDPNPGQCCQCRPNVYGR 780  
Db 742 NSRSVVKTPMTDVCRNIIFISALLHOTGLACEDCPQGSLSVCDPNPGQCCQCRPNVYGR 801  
QY 781 TCNRCAPGTGFGSGCKPCCECHLQGSVNAFONPVTCQCHFCQGVYAROCDCRLPGHGF 840  
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QY 841 PSCQPCQCNHADDCTVPTGECNLQCDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 900  
Db 862 PSCQPCQCNHADDCTVPTGECNLQCDYTMGHNCERCLAGYGDPIIGSGDHCRCPCPCPD 921  
QY 901 GPDGROFABSCYQDPVTLQACVCDPGYIGSRCDPCASGFGNBSVGGSCQPCQCHNN 960  
Db 922 GPDGROFABSCYQDPVTLQACVCDPGYIGSRCDPCASGFGNBSVGGSCQPCQCHNN 981  
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Db 1102 QCQCMFGGRTCEQELFWGDDPVECRACDCDPRGIETPQCDQSTQCQCVCEGVGPR 1161  
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Db 1222 SVKRYSEIKDILAQSPAAEPLKNIKNLPEEAEKLIKOVTEMAQVYKLSDTTSCSNST 1281  
QY 1261 AKELDSIQTEAEASLDNTVKELAEQLEFIKNSDIRGALDSITKYFOMSLAEAEERVNASTTE 1320  
Db 1282 AKELDSIQTEAEASLDNTVKELAEQLEFIKNSDIRGALDSITKYFOMSLAEAEERVNASTTE 1341  
QY 1321 PNSTVQSALMRDRVEDVNMRESOFKQEQEQAELDELAKGLQSLDLSAAAEAMTCCTP 1380  
Db 1342 PNSTVQSALMRDRVEDVNMRESOFKQEQEQAELDELAKGLQSLDLSAAAEAMTCCTP 1401  
QY 1381 PGASCSCTECGPNCRCTDSEGRKCGGPGCGGLVTVAHNAWOKAMVDODVLSALAEVQL 1440  
Db 1402 PGASCSCTECGPNCRCTDSEGRKCGGPGCGGLVTVAHNAWOKAMVDODVLSALAEVQL 1461  
QY 1441 SKVSEAKLRADBAKQSAEDILLKTNATKKNKMDKNEELNLIQIRNPLTQDSADLDSI 1500  
Db 1462 SKVSEAKLRADBAKQSAEDILLKTNATKKNKMDKNEELNLIQIRNPLTQDSADLDSI 1521  
QY 1501 EAVANEVLKXWNPSTPQOLQNLTEDIRERVESLSOVETLQHSADIAAEMLLEAKRA 1560  
Db 1522 EAVANEVLKXWNPSTPQOLQNLTEDIRERVESLSOVETLQHSADIAAEMLLEAKRA 1581  
QY 1561 SKSATDVKYTADVMKAELEAEAKQAQVAAEKAIKQADEDIQGTQNLITSISETAASETL 1620  
Db 1582 SKSATDVKYTADVMKAELEAEAKQAQVAAEKAIKQADEDIQGTQNLITSISETAASETL 1641  
QY 1621 FNASORISELERNVELEKKAQNSGEAEYIEKVYVTVKQSAEDVKTLDGELDEKYYKV 1680  
Db 1642 FNASORISELERNVELEKKAQNSGEAEYIEKVYVTVKQSAEDVKTLDGELDEKYYKV 1701  
QY 1681 ENIIAKTTESADARRKAEMLQNEAKTLIAQANSKLQLLKOLERKYEDNQYLEDKAOEL 1740  
Db 1702 ENIIAKTTESADARRKAEMLQNEAKTLIAQANSKLQLLKOLERKYEDNQYLEDKAOEL 1761  
QY 1741 ARLEGEVRSLLKDIQKQAVYSTCL 1765  
Db 1762 ARLEGEVRSLLKDIQKQAVYSTCL 1786

RESULT 6  
US-10-037-182-10  
; Sequence 10, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jilli  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-10  
Query Match 94.2%; Score 9092; DB 14; Length 1786;  
Best Local Similarity 93.0%; Pred. No. 0;

Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY	1	QEPRESYCAGSCYCPATGDLIGRAOKLSVTSTCGLHKPEPYCIIVSHLOEDKKCFICNS	60
DB	22	QEPRESYCAGSCYCPATGDLIGRAOKLSVTSTCGLHKPEPYCIIVSHLOEDKKCFICDS	81
QY	61	QDPVHETLNPDSHLIENVTTPAPNRLKIWMQSENGVENVTIQDLDEAEFPHLIMTK	120
DB	82	RDVHETLNPDSHLIENVTTPAPNRLKIWMQSENGVENVTIQDLDEAEFPHLIMTK	141
QY	121	TFRPAAMLIERSDDPGKWTGVPYFAYDCEAFSGISTGPMKVDVDDIICDSRYSDIEPST	180
DB	142	TFRPAAMLIERSDDPGKWTGVPYFAYDCEAFSGISTGPMKVDVDDIICDSRYSDIEPST	201
QY	181	EGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKIFVKLHTLGNLLDSRMEIREKYYA	240
DB	202	EGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKIFVKLHTLGNLLDSRMEIREKYYA	261
QY	241	VYDMVVRGNCFCYGHASCAPVDGFNEVEGWVGHGCMCRHNTKGLNCELMDPFYHDLPW	300
DB	262	VYDMVVRGNCFCYGHASCAPVDGFNEVEGWVGHGCMCRHNTKGLNCELMDPFYHDLPW	321
QY	301	RPAEGRNSNACKKCNCEHSSICHFDMAVYLATGNVSGGVCDDCOHNTWGRNCEQCKPFY	360
DB	322	RPAEGRNSNACKKCNCEHSSICHFDMAVYLATGNVSGGVCDDCOHNTWGRNCEQCKPFY	381
QY	361	YOHPERDIRDPNFCRCTCDPAGSNGEGICDSYTDFTGLIAGOCRCKLNVGEHCDVCK	420
DB	382	FQHPREDIRDPNFCRCTCDPAGSNGEGICDSYTDFTGLIAGOCRCKLNVGEHCDVCK	441
QY	421	EGFYDLSSEDPGCKSCACNPLGTIPGNCPCDSTGHCYKRLVTHGCHDQCLPEHWGLS	480
DB	442	EGFYDLSSEDPGCKSCACNPLGTIPGNCPCDSTGHCYKRLVTHGCHDQCLPEHWGLS	501
QY	481	NLDLDCRCPDCLGALANNSCFASGQSCRPBMIGQCNEVEPGYFATLDHYLYEAE	540
DB	502	NLDLDCRCPDCLGALANNSCFASGQSCRPBMIGQCNEVEPGYFATLDHYLYEAE	561
QY	541	ANLPGVSIIVERQYIQDRIPSWTAGFVRVPEGAYLEFFIDNIPYSMEYDILLIRYBPOLP	600
DB	562	ANLPGVSIIVERQYIQDRIPSWTAGFVRVPEGAYLEFFIDNIPYSMEYDILLIRYBPOLP	621
QY	601	DHWEKAVITVQRPGRIPTRSSCGMNTIPDDNQVVSLSFGSRYVVLPRPVCFEKXTNVTYR	660
DB	622	DHWEKAVITVQRPGRIPTRSSCGMNTIPDDNQVVSLSFGSRYVVLPRPVCFEKXTNVTYR	681
QY	661	LELPQYSSDSVSPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE	720
DB	682	LELPQYSSDSVSPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORYRCLE	741
QY	721	NSRSVVKTPMTDVCNIIIFSIALLHQTGLACECDPQGSLSVCDPNNGQCQCRPNVVR	780
DB	742	NSRSVVKTPMTDVCNIIIFSIALLHQTGLACECDPQGSLSVCDPNNGQCQCRPNVVR	801
QY	781	TNRCAPGTGFGPGSGCPCHLOGSVNAPCNVPTGQCHCFQGVYARQCDRCLPGHWGF	840
DB	802	TNRCAPGTGFGPGSGCPCHLOGSVNAPCNVPTGQCHCFQGVYARQCDRCLPGHWGF	861
QY	841	PSCQPCQCNHADDPCDPTGBCLNCQDVTMGHNCERCLAGYVGDPIIGSDHCRPCPCPD	900
DB	862	PSCQPCQCNHADDPCDPTGBCLNCQDVTMGHNCERCLAGYVGDPIIGSDHCRPCPCPD	921
QY	901	GPDSGRQFARSCYQDPVTLQACVDCDPCGYIGSRCDDCASGYFGNPSVSGSCPCCHNN	960
DB	922	GPDSGRQFARSCYQDPVTLQACVDCDPCGYIGSRCDDCASGYFGNPSVSGSCPCCHNN	981
QY	961	IDTTPDPEACDRETGRCLXLYHTEGHCQFCRFYGYGDALRQDCKKVCNLYLTQVHCN	1020
DB	982	IDTTPDPEACDRETGRCLXLYHTEGHCQFCRFYGYGDALRQDCKKVCNLYLTQVHCN	1041
QY	1021	GSDCOCDKATGQCLCLPNVIGQNCDCRCPNWTQLASGTGCDPCNCAHSGFGSCNEFTG	1080
DB	1042	GSDCHCDKATGQCLCLPNVIGQNCDCRCPNWTQLASGTGCDPCNCAHSGFGSCNEFTG	1101

QY	1081	QCQMPFGGRTCSQCQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVGVGEGPR	1140
DB	1102	QCQMPFGGRTCSQCQELFWGDPDVECRACDCDPRGIETPQCDQSTGQCVCVGVGEGPR	1161
QY	1141	CDKTRCYSGVFPDCTCHOCFALNDVILAEALNTHRTHLEKAKALKISGVIGPYETVD	1200
DB	1162	CDKTRCYSGVFPDCTCHOCFALNDVILAEALNTHRTHLEKAKALKISGVIGPYETVD	1221
QY	1201	SVERKVSIEIKDILAQSPAAPLKNIGNLPEAEKLIKDVTEMAQVEVKLSDTTSQSNST	1260
DB	1222	SVERKVSIEIKDILAQSPAAPLKNIGNLPEAEKLIKDVTEMAQVEVKLSDTTSQSNST	1281
QY	1261	AKELDSIQTEAESLDNVTKELAEQLFETKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1320
DB	1282	AKELDSIQTEAESLDNVTKELAEQLFETKNSDIRGALDSITKYFQMSLEAEERVNASTTE	1341
QY	1321	PNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDELALAGLQSLDLSAAAEAMTCGP	1380
DB	1342	PNSTVEQSALMRDRVEDVMMERESQFKEQEQEARLLDELALAGLQSLDLSAAAEAMTCGP	1401
QY	1381	PGASCSITECGGPNCRTRDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLASAEVQL	1440
DB	1402	PGASCSITECGGPNCRTRDEGERKCGGPGCGGLVTVVAHNAWKAMDLDQDVLASAEVQL	1461
QY	1441	SKWSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFLTQPSADLDSI	1500
DB	1462	SKWSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFLTQPSADLDSI	1521
QY	1501	EAVANEVLKWMPTPOOLNLTEDIRERVESLSQVEVILQHSAAADIAEAMLEAEKKA	1560
DB	1522	EAVANEVLKWMPTPOOLNLTEDIRERVESLSQVEVILQHSAAADIAEAMLEAEKKA	1581
QY	1561	SKSATDVKVTADVMYKEALEAEAKQAQVAAEKAKIQAODEDIQGTQNLTSIETSEETL	1620
DB	1582	SKSATDVKVTADVMYKEALEAEAKQAQVAAEKAKIQAODEDIQGTQNLTSIETSEETL	1641
QY	1621	FNASQRISELRNVBELKRAQNSGEAEYIEKVVTYVKSADVDKTLDELDEKVKV	1680
DB	1642	FNASQRISELRNVBELKRAQNSGEAEYIEKVVTYVKSADVDKTLDELDEKVKV	1701
QY	1681	ENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQKLEKRYEDNORYLEDKAQEL	1740
DB	1702	ENLIAKTEESADARRKAEMLQNEAKTLAQANSKLQKLEKRYEDNORYLEDKAQEL	1761
QY	1741	ARLEGEVRSLLKDIQKQVAVYSTCL	1765
DB	1762	VRLEGEVRSLLKDIQKQVAVYSTCL	1786

RESULT 7

US-10-037-182-12  
; Sequence 12, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-12

Query Match 91.9%; Score 9873; DB 14; Length 1725;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 41 EBYCIVSHLQEDKCKFCINSDPQVHETLNPDSHLIENVTTFAPNRLKIWQSENGVENY 100  
DB 1 EBYCIVSHLQEDKCKFCINSDPQVHETLNPDSHLIENVTTFAPNRLKIWQSENGVENY 60

QY 101 TIQDLEAFHFTLHIMFTFRPAAMLIERSDFGKTWGVYFYAYDCEAFPGISTGP 160  
DB 61 TIQDLEAFHFTLHIMFTFRPAAMLIERSDFGKTWGVYFYAYDCEAFPGISTGP 120

QY 161 MKKVDDIICDSRYSDIEBTEGEVIFRALDPAFKIEDPYSPRIQNLKLTNRIRFKVLH 220  
DB 121 MKKVDDIICDSRYSDIEBTEGEVIFRALDPAFKIEDPYSPRIQNLKLTNRIRFKVLH 180

QY 221 TLGDMLLSRMEIRKYYIAYDMVYRGNCFYCHGASECAPYDGFNEVEGVMHGHCMCR 280  
DB 181 TLGDMLLSRMEIRKYYIAYDMVYRGNCFYCHGASECAPYDGFNEVEGVMHGHCMCR 240

QY 281 HNTKGLNCELQWDFYHDLFMRPASGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGV 340  
DB 241 HNTKGLNCELQWDFYHDLFMRPASGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGGV 300

QY 341 CDDCHNTWGRNCBOCKRFFYQHBERDIRDPNFCERTCDPAGSQNEGICDSTDFSTGL 400  
DB 301 CDDCHNTWGRNCBOCKRFFYQHBERDIRDPNFCERTCDPAGSQNEGICDSTDFSTGL 360

QY 401 IAGQCRKLANVEGHCYCKEGFYDLSEDPFGCKSCACNPLGTIPGPNPCDSETHCYC 460  
DB 361 IAGQCRKLANVEGHCYCKEGFYDLSEDPFGCKSCACNPLGTIPGPNPCDSETHCYC 420

QY 461 KELVNGOCHDCLPEHNGSLNDLQCRPCDDCLGGALNNSCPAESQCSRCRPHMIGROCN 520  
DB 421 KELVNGOCHDCLPEHNGSLNDLQCRPCDDCLGGALNNSCPAESQCSRCRPHMIGROCN 480

QY 521 EYEPGYFATLDHYLAEAEANLPGVSIYERQYIQRIPSWTGAQFVRPVGAYLEFFI 580  
DB 481 EYEPGYFATLDHYLAEAEANLPGVSIYERQYIQRIPSWTGAQFVRPVGAYLEFFI 540

QY 581 DNIPIYSMEVDILIRYEPOLPDHWEKAVITVORPGRPTSRRCQNTIPDDNQNVSLSPGS 640  
DB 541 DNIPIYSMEVDILIRYEPOLPDHWEKAVITVORPGRPTSRRCQNTIPDDNQNVSLSPGS 600

QY 641 RYVVLPRVCEKGNVTYRLELQYTSSDSVESPYTLIDSLVLMFYCKSLDIFTVGGS 700  
DB 601 RYVVLPRVCEKGNVTYRLELQYTSSDSVESPYTLIDSLVLMFYCKSLDIFTVGGS 660

QY 701 GGVVNTSAWETFORYRCLNSRSVWKTMTDVCNRIIFSIALLHOTGLACECDPOGSL 760  
DB 661 GGVVNTSAWETFORYRCLNSRSVWKTMTDVCNRIIFSIALLHOTGLACECDPOGSL 720

QY 761 SSVCDPNGGQCCRPVNVGRTCNRCAPGTFGFGPSGCKPCBCHLQGSVNAFCNFTVGOCH 820  
DB 721 SSVCDPNGGQCCRPVNVGRTCNRCAPGTFGFGPSGCKPCBCHLQGSVNAFCNFTVGOCH 780

QY 821 CFQGYVYARQCDRLCPGHWGFPSCQPCQNGHADDCTVGTGECNLCNCDYTMGHNCERCLAG 880  
DB 781 CFQGYVYARQCDRLCPGHWGFPSCQPCQNGHADDCTVGTGECNLCNCDYTMGHNCERCLAG 840

QY 881 YVGDPIIGSDHCRPCPCDPSDGRFARSCVDPTVTLQACVCPGVIGSRCDCAAG 940  
DB 841 YVGDPIIGSDHCRPCPCDPSDGRFARSCVDPTVTLQACVCPGVIGSRCDCAAG 900

QY 941 YFNGPSEVSGSQPCQCHNNITDTPDPAKDKETGRCLKCLYHTEGHCQFCRFGYGDAL 1000  
DB 901 YFNGPSEVSGSQPCQCHNNITDTPDPAKDKETGRCLKCLYHTEGHCQFCRFGYGDAL 960

QY 1001 RODCRKVCNVLGTVOEHNCNSGDCOCKATGQCLCLPNVIGONCDRCAPNTWOLASGTGC 1060  
DB 961 RODCRKVCNVLGTVOEHNCNSGDCOCKATGQCLCLPNVIGONCDRCAPNTWOLASGTGC 1020

## RESULT 8

US-10-443-349-4

; Sequence 4, Application US/10443349

; Publication No. US20040023856A1

; GENERAL INFORMATION:

; APPLICANT: Burgeson, Robert E.

; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE

; FILE REFERENCE: 10287/021003

; CURRENT FILING DATE: 2003-05-22

; PRIOR FILING DATE: 1998-09-28

; PRIOR FILING DATE: 1998-09-28

; PRIOR FILING DATE: 1996-10-23

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1196

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (1)...(250)

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; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (251)...(437)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (438)...(807)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (808)...(840)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (841)...(1196)
; OTHER INFORMATION: Human B1 chain
; US-10-443-349-4

Query Match      62.6%; Score 6044.5; DB 16; Length 1196;
Best Local Similarity 67.6%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;

QY 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIYSHLQEDKKCFICN 59
DB 1 QPEFSYGCAGSCYPATGDLIGRAQKLSVTSITCG-LHKPEPYCIYSHLQEDKKCFICN 60
QY 60 SODPHETLNPSHLIENVTTFAPNRLKIWQSENGVENVTIOGLDEAEFPHFLIMTF 119
DB 61 SODPHETLNPSHLIENVTTFAPNRLKIWQSENGVENVTIOGLDEAEFPHFLIMTF 120
QY 120 KTFRAAAMLIERSDFGTGWYRYFAYDCEASFFGISTGPMKKVDDIIICDSRYSDIEPS 179
DB 121 KTFRAAAMLIERSDFGTGWYRYFAYDCEASFFGISTGPMKKVDDIIICDSRYSDIEPS 180
QY 180 TEGEVI FRALDPAFKIEPYSPRIQNLKLTNLRKFVKLHTGLGNLDSRMEIREKYY 239
DB 181 TEGEVI FRALDPAFKIEPYSPRIQNLKLTNLRKFVKLHTGLGNLDSRMEIREKYY 240
QY 240 AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGVHGHCMCRHNTKGLNCLMDFYHDL 299
DB 241 AVYDMVVRGNCFCYGHASECAPVDGFNEEVEGVHGHCMCRHNTKGLNCLMDFYHDL 300
QY 300 WPAEGRNSNACKCNNEHSISCHFDMAVLTATGNVSGVCCDCHQNTWGRNCEQCKPF 359
DB 301 WPAEGRNSNACKCNNEHSISCHFDMAVLTATGNVSGVCCDCHQNTWGRNCEQCKPF 360
QY 360 YYQHPERDIRDPNFCERTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVC 419
DB 361 YYQHPERDIRDPNFCERTCDPAGSQNEGICDSYTFSTGLIAGQCRCKLNVEGEHCDVC 420
QY 420 KEGFYDLASEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTSQHCQCLPERHGL 479
DB 421 KEGFYDLASEDPFGCKS----- 437
QY 480 SNDLDCRCPDCDGLGALNNSCFABSGQSCRPMMIGRQCNVEPYPATLDHYLYAE 539
DB 438 ----- 437
QY 540 EANLPGVSIYERQIQDIRIPSWTCAGFVRVPEGAYLEFFIDNIPYSMEYDILLIRYEPQL 599
DB 438 ----- 437
QY 600 PDHWEKAVITVQRPGRIPTSRCGNTPDDDNQVWSLSPGSRYYVLPFRPVCFEKGNYTV 659
DB 438 ----- 437
QY 660 RLELPQYTSDDSVESPYTLIDSLVLMYPCKSLDIFTVGGSGDGVWINSAWETFORYRCL 719
DB 438 ----- 437
QY 720 ENSRSVVKTPMTDVCRNIIIFISALLHOTGLACECDPQGLSSVCDPNGGQCCQCRPNVNG 779

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DB 438 ----- 437
QY 780 RTNRCAPGTFGFGPSGCKPECHLQGSVNAFCNPVTGQCHCFQGVYARQCDRLPQHWG 839
DB 438 ----- 437
QY 840 PFCQPCQCNHADDCDPVTGECLNCQDYMTHNCERCLAGYVGDPIIGSGDHCRCPCPCP 899
DB 438 ----- 437
QY 900 DGPDSGRPARSCYQDPVTIQLACVCDPGYIGSRCDCCASGYFNGPSEVGSGCQPCQCHN 959
DB 438 ----- 437
QY 960 NIDTTPCADKERTGRCLKLYHTEGHEHCQFCRFGYGDALRQDRCRKCVCNLYGTVOEHC 1019
DB 438 ----- CVCNLYGTVOEHC 450
QY 1020 NGSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFT 1079
DB 451 NGSDCCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPGSCNEFT 510
QY 1080 QCCQMPFGGRTCSHCQELFWGDPDVECRACDPRGIEPTQCDQSTGQCVGVEGVP 1139
DB 511 QCCQMPFGGRTCSHCQELFWGDPDVECRACDPRGIEPTQCDQSTGQCVGVEGVP 570
QY 1140 RCDKTRGYSVFPDCTPCHQCPALMDVIIAELTNRTHRELEKAKALKISGIVGPYRETV 1199
DB 571 RCDKTRGYSVFPDCTPCHQCPALMDVIIAELTNRTHRELEKAKALKISGIVGPYRETV 630
QY 1200 DSVRKYSEIKDIIAQSAPAAEPLKNIGNLPEEAELIKOVTEMAQVEVKLSDTTQSNS 1259
DB 631 DSVRKYSEIKDIIAQSAPAAEPLKNIGNLPEEAELIKOVTEMAQVEVKLSDTTQSNS 690
QY 1260 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVASTT 1319
DB 691 TAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVASTT 750
QY 1320 EPNSTVEQSALMRDVRDVMERESQFKEQEQAALDELALAGKLSLDLSAAAEVTCGT 1379
DB 751 EPNSTVEQSALMRDVRDVMERESQFKEQEQAALDELALAGKLSLDLSAAAEVTCGT 810
QY 1380 PPGASCSETCGGNCRTDGERKCGGPGGGLVTVVAHNAWOKAMDLDQDVLALAEVEQ 1439
DB 811 PPGASCSETCGGNCRTDGERKCGGPGGGLVTVVAHNAWOKAMDLDQDVLALAEVEQ 870
QY 1440 LSKWVSEAKLRADBAKQSAEDILLKTNATKEXMDKNEELRNLIKOIRNFLTQDSADLDS 1499
DB 871 LSKWVSEAKLRADBAKQSAEDILLKTNATKEXMDKNEELRNLIKOIRNFLTQDSADLDS 930
QY 1500 IEAVANEVLKXEMPSPTQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEAEKR 1559
DB 931 IEAVANEVLKXEMPSPTQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEAEKR 990
QY 1560 ASKATDVKTADVMKALBEAEKAQVAABKAIKQADEDIQGTQNLTTSEETAASEET 1619
DB 991 ASKATDVKTADVMKALBEAEKAQVAABKAIKQADEDIQGTQNLTTSEETAASEET 1050
QY 1620 LFNASQRISELERNVBELKRAQNGSEAEYIEKVYTVTKQSAEDVKKTLDGELDEKYYK 1679
DB 1051 LFNASQRISELERNVBELKRAQNGSEAEYIEKVYTVTKQSAEDVKKTLDGELDEKYYK 1110
QY 1680 VENLIAKTTESADARKAEMLQNEAKTLIAQNSKLQLLKDLERYEDNQRYLEDKQAE 1739
DB 1111 VENLIAKTTESADARKAEMLQNEAKTLIAQNSKLQLLKDLERYEDNQRYLEDKQAE 1170
QY 1740 LARLEGEVRSLLKXDISOKVAVYSTCL 1765
DB 1171 LARLEGEVRSLLKXDISOKVAVYSTCL 1196

```

RESULT 9  
US-09-938-275-8

Sequence 8, Application US/09938275  
Patent No. US20020111309A1  
GENERAL INFORMATION:  
APPLICANT: Gerardo Castillo  
APPLICANT: Alan Snow  
TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
FILE REFERENCE: PROTEO.P03  
CURRENT APPLICATION NUMBER: US/09/938,275  
CURRENT FILING DATE: 2001-08-16  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 1801  
TYPE: PRT  
ORGANISM: Rattus No. U920020111309Alveigicus  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: Swissprot P15800  
DATABASE ENTRY DATE: 1990-04-01  
US-09-938-275-8

Query Match 52.7%; Score 5084; DB 9; Length 1801;  
Best Local Similarity 51.5%; Pred. No. 2.9e-280;  
Matches 910; Conservative 303; Mismatches 534; Indels 20; Gaps 8;

QY 8 GCAGSCYPATGDLILIGRAOKLSTVSTCGLHKPEPYCIIVSHLQEDKKCFICNSQDPYHET 67  
DB 44 GCSGSCYPATGDLILIGRAOKLSTVSTCGLHKPEPYCIIVSHLQEDKKCFICNSQDPYHET 103

QY 68 LNPDSHLIENVVTFAPNRUKIKWQSENGVENVTIQLDEAFHFTHLIMTKTPRPAAM 127  
DB 104 DNPNSHRIQNVVTFAPNRUKIKWQSENGVENVTIQLDEAFHFTHLIMTKTPRPAAM 163

QY 128 LIERSDFGKWTGVYFAYDCASPGIISTGPMKVVDDIICDSRYSDIETPSTEGEVIFR 187  
DB 164 LVESADFGRTWYRVFSDGADPGIPLAPRWDVDCESRYSEIETPSTEGEVIFR 223

QY 188 ALDPAFKIEDPYSPRIQNLKIKTNLRIKFKVHLTGONLLDSRMEIREKYYIYAVDMVR 247  
DB 224 VLDPAIPDPYSSRIQNLKIKTNLRIKFKVHLTGONLLDSRMEIREKYYIYAVDMVR 283

QY 248 GNCFCYGHASECAPVDGNEVEGWHGCMCHRNKGLNCLMDPFYHDLFWPABGRN 307  
DB 284 GNCFCYGHASECAPVDGNEVEGWHGCMCHRNKGLNCLMDPFYHDLFWPABGRN 343

QY 308 SNACKKCNHSHSIFDFMAVYLATGNVSGVCDCCQNTWGRNCEQCKPFIYHPERD 367  
DB 344 THACKKCEGNHSHSIFDFMAVYLATGNVSGVCDCCQNTWGRNCEQCKPFIYHPERD 403

QY 368 IRDENFCERTCDPAGONEGICDSYDTSTGLIAGQCKKLNVEGEHCDVCKEGFYDLS 427  
DB 404 MEDPAAACPCDCDPMGSDGGRCDSDHDDPVLGLVSGQCKKEHVYVTRCQCCRDGFFGLS 463

QY 428 SEDPFGCKSCNPLGTHPGNCDSDSETGHCYCKRLVTGQCDQCLPHEWGLSNDLDCR 487  
DB 464 ASNPRGQRCQCNRSRGTVPGGTFCCKRLVTGQCDQCLPHEWGLSNDLDCR 523

QY 488 PCDCDLGALNNSCFABSGQSCRPIMIGRCQNEVEPGYVFATLDHLYLAEANLPGV 547  
DB 524 PCDCDLGALNNSCFABSGQSCRPIMIGRCQNEVEPGYVFATLDHLYLAEANLPGV 582

QY 548 SIVERQVQDRIPSWTCAGTVPEGAYLEFFIDNTPYSMEYDILIRYEPOLPDWEKAV 607  
DB 593 EVVERLVNRETPTSWTGVFRLEGEVEFLVSLDPRAWDYLLEWEPQVPEQWASLE 642

QY 608 ITVQPRGRIPTSSRCGNTIPDDNQVVSLSPGSRVYVLPVPCFEKGTNTYVRLPQYT 667  
DB 643 LVQRPQGVSAHSPCGHVLPRDRIQGLMHPNTRVLVPRPVCLEPGLSKLKLXTG-T 701

QY 668 SSDSDVESPT-LLDSLVLPYCKSLDIFTVGGSGGVWTSNAWETFORVCLNSR 723  
DB 702 GGRAPHPETPYSGGILLIDSLVLPYCKSLDIFTVGGSGGVWTSNAWETFORVCLNSR 757

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 16.2434 Seconds

(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-8

Perfect score: 9654

Sequence: 1 QEPFESYGAEGSCYPATGD.....EVRSLKDISQVAVYSTCL 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: pirl:\*

2: pirl2:\*

3: pirl3:\*

4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9654	100.0	1786	1 MMHUB1	laminin beta-1 cha
2	9092	94.2	1786	1 MMMSB1	laminin beta-1 cha
3	5084	52.7	1801	1 MMRTS	laminin beta-2 cha
4	5050	52.3	1798	2 S53869	laminin beta-2 cha
5	4884.5	50.6	1797	2 A55677	laminin beta-2 cha
6	3844.5	39.8	1790	1 MMFBE1	laminin beta-1 cha
7	3765	39.0	1808	2 T15099	hypothetical prote
8	1755	18.2	1639	1 MMFBE2	laminin gamma-1 ch
9	1729.5	17.9	3672	2 T23433	hypothetical prote
10	1729.5	17.9	3704	2 T37316	probable laminin a
11	1696.5	17.6	1557	2 T28811	hypothetical prote
12	1676.5	17.4	1609	1 MMHUB2	laminin gamma-1 ch
13	1653	17.1	1607	1 MMMSB2	laminin gamma-1 ch
14	1637	17.0	3712	2 S18253	laminin alpha-1 ch
15	1605	16.6	3635	2 T10053	laminin alpha 5 ch
16	1583	16.4	303	2 B45067	laminin B1 chain -
17	1538.5	15.9	1170	2 A53612	laminin B1 chain
18	1535.5	15.9	3106	1 S53868	laminin alpha-2 ch
19	1525	15.8	3075	2 S14458	laminin alpha-1 ch
20	1507.5	15.6	3084	1 MMMSA	laminin alpha-1 ch
21	1485.5	15.4	1168	2 T56885	kalinin B1 - mouse
22	1307.5	13.5	2823	2 T23064	hypothetical prote
23	1307.5	13.5	2823	2 F87908	protein T2A3.8 li
24	1307.5	13.5	3102	2 T43291	laminin alpha cha
25	1001.5	10.4	616	2 I38231	S-laminin - human
26	871	9.0	1193	2 A44018	laminin B2t chain
27	862.5	8.9	1192	2 S69000	laminin gamma 2 ch
28	690.5	7.2	606	2 A54665	netrin-1 precursor
29	679	7.0	1620	2 T27283	hypothetical prote

30 669.5 6.9 1574 2 T13954  
31 666 6.9 3707 2 S18252  
32 663.5 6.9 1111 2 T26972  
33 657 6.8 4391 2 A38096  
34 600 6.2 581 2 B54665  
35 580.5 6.0 1816 1 S68960  
36 579 6.0 612 2 JH0799  
37 577.5 6.0 1751 1 MMHUMH  
38 568 5.9 400 2 T46383  
39 527 5.5 2555 2 A40043  
40 526 5.4 2295 2 C83369  
41 526 5.4 2375 2 T19821  
42 523 5.4 1160 2 F88369  
43 511 5.3 198 2 A45067  
44 509 5.3 2524 2 A35844  
45 506.5 5.2 2703 1 A24420

#### ALIGNMENTS

##### RESULT 1

MMHUB1

laminin beta-1 chain precursor - human

N:Alternate names: laminin chain B1

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1991 #sequence, revision 30-Jun-1991 #text\_change 19-Jan-2001

C:Accession: S13547; A28483; A26994; S29566

R:Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.

J. Biol. Chem. 265, 15611-15616, 1990

A>Title: Structure of the human laminin B1 chain gene.

A:Reference number: S13547; MUID:90368768; PMID:1975589

A:Accession: S13547

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1786 <VUO>

A:Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

A>Note: the nucleotide sequence was submitted to GenBank, February 1991

R:Piikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Sar

J. Biol. Chem. 262, 10454-10462, 1987

A>Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q

A:Reference number: A28483; MUID:87280097; PMID:3611077

A:Accession: A28483

A:Molecule type: mRNA

A:Residues: 1-1786 <PIK>

A:Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913

R:Jaya, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.

Am. J. Hum. Genet. 41, 605-615, 1987

A>Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localiza

A:Reference number: A26994; MUID:88021029; PMID:3661559

A:Accession: A26994

A:Molecule type: mRNA

A:Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>

A:Cross-references: EMBL:IM20206; NID:G186914; PIDN:AAA59487.1; PID:G186915

R:Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Piikkarainen, T.; Tryggvason, K.

in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic

A>Title: Genes for the human laminin B1 and B2 chains.

A:Reference number: S23566

A:Accession: S23566

A:Molecule type: DNA

A:Residues: 762-1786 <VUO>

A>Note: mRNA was also sequenced

C:Genetics:

A:Gene: GDB:LAMB1

A:Cross-references: GDB:119357; OMIM:150240

A:Map position: 7q31.1-7q31.3

A:Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 5

64/3; 1513/1; 1582/2; 1629/3; 1686/3; 1742/1

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type BGP-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular



F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>  
 F:22-270/Domain: VI <DOM6>  
 F:271-548/Domain: V <DOM5>  
 F:271-332/Domain: laminin-type EGF-like homology <LE01>  
 F:335-395/Domain: laminin-type EGF-like homology <LE02>  
 F:398-455/Domain: laminin-type EGF-like homology <LE03>  
 F:458-507/Domain: laminin-type EGF-like homology <LE04>  
 F:463-468/Region: cell adhesion #status predicted  
 F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F:548-774/Domain: IV <DOM4>  
 F:568-668/Region: cell adhesion #status predicted  
 F:773-818/Domain: laminin-type EGF-like homology <LE06>  
 F:775-1178/Domain: III <DOM3>  
 F:821-864/Domain: laminin-type EGF-like homology <LE07>  
 F:867-914/Domain: laminin-type EGF-like homology <LE08>  
 F:917-973/Domain: laminin-type EGF-like homology <LE09>  
 F:923-927/Region: cell adhesion #status predicted  
 F:950-954/Region: cell adhesion #status predicted  
 F:976-1025/Domain: laminin-type EGF-like homology <LE10>  
 F:1028-1081/Domain: laminin-type EGF-like homology <LE11>  
 F:1084-1129/Domain: laminin-type EGF-like homology <LE12>  
 F:1132-1176/Domain: laminin-type EGF-like homology <LE13>  
 F:1179-1397/Domain: II <DOM2>  
 F:1179-1397/Region: heptad repeats  
 F:1398-1430/Domain: alpha <ALP>  
 F:1431-1786/Domain: I <DOM1>  
 F:1431-1786/Region: heptad repeats  
 F:130-357/Disulfide bonds: #status Predicted  
 F:120,356,519,577,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate  
 F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 9654; DB 1; Length 1786;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QEPFSGYAGSGCYPATGDLIGRAQKLSVTSTGLHKPEPYCVSHVQEDKFCFNS	60
Db	22	QEPFSGYAGSGCYPATGDLIGRAQKLSVTSTGLHKPEPYCVSHVQEDKFCFNS	81
Qy	61	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGENVVITQLDLAEFPHTHLIMTFK	120
Db	82	QDPVHETLNPDSHLIENVVTFAPNRLKIWQSENGENVVITQLDLAEFPHTHLIMTFK	141
Qy	121	TFRPAAMLIERSSDFGTWGYRYFAYDCEASPGISTGPMKKVDDIICDSRYSDIEPST	180
Db	142	TFRPAAMLIERSSDFGTWGYRYFAYDCEASPGISTGPMKKVDDIICDSRYSDIEPST	201
Qy	181	EGEVI FRALDPAPKIEDPYSPRIQNLKITNLRIKFKVLHTIGDNLDSRMEIREKYTA	240
Db	202	EGEVI FRALDPAPKIEDPYSPRIQNLKITNLRIKFKVLHTIGDNLDSRMEIREKYTA	261
Qy	241	YDMVVRGNCFCYGHASECAPVDGFNEVEGVMVGHGCMCRHNTKGLNCELMDPFYHDLWP	300
Db	262	YDMVVRGNCFCYGHASECAPVDGFNEVEGVMVGHGCMCRHNTKGLNCELMDPFYHDLWP	321
Qy	301	RPAGRNACKKNCNEHSISCHFDMAVYATATGNSVGGVCDCCQNTWGRNCECKPFY	360
Db	322	RPAGRNACKKNCNEHSISCHFDMAVYATATGNSVGGVCDCCQNTWGRNCECKPFY	381
Qy	361	YQHPERDIRPNCERTCTDPAGSQNEGICDSYTFDSTGLIAGQCRKLNVEGEHCYCK	420
Db	382	YQHPERDIRPNCERTCTDPAGSQNEGICDSYTFDSTGLIAGQCRKLNVEGEHCYCK	441
Qy	421	EGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETHCYCKELVTGQHCDOCLPEHWGLS	480
Db	442	EGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETHCYCKELVTGQHCDOCLPEHWGLS	501
Qy	481	NLDGCRPCDCDGLGALNNSCFASQCCSRPHMGRQCNVEPGYYPATLDHYLYEABE	540
Db	502	NLDGCRPCDCDGLGALNNSCFASQCCSRPHMGRQCNVEPGYYPATLDHYLYEABE	561
Qy	541	ANLPGVSVIVERQVIQDRIPSWTGAGFVRVPSGAVLEFIDNIPSYMEYDILIRYEPOLP	600

Db	562	ANLPGVSVIVERQVIQDRIPSWTGAGFVRVPSGAVLEFIDNIPSYMEYDILIRYEPOLP	621
Qy	601	DHWEKAVITVQREGRIPTSRGNTIPDDDNQVSVLSPGSRVVLPRPVPCEPKGNTYVR	660
Db	622	DHWEKAVITVQREGRIPTSRGNTIPDDDNQVSVLSPGSRVVLPRPVPCEPKGNTYVR	681
Qy	661	LELPQVTSDDSDVESYTTIDSLVLMYPYCKSLDITFVGGSGDGVVTVNSAWETFYRCL	720
Db	682	LELPQVTSDDSDVESYTTIDSLVLMYPYCKSLDITFVGGSGDGVVTVNSAWETFYRCL	741
Qy	721	NSRSVVKTPMTDVCNRIIFSIALLHQTGLACEDCPQGSLSVCDPNGGQCCQCRNVVGR	780
Db	742	NSRSVVKTPMTDVCNRIIFSIALLHQTGLACEDCPQGSLSVCDPNGGQCCQCRNVVGR	801
Qy	781	TCNRCAPGTGFGPSPCKCECHLQGSVNAFCNPTVGTQCHQCHQGYARQCDCLPCHWGF	840
Db	802	TCNRCAPGTGFGPSPCKCECHLQGSVNAFCNPTVGTQCHQCHQGYARQCDCLPCHWGF	861
Qy	841	PSQPCQCNHADDCCDPTVTEGCLNCQDVTMGNHCERCLAGYGGDPIIGSGDHCRCPCPD	900
Db	862	PSQPCQCNHADDCCDPTVTEGCLNCQDVTMGNHCERCLAGYGGDPIIGSGDHCRCPCPD	921
Qy	901	GPDSGRQFARSCYQDPTVITQLACVCDPGYIGSRCDGAGYGNPSEVGGSCQPCCHNN	960
Db	922	GPDSGRQFARSCYQDPTVITQLACVCDPGYIGSRCDGAGYGNPSEVGGSCQPCCHNN	981
Qy	961	IDTTPDPAACDKETGRCLKCLYHTEGHCQFCRFYGGYDALRQDCRCKVCNYLGTVQECN	1020
Db	982	IDTTPDPAACDKETGRCLKCLYHTEGHCQFCRFYGGYDALRQDCRCKVCNYLGTVQECN	1041
Qy	1021	GSQCCQDKATGQCLPNNVIGQNCRCAPNTWQASGTCPCNCAHSPGSCNFTG	1080
Db	1042	GSQCCQDKATGQCLPNNVIGQNCRCAPNTWQASGTCPCNCAHSPGSCNFTG	1101
Qy	1081	QCCMFPFGRTCSBQELFWGDDPVECRACDPCDPRGIETPCCQSTQCCVCEVGEZPR	1140
Db	1102	QCCMFPFGRTCSBQELFWGDDPVECRACDPCDPRGIETPCCQSTQCCVCEVGEZPR	1161
Qy	1141	CDKCTGYSVGPDPCTPCHQCFALWDVIAELTNTRHFLKAKALKISGIVGYRETVD	1200
Db	1162	CDKCTGYSVGPDPCTPCHQCFALWDVIAELTNTRHFLKAKALKISGIVGYRETVD	1221
Qy	1201	SVERKYSBKIDILASQAPAAEPLKNTGNLFEBEAKLIKDVTEMMAQVEVKLSQSTNS	1260
Db	1222	SVERKYSBKIDILASQAPAAEPLKNTGNLFEBEAKLIKDVTEMMAQVEVKLSQSTNS	1281
Qy	1261	AKELDSLOTAEASLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERVNAS	1320
Db	1282	AKELDSLOTAEASLNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABERVNAS	1341
Qy	1321	PNSVTEQSALMDRVEDVNMERESQFKQBEQARLDELAKGLQSLDLSAAEMTCGTP	1380
Db	1342	PNSVTEQSALMDRVEDVNMERESQFKQBEQARLDELAKGLQSLDLSAAEMTCGTP	1401
Qy	1381	PGASCSETECGGPNCRDTEGERKCGGCGGLVTVAHNAWQKAMDLDODVLSALAEVQL	1440
Db	1402	PGASCSETECGGPNCRDTEGERKCGGCGGLVTVAHNAWQKAMDLDODVLSALAEVQL	1461
Qy	1441	SKWSEAKLRADEAKQSAEDILLKTNATKQKMSNEELNLIKQIRNFLTQDSADLDSI	1500
Db	1462	SKWSEAKLRADEAKQSAEDILLKTNATKQKMSNEELNLIKQIRNFLTQDSADLDSI	1521
Qy	1501	EAVANEVLKQVEMPTPQQLQNLITEDIRVERVESLSQVEVILQHSAAIDARAEMLLEAKRA	1560
Db	1522	EAVANEVLKQVEMPTPQQLQNLITEDIRVERVESLSQVEVILQHSAAIDARAEMLLEAKRA	1581
Qy	1561	SKSATDVKTADMKVEALEEAKQAABEAKIQAEDDIQGTQNLITSISETAASETL	1620
Db	1582	SKSATDVKTADMKVEALEEAKQAABEAKIQAEDDIQGTQNLITSISETAASETL	1641
Qy	1621	FNASORISELENNBELKRAQNSGEAFYIEKVYVTVKQSAEDVKKTLDELDEKTKV	1680

Db 1642 FNASQRISELRNVEELKKAAQNGEAEYIEKVTVVTKQSAEDVKKTLDELDEKVKV 1701

QY 1691 ENLIAKTESADARRKAEMLQNEAKTLQAQNSKLQLKDLERYEDNQRYLEDKQAE 1740  
|||||

Db 1702 ENLIAKTESADARRKAEMLQNEAKTLQAQNSKLQLKDLERYEDNQRYLEDKQAE 1761  
|||||

QY 1741 ARLEGEVRLLKDISQKAVYVSTCL 1765  
|||||

Db 1762 ARLEGEVRLLKDISQKAVYVSTCL 1786  
|||||

RESULT 2

MMMSB1

N; Alternates names: laminin chain B1

C; Species: Mus musculus (house mouse)

C; Date: 28-Feb-1986 #sequence revision 30-Jun-1991 #text change 10-Dec-1999

C; Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543

R; Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.

Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987

A; Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein

A; Reference number: A26413; MUID:87147212; PMID:3493487

A; Accession: A26413

A; Molecule type: mRNA

A; Residues: 1-1786 <SAS>

A; Cross-references: EMBL:M15525; NID:G198700

A; Note: translation in Genbank has additional 48 residues at the amino end

R; Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A; Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A; Reference number: S02678; MUID:88326259; PMID:2458101

A; Accession: S02679

A; Molecule type: protein

A; Residues: 28-42; 932-946 <FUJ>

R; Hartl, L.; Oberbaumer, I.; Deutzmann, R.

Eur. J. Biochem. 173, 629-635, 1988

A; Title: The N terminus of laminin A chain is homologous to the B chains.

A; Reference number: S00624; MUID:88225080; PMID:3267223

A; Accession: S05326

A; Molecule type: protein

A; Residues: 457-466; 854-868; 932-946 <HAR>

R; Mann, K.; Deutzmann, R.; Timpl, R.

Eur. J. Biochem. 178, 71-80, 1988

A; Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th

A; Reference number: S08895; MUID:89078415; PMID:2462498

A; Accession: S14877

A; Molecule type: protein

A; Residues: 590-620 <MAN>

R; Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.

EMBO J. 3, 2355-2362, 1984

A; Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a

A; Reference number: A02870; MUID:85051302; PMID:6209134

A; Accession: A02871

A; Molecule type: mRNA

A; Residues: 1293-1530, 'MEMP', 1535-1591, 'C', 1693-1748, 'N', 1750-1786 <BAR>

A; Cross-references: EMBL:X05212; NID:G52861; PIDN:CAA28839.1; PID:G809042

R; Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988

A; Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te

A; Reference number: S01790; MUID:89030693; PMID:3181157

A; Accession: S02036

A; Molecule type: protein

A; Residues: 1561-1597 <DEU>

R; Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalozzo, D.; Odermatt, E.; Engel, J.

EMBO J. 4, 309-316, 1985

A; Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.

A; Reference number: S13543; MUID:86257455; PMID:3848400

A; Accession: S13543

A; Molecule type: protein

A; Residues: 1700-1748, 'N', 1750-1759 <PAU>

C; Genetics:

A; Gene: Lamb-1

A; Map position: 12

C; Complex: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C; Function:

A; Description: interact with cells and with other basement membrane proteins to promote

C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C; Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F; 1-21/Domain: signal sequence #status predicted <SIG>

F; 22-1786/Product: laminin beta-1 chain #status predicted <MAT>

F; 22-270/Domain: VI <DOM6>

F; 271-540/Domain: V <DOM5>

F; 271-332/Domain: laminin-type EGF-like homology <LE01>

F; 335-395/Domain: laminin-type EGF-like homology <LE02>

F; 398-455/Domain: laminin-type EGF-like homology <LE03>

F; 458-507/Domain: laminin-type EGF-like homology <LE04>

F; 510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>

F; 541-772/Domain: IV <DOM4>

F; 773-1182/Domain: III <DOM3>

F; 773-818/Domain: laminin-type EGF-like homology <LE06>

F; 821-864/Domain: laminin-type EGF-like homology <LE07>

F; 867-914/Domain: laminin-type EGF-like homology <LE08>

F; 917-973/Domain: laminin-type EGF-like homology <LE09>

F; 976-1025/Domain: laminin-type EGF-like homology <LE10>

F; 1028-1081/Domain: laminin-type EGF-like homology <LE11>

F; 1084-1129/Domain: laminin-type EGF-like homology <LE12>

F; 1132-1176/Domain: laminin-type EGF-like homology <LE13>

F; 1183-1397/Domain: II <DOM2>

F; 1183-1397/Region: heptad repeats

F; 1398-1430/Domain: alpha <ALP>

F; 1431-1786/Domain: I <DOM1>

F; 22/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted

F; 30-35/Disulfide bonds: #status predicted

F; 120, 356, 519, 677, 1041, 1195, 1279, 1336, 1343, 1487, 1533, 1542, 1643/Binding site: carbohydrate

F; 1179, 1182, 1785/Disulfide bonds: interchain #status predicted

Query Match 94.2%; Score 9092; DB 1; Length 1786;

Best Local Similarity 93.0%; Pred. No. 0;

Matches 1642; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

QY 1 QEPFSGYGCAGSCYVATGDLIGRAOKLSVTSTGLHKPEPYCIIVSHLOEDKKCFICNS 60  
|||||

Db 22 QEPFSGYGCAGSCYVATGDLIGRAOKLSVTSTGLHKPEPYCIIVSHLOEDKKCFICDS 81  
|||||

QY 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGENVTIQDLLEAEHFHLLMTFK 120  
|||||

Db 82 RDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGENVTIQDLLEAEHFHLLMTFK 141  
|||||

QY 121 TFRPAAMLIERSPPGKTGWYRYFAYDCEASFPSTGPMKKVDDIICDSRYSDIEPST 180  
|||||

Db 142 TFRPAAMLIERSPPGKTGWYRYFAYDCEASFPSTGPMKKVDDIICDSRYSDIEPST 201  
|||||

QY 181 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYIYA 240  
|||||

Db 202 EGEVIFRALDPAFKIEDPYSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYIYA 261  
|||||

QY 241 VYDMVVRGNCFCYGHASCAPVDGFEVEGVHGHQCRHNTKGLNCELMDPFYHDLPW 300  
|||||

Db 262 VYDMVVRGNCFCYGHASCAPVDGFEVEGVHGHQCRHNTKGLNCELMDPFYHDLPW 321  
|||||

QY 301 RPAEGRNACKNCNEHSTCHDFMAVILATGNSGGVCDCCQHTMGRCNEQCKPFY 360  
|||||

Db 322 RPAEGRNACKNCNEHSSCHDFMAVILATGNSGGVCDCCQHTMGRCNEQCKPFY 381  
|||||

QY 361 YQHPERDIRDPNFCERTCTDPAGSQNEGICDSTYDFSTGLIAGQCRKLVNVEGHCDCVCK 420  
|||||

Db 382 FQHPERDIRDPNFCERTCTDPAGSQNEGICDSTYDFSTGLIAGQCRKLVNVEGHCDCVCK 441  
|||||

QY 421 EGFYDLSSDFPGCKSCACPLGTIPGNGPCDSETHCYCKRLVTGQHCDCQCLPEHGLS 480  
|||||

Db 442 EGFYDLSSDFPGCKSCACPLGTIPGNGPCDSETHCYCKRLVTGQHCDCQCLPEHGLS 501  
|||||

QY 481 NDLDGCRPCDCDLGALNNSCFASGQSCSRPMIGRCQNEVPFGYFATLDHYLVEAE 540  
|||||

Db 502 NDLDGCRPCDCDLGALNNSCFASGQSCSRPMIGRCQNEVPFGYFATLDHYLVEAE 561  
|||||

QY 541 ANLGPGVSVIRQVYIODRIPSWTQAGFVRVPEGAAYLEFFIDNIPYMEVDILLIRPEPOLP 600  
DB 542 ANLGPGVSVIRQVYIODRIPSWTQAGFVRVPEGAAYLEFFIDNIPYMEVDILLIRPEPOLP 621  
QY 601 DHWEKAVITVQRPGRIPSSRCGNTIPDDNQVVSLSFGSRVYVVLPRPVCFFKGNVTVR 660  
DB 602 DHWEKAVITVQRPGRIPSSRCGNTIPDDNQVVSLSFGSRVYVVLPRPVCFFKGNVTVR 681  
QY 661 LELPQYTSDDSVSPYTLIDSLVMPYCKSLDIFVGGSGDGVNTNSAWETFORYRCLE 720  
DB 662 LELPQYTSDDSVSPYTLIDSLVMPYCKSLDIFVGGSGDGVNTNSAWETFORYRCLE 741  
QY 721 NSRSVVTPTMTDVCNRIIFISALLHQTGLACEDCPQGSLSVSCDPPNGQCCRCRPNVWGR 780  
DB 742 NSRSVVTPTMTDVCNRIIFISALLHQTGLACEDCPQGSLSVSCDPPNGQCCRCRPNVWGR 801  
QY 781 TCNRCAPGTGFGSGCKPECHLOGSVNAPNPVTGCHCQGVYARCDCLPHWGF 840  
DB 802 TCNRCAPGTGFGSGCKPECHLOGSVNAPNPVTGCHCQGVYARCDCLPHWGF 861  
QY 841 PSCQPCQCNHADDPCDPTVTECLNQCQDYTMGHNCERCLAGYTGDPITIGSGDRCRCPCPD 900  
DB 862 PSCQPCQCNHADDPCDPTVTECLNQCQDYTMGHNCERCLAGYTGDPITIGSGDRCRCPCPD 921  
QY 901 GPDGROFARSCYODPVTLQACVCPGYIGSCDPCASGYGNSPSEVGGSCQPCCHN 960  
DB 922 GPDGROFARSCYODPVTLQACVCPGYIGSCDPCASGYGNSPSEVGGSCQPCCHN 981  
QY 961 IDTTDPEACDKTGRCLKCLYHTEGHCQFCRFGYGDALRQDCRCKVCNVLGTVEHCN 1020  
DB 982 IDTTDPEACDKTGRCLKCLYHTEGHCQFCRFGYGDALRQDCRCKVCNVLGTVEHCN 1041  
QY 1021 GSDCQCKATGOCCLCNVIGQNCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNFTG 1080  
DB 1042 GSDCQCKATGOCCLCNVIGQNCRCAPNTWQLASGTGCDPCNCAHSGFSPSCNFTG 1101  
QY 1081 QCQMPGFGGTCSECELFWGPDPVECRACDPRIGETPOCQDSTGQCVCEVGEPR 1140  
DB 1102 QCQMPGFGGTCSECELFWGPDPVECRACDPRIGETPOCQDSTGQCVCEVGEPR 1161  
QY 1141 CDKTRGVSGVFPDCTCHOCFALWVIAELNTRHLEKAKALKISGVIGPVRETV 1200  
DB 1162 CDKTRGVSGVFPDCTCHOCFALWVIAELNTRHLEKAKALKISGVIGPVRETV 1221  
QY 1201 SVERKVEIKDILAQSPAAPLKNIGLFEAEKLIKVTETMAQVVEVKLSDTTSQSNST 1260  
DB 1222 SVERKVEIKDILAQSPAAPLKNIGLFEAEKLIKVTETMAQVVEVKLSDTTSQSNST 1281  
QY 1261 AKELDSLQTEAESLDNVTVELABQLFINKSDIRGALDSITKYFQMSLEAEKRVNASTTD 1320  
DB 1282 AKELDSLQTEAESLDNVTVELABQLFINKSDIRGALDSITKYFQMSLEAEKRVNASTTD 1341  
QY 1321 PNSTVBOSALWRDVEDVMMERESQKEQEQEQLLDELAKLQSLDLSAAAEWTCGTP 1380  
DB 1342 PNSTVBOSALWRDVEDVMMERESQKEQEQEQLLDELAKLQSLDLSAAAEWTCGTP 1401  
QY 1381 PGASCSSTEGGPNCRITDEGERKCGGPGGGLVVAHNAWQKAMDQDVLSALAEVQL 1440  
DB 1402 PGASCSSTEGGPNCRITDEGERKCGGPGGGLVVAHNAWQKAMDQDVLSALAEVQL 1461  
QY 1441 SKMVEAKLRADAEKQSAEDILLKTAATKWDKNEELRNLIKQIRNPLFQDSADLDSI 1500  
DB 1462 SKMVEAKLRADAEKQSAEDILLKTAATKWDKNEELRNLIKQIRNPLFQDSADLDSI 1521  
QY 1501 EAVANEVLKMPSTPQOLQNTLTERVESLSQVEVTLQSAADIAARAEMLEEAKRA 1560  
DB 1522 EAVANEVLKMPSTPQOLQNTLTERVESLSQVEVTLQSAADIAARAEMLEEAKRA 1581  
QY 1561 SKSATDVKTADVMKALEAEKQAAKAKQADEDIQCTONLLTSEETASSETL 1620  
DB 1582 SKSATDVKTADVMKALEAEKQAAKAKQADEDIQCTONLLTSEETASSETL 1641

QY 1621 FNASQRISELERNVZELKRAAQNSEGEAYITEKVVYTVKQSAEDVKKTLGDELDEKVKY 1680  
DB 1642 FNASQRISELERNVZELKRAAQNSEGEAYITEKVVYTVKQSAEDVKKTLGDELDEKVKY 1701  
QY 1681 ENLIKTTEESADARRKAEMLQNEAKTLAANSKLOLLKDLERKYSDNORYLEDKAQL 1740  
DB 1702 ENLIKTTEESADARRKAEMLQNEAKTLAANSKLOLLKDLERKYSDNORYLEDKAQL 1761  
QY 1741 ARLEGEVRSLLKXISQKAVVYSTCL 1765  
DB 1762 VRLEGEVRSLLKXISQKAVVYSTCL 1786

RESULT 3  
MMRTS  
laminin beta-2 chain precursor - rat  
N/Alternate names: laminin chain B3; S-laminin  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C/Accession: S03539  
R/Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
Nature 338, 229-234, 1989  
A/Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur.  
A/Reference number: S03539; MUID:89159410; PMID:2922051  
A/Accession: S03539  
A/Molecule type: mRNA  
A/Residues: 1-1801 <HUN>  
C/Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251  
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C/Function:  
A/Description: Interact with cells and with other basement membrane proteins to promote  
C/Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F/1-35/Domain: signal sequence #status Predicted <SIG>  
F/36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F/36-285/Domain: VI <DOM6>  
F/286-555/Domain: V <DOM5>  
F/286-347/Domain: laminin-type EGF-like homology <LE01>  
F/350-410/Domain: laminin-type EGF-like homology <LE02>  
F/413-470/Domain: laminin-type EGF-like homology <LE03>  
F/473-522/Domain: laminin-type EGF-like homology <LE04>  
F/525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F/556-784/Domain: IV <DOM4>  
F/786-831/Domain: laminin-type EGF-like homology <LE06>  
F/788-1196/Domain: III <DOM3>  
F/834-877/Domain: laminin-type EGF-like homology <LE07>  
F/880-927/Domain: laminin-type EGF-like homology <LE08>  
F/930-986/Domain: laminin-type EGF-like homology <LE09>  
F/989-1038/Domain: laminin-type EGF-like homology <LE10>  
F/1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F/1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F/1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F/1197-1412/Domain: II <DOM2>  
F/1197-1412/Region: heptad repeats  
F/1413-1445/Domain: alpha <ALP>  
F/1446-1801/Region: heptad repeats  
F/1446-1801/Domain: I <DOM1>  
F/45-50/Bisulfide bonds: #status predicted  
F/251,371,1098,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status I  
F/1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 52.7%; Score 5084; DB 1; Length 1801;

Best Local Similarity 51.5%; Pred.No.7.6e-186;

Matches 910; Conservative 303; Mismatches 534; Indels 20; Gaps 8;

QY 8 CGAGSCYPATGDLIGRAQKLSVTSTGHLKPEPCYIVSHLQEDKKKFCICNSQDPYHET 67

DB 44 GCSRGSCYPATGDLIGRAQKLSVTSTGHLKPEPCYIVSHLQEDKKKFCICNSQDPYHET 103

QY 68 LNPDSHLNENVVTFAPNKLKIQWQSENGVNTIOLDLEAEHFHLLMTKTRPRAM 127

DB 104 DPNSHRIQNVTSFAPQRTAMWQSENGVPMVTIQDLEAEHFHLLMTKTRPRAM 163

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 98.6077 Seconds  
(without alignments)

11631.021 Million cell updates/sec

Title: US-10-037-182-4

Perfect score: 19876

Sequence: 1 DLYCKLVGPGVAGDPNQTI.....QKALTQRHAKFSVSLLMH 3635

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15839	79.7	3695	4 Q8TDF8	Q8tdf8 homo sapien
2	5012.5	25.2	3712	5 Q5VRW0	Q5vrw0 drosophila
3	4820.5	24.3	3704	5 P51904	P51904 caenorhabdi
4	4129	20.8	794	11 Q8R3Y7	Q8r3y7 mus musculu
5	3934.5	19.8	1486	4 O14637	O14637 homo sapien
6	2530	12.7	3102	5 O45614	O45614 caenorhabdi
7	2450	12.3	1806	4 Q9BTG0	Q9btg0 homo sapien
8	2407.5	12.1	670	4 Q9BTP3	Q9btp3 homo sapien
9	2380	12.0	3375	5 Q81P51	Q81p51 drosophila
10	2359	11.9	3367	5 Q5XZC9	Q5xzcz9 drosophila
11	2320	11.7	452	11 Q80VE8	Q80ve8 mus musculu
12	2154	10.8	1725	6 Q867A1	Q867a1 canis fami
13	2084.5	10.5	2731	5 Q5VJT5	Q5vjts drosophila
14	2067	10.4	1725	11 P70570	P70570 rattus norv
15	1683.5	8.5	1799	11 Q8ROY0	Q8roy0 mus musculu
16	1676	8.4	1792	13 O57484	O57484 gallus gall

#### ALIGNMENTS

#### RESULT 1

ID	Q8TDF8	PRELIMINARY;	PRT;	3695 AA.
AC	Q8TDF8;			
DT	01-JUN-2002 (TREMELrel. 21, Created)			
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)			
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)			
DE	Laminin alpha5 chain precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21935381; PubMed=11821406;			
RA	Doi M., Thyboll J., Kortessmaa J., Jansson K., Iivanainen A.,			
RA	Farwarden M., Timpi R., Hedin U., Swenberg J., Tryggvason K.;			
RT	"Recombinant Human Laminin-10 (alpha5beta3gamma1). Production,			
RT	Purification, and Migration-Promoting Activity on Vascular Endothelial			
RT	Cells."			
RL	J. Biol. Chem. 277:12741-12748(2002).			
DR	EMBL; AF443072; AM12527.1;			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0003743; F:translation initiation factor activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0008410; F:transport; IEA.			
DR	InterPro; IPR008995; ConA_like lec_gl.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR000334; Laminin B.			
DR	InterPro; IPR002049; Laminin EGF.			
DR	InterPro; IPR001791; Laminin_G.			
DR	InterPro; IPR008211; LamNT.			
DR	InterPro; IPR008212; Lam_N2.			
DR	InterPro; IPR001638; SBP_bac_3.			
DR	InterPro; IPR001950; TIF_SUI1.			

Q8jhw7 brachydanio  
Q86xn2 homo sapien  
Q8jhw6 brachydanio  
Q9y6u6 homo sapien  
Q9u3u7 anopheles g  
Q91vv0 mus musculu  
Q8jhw8 brachydanio  
P70636 rattus norv  
Q90zn3 gallus gall  
Q9ns27 homo sapien  
Q8c9j2 mus musculu  
Q75445 homo sapien  
Q8bjp3 mus musculu  
Q44565 caenorhabdi  
Q8k3k1 rattus norv  
Q88281 rattus norv  
Q8irv9 drosophila  
Q9w4v4 drosophila  
Q8irv8 drosophila  
Q8mpn3 drosophila  
Q8tvq2 caenorhabdi  
Q8ta66 homo sapien  
Q867a2 canis fami  
Q8hz19 equus caball  
Q8swy0 drosophila  
Q967s8 schistocerc  
Q8irv7 drosophila  
Q9nef9 drosophila



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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 48.4494 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-6  
Perfect score: 9754  
Sequence: 1 MGLQLLAFSFLACRAVR.....EVRSLKDISQKAVYVSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9754	100.0	1786	2 AAW50893	Human lam
2	9754	100.0	1786	3 AAB16522	Human lam
3	9754	100.0	1786	3 AAB19797	Human lam
4	9754	100.0	1786	3 AAB48448	Human lam
5	9754	100.0	1786	4 AAB30788	Human she
6	9754	100.0	1786	5 ABB81590	Human lam
7	9738	99.8	1786	5 AAM48896	Laminin p
8	9718	99.6	1785	2 AAY15461	Human lam
9	9654	99.0	1785	3 AAB19798	Human lam
10	9654	99.0	1785	3 AAB48449	Human lam
11	9654	99.0	1785	3 ABB81591	Human lam
12	9144	93.7	1786	3 AAB19799	Mouse lam
13	9144	93.7	1786	3 AAB48450	Mouse lam
14	9144	93.7	1786	5 ABB81592	Mouse lam
15	9087	93.2	1776	2 AAW50894	Mouse lam
16	8967	91.9	1764	1 AAP31672	Primary a
17	8873	91.0	1725	3 AAB19800	Mouse lam
18	8873	91.0	1725	3 AAB48451	Mouse lam
19	8873	91.0	1725	5 ABB81593	Mouse lam
20	5088	52.2	1801	2 AAW50895	Rat lamin
21	5088	52.2	1801	7 ADE60383	Rat Prote
22	5088	52.2	1801	7 ADE60386	Human lam
23	5052	51.8	1798	7 ADE60385	Human Pro
24	5051	51.8	1799	7 ADE60359	Mouse lam
25	4921	50.5	1799	5 AAU84346	Protein L

26	4921.5	50.5	1798	5	AAW50360	Human lam
27	3881	39.8	822	5	AAM48897	Laminin p
28	3852	39.5	1788	4	ABB62995	Drosophil
29	3832.5	39.3	1761	2	AAI15457	Human lam
30	3625.5	37.2	1670	7	ADE07851	Novel pro
31	3076.5	31.5	1101	7	ADE28641	Human NOV
32	3044.5	31.2	1105	2	AAI15459	SEQ ID 5
33	2776	28.5	466	2	AAR07447	Human lam
34	2348	24.1	527	3	AB55995	Breast an
35	2115	21.7	434	1	ABP0109	Human B1
36	1787	18.3	315	6	ABU70520	Human adi
37	1762.5	18.1	1639	4	ABBS9807	Drosophil
38	1682	17.2	1605	3	AAB19805	Mouse lam
39	1682	17.2	1605	3	AAB48454	Mouse lam
40	1682	17.2	1605	5	ABB81596	Mouse lam
41	1680.5	17.2	1609	3	AAB19801	Human lam
42	1680.5	17.2	1609	3	AAB48452	Human lam
43	1680.5	17.2	1609	5	ABB81594	Human lam
44	1680.5	17.2	1609	7	ADC01887	Human lam
45	1680.5	17.2	1617	3	AAB19803	Human lam

ALIGNMENTS

RESULT 1  
AAW50893  
ID AAW50893 standard; protein; 1786 AA.

AC AAW50893;  
XX  
DT 07-DEC-1998 (first entry)  
XX  
DE Human laminin B1 chain.

KW Laminin; human; beta-amyloid; amyloidosis; Alzheimer's disease;  
KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
KW Gertsmann-Straussler syndrome; Kuru; scrapie; haemodialysis;  
KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
therapy.

XX Homo sapiens.

XX WO9815179-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P;

XX (UNIW ) UNIV WASHINGTON.

XX Castillo G, Snow AD;

XX WPI; 1998-240534/21.

PT Use of laminin and fragments - for developing products for use in the  
PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
PT CJD.

XX Claim 15; Page 86-89; 132pp; English.

XX This is the amino acid sequence of the human laminin B1 chain. The  
CC primary object of the invention is to use laminin, laminin-derived  
CC protein fragments and/or laminin-derived polypeptides as potent  
CC inhibitors of amyloid formation, deposition, accumulation and/or  
CC persistence in Alzheimer's disease and other amyloidoses. The laminin  
CC products (see AAW50888-98) may include mouse or human laminin A or A1  
CC chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1

chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin)

xx  
sq  
Sequence 1786 AA;  
Query Match 100.0%; Score 9754; DB 2; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLQLLAFSLCARVRAQEPFSGYGAEGSCYPATGDLIGRAKLSVTSTGLHK 60  
Db 1 MGLQLLAFSLCARVRAQEPFSGYGAEGSCYPATGDLIGRAKLSVTSTGLHK 60

Qy 61 PEPYCVIYSHLQEDKKFCICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120  
Db 61 PEPYCVIYSHLQEDKKFCICNSQDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120

Qy 121 VTIQDLLEAPHFTHLIMTFKTPFAAMLIERSDFKGTGVTYFAYDCSEAFPGISTG 180  
Db 121 VTIQDLLEAPHFTHLIMTFKTPFAAMLIERSDFKGTGVTYFAYDCSEAFPGISTG 180

Qy 181 PMKVVDDIIICDSRYSIDPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIKFVKL 240  
Db 181 PMKVVDDIIICDSRYSIDPSTEGEVIIFRALDPAFKIEDPYSPIQNLLKITNLRIKFVKL 240

Qy 241 HTLGNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGFEVEGVHGHCMC 300  
Db 241 HTLGNLLDSRMEIREKYIYAYVDMVVRGNCFCYGHASECAPVDGFEVEGVHGHCMC 300

Qy 301 RHNTKGLNCELMDPFYHDLPRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360  
Db 301 RHNTKGLNCELMDPFYHDLPRPAEGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360

Qy 361 VCDCCQNTMGRNCEQCKPFYIYQHPERDIRDPNFCERTCDPAGSQNEGICDSYTFDFTG 420  
Db 361 VCDCCQNTMGRNCEQCKPFYIYQHPERDIRDPNFCERTCDPAGSQNEGICDSYTFDFTG 420

Qy 421 LIAGQCRKLVNVEGHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCY 480  
Db 421 LIAGQCRKLVNVEGHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCY 480

Qy 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABESQCCSCRPMMIGRQC 540  
Db 481 CKRLVTGQHCDOCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABESQCCSCRPMMIGRQC 540

Qy 541 NEVEPGYFATLDHYLYEAEANLPGVSIYVERQIYQIRPSWTGAGFVRVPEGAYLEFF 600  
Db 541 NEVEPGYFATLDHYLYEAEANLPGVSIYVERQIYQIRPSWTGAGFVRVPEGAYLEFF 600

Qy 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPG 660

601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRPGRIPTSRRCGNTIPDDDNQVVSLSPG 660  
661 SRYVVLPRPVCFEKGNTYVRLLELPQVTSDDSDVESPYTLIDSVLVMPYCKSLDIFTVGG 720  
661 SRYVVLPRPVCFEKGNTYVRLLELPQVTSDDSDVESPYTLIDSVLVMPYCKSLDIFTVGG 720  
721 SGDGVVTNSAMETFORVRCLENSSVKVTMTVCRNIIIFSISALLHQTGLACEDCPQGS 780  
721 SGDGVVTNSAMETFORVRCLENSSVKVTMTVCRNIIIFSISALLHQTGLACEDCPQGS 780  
781 LSSVCDPNNGGOCQCRPNVVGSTCNRCAPGTFGFGPSGCKPCCECHLOGSVNAFCNPVTGQC 840  
781 LSSVCDPNNGGOCQCRPNVVGSTCNRCAPGTFGFGPSGCKPCCECHLOGSVNAFCNPVTGQC 840  
841 HCFQGVYARQCDRLCPGHGWPSPQPCQCNHAGDCCPVTGECNLCODYTWGHCRCCLA 900  
841 HCFQGVYARQCDRLCPGHGWPSPQPCQCNHAGDCCPVTGECNLCODYTWGHCRCCLA 900  
901 GYGDPIIGSDGHCRCPCPDGPGSGRQFARSCYQDPVTQLQACVCPGPGYIGSSCDDCAS 960  
901 GYGDPIIGSDGHCRCPCPDGPGSGRQFARSCYQDPVTQLQACVCPGPGYIGSSCDDCAS 960  
961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQCFRGYGYGDA 1020  
961 GYFGNPSVGGSCQPCQCHNNIDTTDPEACDKETGRCLKCLYHTEGHCQCFRGYGYGDA 1020  
1021 LRQDCKVCYNLGTVOEHGNGSDCCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTG 1080  
1021 LRQDCKVCYNLGTVOEHGNGSDCCDKATGQCLCLPNVIGQNCDCRCAPNTWOLASGTG 1080  
1081 CDPNCNNAHSGFSGSCNEFTGQCQCMFGFGGRTCEQCLFWGDPDVECRACDCDPRGIE 1140  
1081 CDPNCNNAHSGFSGSCNEFTGQCQCMFGFGGRTCEQCLFWGDPDVECRACDCDPRGIE 1140  
1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSVFPDCTFCHOCFALMDVITAELENRTHRF 1200  
1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSVFPDCTFCHOCFALMDVITAELENRTHRF 1200  
1201 LEKAKALISGIVGYRETVDSEVERKVESEIKDIIAQSPAAPLKNIGNLFEAEKLIKDV 1260  
1201 LEKAKALISGIVGYRETVDSEVERKVESEIKDIIAQSPAAPLKNIGNLFEAEKLIKDV 1260  
1261 TEMMAQVEKLSDDTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
1261 TEMMAQVEKLSDDTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
1321 ITKYFQMSLEAEERNVASTTEPNSTVEQSALMRVEDVMMERESQFKEKEQEARLLDE 1380  
1321 ITKYFQMSLEAEERNVASTTEPNSTVEQSALMRVEDVMMERESQFKEKEQEARLLDE 1380  
1381 LAGKLQSLDLSAAAEMLTCTGTPPGASCSETGCGPNCRDTDEGERKCGGPGCGGLVTVAHA 1440  
1381 LAGKLQSLDLSAAAEMLTCTGTPPGASCSETGCGPNCRDTDEGERKCGGPGCGGLVTVAHA 1440  
1441 WOKAMDLDQDVLALAEVEQLSKMVSEAKRADSAKQSAEDILLKTNATKEKMDKSNBEEL 1500  
1441 WOKAMDLDQDVLALAEVEQLSKMVSEAKRADSAKQSAEDILLKTNATKEKMDKSNBEEL 1500  
1501 RNLIQIRNFLTQDSADLDSIEAVANEVLKVMEMPSTPOQLNLTEDIRERVESLSQVEVI 1560  
1501 RNLIQIRNFLTQDSADLDSIEAVANEVLKVMEMPSTPOQLNLTEDIRERVESLSQVEVI 1560  
1561 LQHSAADTARAEMLLEAKRASKSTDKVTADVKKEALEEAEAKQVAEAKAKQADEDI 1620  
1561 LQHSAADTARAEMLLEAKRASKSTDKVTADVKKEALEEAEAKQVAEAKAKQADEDI 1620  
1621 QGTQNLTSISETAASSETLFFNASQRISELEARNVEELKRAAQNQSGEAEYKVVYTVK 1680  
1621 QGTQNLTSISETAASSETLFFNASQRISELEARNVEELKRAAQNQSGEAEYKVVYTVK 1680  
1681 QSAEDVKKTLDELDEKYYKENLIKAKTESADARRKAEMLQNEAKTLQAQNSKQLL 1740  
1681 QSAEDVKKTLDELDEKYYKENLIKAKTESADARRKAEMLQNEAKTLQAQNSKQLL 1740







QY 421 LIAGQCRKLVNVEGHCDCVCKGFFYDLSSDDPFGCKSCACNPLGTIPGNCPCDSTGHY 480  
DB 421 LIAGQCRKLVNVEGHCDCVCKGFFYDLSSDDPFGCKSCACNPLGTIPGNCPCDSTGHY 480  
QY 481 CKELVTGQHCDCQCLPEHMGSLNDLDCRCDCDGLGALNNSCFABSGQSCSRPHMIGQC 540  
DB 481 CKRLVTGQHCDCQCLPEHMGSLNDLDCRCDCDGLGALNNSCFABSGQSCSRPHMIGQC 540  
QY 541 NEVEPGYYFATLDHYLYEAEANLGVSVIVRQYIQDRIPSWTGAGFVRVPEGAYLEFF 600  
DB 541 NEVEPGYYFATLDHYLYEAEANLGVSVIVRQYIQDRIPSWTGAGFVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEVDILIRYEPQLDHEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSFG 660  
DB 601 IDNIPYSMEVDILIRYEPQLDHEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSFG 660  
QY 661 SRYVVLPRPVCFEKGNTYVRLSLPQVTSDDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
DB 661 SRYVVLPRPVCFEKGNTYVRLSLPQVTSDDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
QY 721 SGQGVVNSAWETFORVRCLENSRSVVKTPMTDVCNIIFISALLHQTGLACEDPOGS 780  
DB 721 SGQGVVNSAWETFORVRCLENSRSVVKTPMTDVCNIIFISALLHQTGLACEDPOGS 780  
QY 781 LSSVCDPNGQCCQCRPNVGRVTCNRCAPTGFGPSCGCKPCECHLOGSVNAFCNPVTGQC 840  
DB 781 LSSVCDPNGQCCQCRPNVGRVTCNRCAPTGFGPSCGCKPCECHLOGSVNAFCNPVTGQC 840  
QY 841 HCFQGVVAROCDRLPGHWGFPSCQCCNGHADDQDPTVTECLNCODYTMGHNCERCLA 900  
DB 841 HCFQGVVAROCDRLPGHWGFPSCQCCNGHADDQDPTVTECLNCODYTMGHNCERCLA 900  
QY 901 GYVGDPIIGSDHCRPCPCPDGSDGRQFARSCVQDPVTLLQACVCDPGVIGSRCDCCAS 960  
DB 901 GYVGDPIIGSDHCRPCPCPDGSDGRQFARSCVQDPVTLLQACVCDPGVIGSRCDCCAS 960  
QY 961 GYFQNPSEVGSCQPCQCHNIDTTPDCAKGTGRCLKCLXHTGEHCQFCRFGYVGA 1020  
DB 961 GYFQNPSEVGSCQPCQCHNIDTTPDCAKGTGRCLKCLXHTGEHCQFCRFGYVGA 1020  
QY 1021 LRQDCRCVCNLTGVQEHNGSCQCDKATGQCLCLPNVIGNCQDCRCAPTWQLASGTG 1080  
DB 1021 LRQDCRCVCNLTGVQEHNGSCQCDKATGQCLCLPNVIGNCQDCRCAPTWQLASGTG 1080  
QY 1081 CDPNCNAAHSFGPSCNEFTGQCCQCMFPGRTSCQELFWGDPVVECRACDCDPRGIE 1140  
DB 1081 CDPNCNAAHSFGPSCNEFTGQCCQCMFPGRTSCQELFWGDPVVECRACDCDPRGIE 1140  
QY 1141 TPQCDQSTGQCVGVGEGPRCDKTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHR 1200  
DB 1141 TPQCDQSTGQCVGVGEGPRCDKTRGYSGVFPDCTPCHQCFALMDVIIAELTNRTHR 1200  
QY 1201 LEKAKALKISGIVGYRETVDVSRKVSIEIKDIIAQSPAAPLKNIGNLFEEAEKLIKDV 1260  
DB 1201 LEKAKALKISGIVGYRETVDVSRKVSIEIKDIIAQSPAAPLKNIGNLFEEAEKLIKDV 1260  
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSIQTEABSLDNTVKELASQLEFIKNSDIRGALDS 1320  
DB 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSIQTEABSLDNTVKELASQLEFIKNSDIRGALDS 1320  
QY 1321 ITKQFQMSLEAEERVNASTTBNPSTVQSAALMRDRVEDVMMERESQFKQEQEQLLDE 1380  
DB 1321 ITKQFQMSLEAEERVNASTTBNPSTVQSAALMRDRVEDVMMERESQFKQEQEQLLDE 1380  
QY 1381 LAGKLSLDLSAAABMTCTGTPPGASCSTEGGPNCRDTEGERKCGGPGGGLVVAHNA 1440  
DB 1381 LAGKLSLDLSAAABMTCTGTPPGASCSTEGGPNCRDTEGERKCGGPGGGLVVAHNA 1440  
QY 1441 WCKAMLDQDVLISALAEVQSLSKMVSEAKLRADAKQSAEDILLKTNATKMKDKSNEEL 1500  
DB 1441 WCKAMLDQDVLISALAEVQSLSKMVSEAKLRADAKQSAEDILLKTNATKMKDKSNEEL 1500  
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTDIERVESLSQVEVI 1560

DB 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKMEPSTPQOLQNLTDIERVESLSQVEVI 1560  
QY 1561 LOHSAADIARAEMLLBEAKRASKSATDVKTADWKEALEEAEKAQVAAEKAIKQADEDI 1620  
DB 1561 LOHSAADIARAEMLLBEAKRASKSATDVKTADWKEALEEAEKAQVAAEKAIKQADEDI 1620  
QY 1621 QGTQNLITSIESETPAASEETLFNASQISIELENVEELKRAAQNSEAEYIEKVVYTVK 1680  
DB 1621 QGTQNLITSIESETPAASEETLFNASQISIELENVEELKRAAQNSEAEYIEKVVYTVK 1680  
QY 1681 QSAEDVKTLDGELDEKVKVENLIAKTBESADARRKAEMLQNEAKTLAQAANSKLQLL 1740  
DB 1681 QSAEDVKTLDGELDEKVKVENLIAKTBESADARRKAEMLQNEAKTLAQAANSKLQLL 1740  
QY 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLDKDISOKVAVYSTCL 1786  
DB 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLDKDISOKVAVYSTCL 1786

## RESULT 4

AAB48448

ID AAB48448 standard; protein; 1786 AA.

XX AAB48448;

AC AAB48448;

XX DT 02-WAR-2001 (first entry)

XX DT Human laminin 8 polypeptide, SEQ ID NO: 14.

DE Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.

OS Homo sapiens.

XX WO200006732-A2.

XX PD 09-NOV-2000.

XX PF 28-APR-2000; 2000WO-US011543.

XX PR 30-APR-1999; 99US-0131720P.

XX PR 21-AUG-1999; 99US-0149738P.

XX PR 24-SEP-1999; 99US-0155945P.

XX PR 11-FEB-2000; 2000US-0182012P.

XX PA (BIOS-) BIOSTRATUM INC.

XX PI Kortessmaa J, Tryggvason K;

XX DR WPI; 2000-687539/67.

XX DR N-PSDB; AAC83709.

XX PT Purified laminin 8 protein, useful for research and therapeutic purposes  
XX PT including peripheral nerve regeneration, treatment of degenerative muscle  
XX PT disorders, angiogenesis regulation, and ex vivo cell therapy.

XX PS Claim 5; Page 150-155; 245pp; English.

XX CC The present sequence is a laminin 8 polypeptide chain. Laminins are a  
XX CC family of heterotrimeric glycoproteins that function via binding  
XX CC interactions with neighbouring cell receptors and by forming laminin  
XX CC networks. They are signalling molecules which influence cellular  
XX CC function. Laminin 8 is useful for treating injuries to tissue of  
XX CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
XX CC treating injuries to vascular tissue, promoting cell attachment and  
XX CC migration, ex vivo cell therapy, improving the biocompatibility of  
XX CC medical devices, and preparing improved cell culture devices and media.  
XX CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
XX CC of vascular injuries, improving the take of grafts, improving the  
XX CC biocompatibility of medical devices, treating neural injuries (neural  
XX CC regeneration), regulating angiogenesis, and promoting cell attachment and



XX	02-OCT-2000; 2000WO-JP006840.	
PF		
XX	01-OCT-1999; 99JP-00280976.	
PR		
XX	(KYOW ) KYOWA HAKKO KOGYO KK.	
PA	(NOJI/) NOJIMA H.	
PA		
XX	Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;	
PI	Kuga T, Sekine S, Nakamura Y, Sugano S;	
PI		
XX	WPI; 2001-266308/27.	
DR	N-PSDB; AAH02911.	
XX		
XX	DNA sequences, proteins encoded by them and antibodies against them	
PT	useful in diagnosis and treatment of vascular disease caused by	
PT	arteriosclerosis.	
PT		
XX	Claim 60; Page 440-449; 678pp; Japanese.	
PS		
XX	The present invention provides the protein and coding sequences of a	
CC	number of human shear stress response proteins. These are useful in the	
CC	diagnosis, treatment and screening of vascular diseases caused by	
CC	arteriosclerosis, including heart failure, post-PTCA restenosis and	
CC	hypertension	
XX		
SQ	Sequence 1786 AA;	
	Query Match 100.0%; Score 9754; DB 4; Length 1786;	
	Best Local Similarity 100.0%; Pred. NO. 0;	
	Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MGLQLLAFALCARVRAQPEFSYGCAGSCYPATGDLIGRAQKLSVTSICGLHK 60	
DB	1 MGLQLLAFALCARVRAQPEFSYGCAGSCYPATGDLIGRAQKLSVTSICGLHK 60	
QY	61 PEYICVSHLQEDKCFICNSDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120	
DB	61 PEYICVSHLQEDKCFICNSDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVEN 120	
QY	121 VTIQDLAEAFHFLIMTKFRPAAMLIERSDFGKTWGYRYFAYDCEASFPGISTG 180	
DB	121 VTIQDLAEAFHFLIMTKFRPAAMLIERSDFGKTWGYRYFAYDCEASFPGISTG 180	
QY	181 PMKKVDDIICDSYSIDPSTEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKIFVKL 240	
DB	181 PMKKVDDIICDSYSIDPSTEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKIFVKL 240	
QY	241 HTLGDNLLDSRMPIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHC 300	
DB	241 HTLGDNLLDSRMPIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVHGHC 300	
QY	301 RHNTKGLNCELMDFYHDLWPRAEGRNNAKCKNCNEHSISCHFDMAVYLATGNVSGG 360	
DB	301 RHNTKGLNCELMDFYHDLWPRAEGRNNAKCKNCNEHSISCHFDMAVYLATGNVSGG 360	
QY	361 VCDQCQHTMGRNCEQKPFYVYOHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420	
DB	361 VCDQCQHTMGRNCEQKPFYVYOHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTG 420	
QY	421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSDDPGCKSCACNPLGTPGNPCDSETGHY 480	
DB	421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSDDPGCKSCACNPLGTPGNPCDSETGHY 480	
QY	481 CKRLVVGQHCDCQLPEHFWGLSNDLDCRCDLGGALNNSCFABSGQSCSRPHMIGRQC 540	
DB	481 CKRLVVGQHCDCQLPEHFWGLSNDLDCRCDLGGALNNSCFABSGQSCSRPHMIGRQC 540	
QY	541 NEVEPGYFATLDHYLYEAEANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600	
DB	541 NEVEPGYFATLDHYLYEAEANLPGVSIYERQYIQDRIPSWTGAGFVRVPEGAYLEFF 600	
QY	601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCGNTIPDDNQVLSLSPG 660	

DB	601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVORPGRIPTSSRCGNTIPDDNQVLSLSPG 660	
QY	661 SRVYVLPKPRVCFKGTNTYVLELPOVTSDDSVESPYTLIDSLVLMFYCKSLDITVGG 720	
DB	661 SRVYVLPKPRVCFKGTNTYVLELPOVTSDDSVESPYTLIDSLVLMFYCKSLDITVGG 720	
QY	721 SGDGVTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSISALLHQTLGACCECPQGS 780	
DB	721 SGDGVTNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFSISALLHQTLGACCECPQGS 780	
QY	781 LSSVCDPENGOCOCRPNVWGRTCNRCAPTGFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840	
DB	781 LSSVCDPENGOCOCRPNVWGRTCNRCAPTGFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840	
QY	841 HCFQGVYARQCDRLPGHWGFPSCQPCQCNHADDODPVTGECINQDITYTMHNCERCLA 900	
DB	841 HCFQGVYARQCDRLPGHWGFPSCQPCQCNHADDODPVTGECINQDITYTMHNCERCLA 900	
QY	901 GYVGDPIIGSGDHCRPCPCPDGPDGSRQFARSCVQDPVTLQACVCDPGVIGSRCDCCAS 960	
DB	901 GYVGDPIIGSGDHCRPCPCPDGPDGSRQFARSCVQDPVTLQACVCDPGVIGSRCDCCAS 960	
QY	961 GYFQNPSEVGGSCQPCQCHNNIDITTPDEACDKETGRCLKCLYHTEGHEHCFRFGYVGA 1020	
DB	961 GYFQNPSEVGGSCQPCQCHNNIDITTPDEACDKETGRCLKCLYHTEGHEHCFRFGYVGA 1020	
QY	1021 LRQCRKVCNVLGTVOEHGNCSDCCDKATGOCCLCPNVIGONCDRCAPTWQLASGTG 1080	
DB	1021 LRQCRKVCNVLGTVOEHGNCSDCCDKATGOCCLCPNVIGONCDRCAPTWQLASGTG 1080	
QY	1081 CDPCNCAAHSGFPCSCNEFTGQCQCMFPGFGRGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140	
DB	1081 CDPCNCAAHSGFPCSCNEFTGQCQCMFPGFGRGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140	
QY	1141 TPQCDQSTGQCVCEGVEGPRCKTRGYSVGPDPCTPCHQCCFALMDVILIAETNTRHF 1200	
DB	1141 TPQCDQSTGQCVCEGVEGPRCKTRGYSVGPDPCTPCHQCCFALMDVILIAETNTRHF 1200	
QY	1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNTGNLFEEAEKLIKDV 1260	
DB	1201 LEKAKALKISGVIGPYRETVDVSVERKVSEIKDILAQSPAAEPLKNTGNLFEEAEKLIKDV 1260	
QY	1261 TEMMAQVEVKLSDTTSSQNSTAKELSLQTEASLDMNTVVELAEQLEFIKNSDIRGALDS 1320	
DB	1261 TEMMAQVEVKLSDTTSSQNSTAKELSLQTEASLDMNTVVELAEQLEFIKNSDIRGALDS 1320	
QY	1321 ITKYFQVSLAEAEERVNASTTEPNSTVQSALMDRVEDVMMERESQFKEQEQAARLLDE 1380	
DB	1321 ITKYFQVSLAEAEERVNASTTEPNSTVQSALMDRVEDVMMERESQFKEQEQAARLLDE 1380	
QY	1381 LAGKLQSLDLSAAAEAMTCGTPPGASCSETCGGPNCTDEGERKCGGCGGLVTVAHNA 1440	
DB	1381 LAGKLQSLDLSAAAEAMTCGTPPGASCSETCGGPNCTDEGERKCGGCGGLVTVAHNA 1440	
QY	1441 WQKAWDLDDQVLSALAEVOLSKMVSSEAKLRADEAKQSAEDILLKTNAKEKMDKSNEL 1500	
DB	1441 WQKAWDLDDQVLSALAEVOLSKMVSSEAKLRADEAKQSAEDILLKTNAKEKMDKSNEL 1500	
QY	1501 RNLIQIRNFLTQDSADLDSIEAVANEVLKXEMPSTPQQLQNLTEDIRVERSELQSVEVI 1560	
DB	1501 RNLIQIRNFLTQDSADLDSIEAVANEVLKXEMPSTPQQLQNLTEDIRVERSELQSVEVI 1560	
QY	1561 LQHSAAIDQVLSALAEVOLSKMVSSEAKLRADEAKQSAEDILLKTNAKEKMDKSNEL 1620	
DB	1561 LQHSAAIDQVLSALAEVOLSKMVSSEAKLRADEAKQSAEDILLKTNAKEKMDKSNEL 1620	
QY	1621 QGTQNLTLTSEISETAASEETLFNASQRISELERNVEELKEKAAQNSGEAEYIEKVYTVK 1680	
DB	1621 QGTQNLTLTSEISETAASEETLFNASQRISELERNVEELKEKAAQNSGEAEYIEKVYTVK 1680	
QY	1681 QSAEDVKKTLDDGELDEKVKVENLIAKTTESADARKAEMLQNEAKTILAAQNSKLQLL 1740	

Db 1681 QSAEDVKTLDGELDEKYKVENLIAKTTESADARRKAEMQLONEAKTLLAQANSKLQLL 1740

Qy 1741 KDLERKYEDNORYLEDKAOELARLEGEVRSLLKDISQKAVYSTCL 1786

Db 1741 KDLERKYEDNORYLEDKAOELARLEGEVRSLLKDISQKAVYSTCL 1786

RESULT 6

ABB81590

ID ABB81590 standard; protein; 1786 AA.

AC ABB81590;

XX 19-SEP-2002 (first entry)

XX Human laminin 10 second chain protein sequence SEQ ID NO:6.

XX Laminin alpha 5; laminin 10; vulnarary; cell growth; differentiation;

KW tissue repair development; laminin; healing; vascular tissue;

KW re-endothelialisation; vascular injury; cell attachment; cell stasis;

KW proliferation; migration.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein /label= signal

FT 22..1786

XX /label= laminin\_10\_second\_chain

XX WO200250111-A2.

XX 27-JUN-2002.

XX 21-DEC-2001; 2001WO-US051035.

XX 21-DEC-2000; 2000US-0257449P.

PR 28-MAR-2001; 2001US-0279282P.

PR 13-NOV-2001; 2001US-00279282.

XX (BIOS-) BIOSTRATUM INC.

XX Trygsvason K, Doi M, Thyboll J;

XX WPI: 2002-557650/59.

DR N-PSDB; ABQ72908.

XX New human laminin-10 proteins, useful for accelerating the healing of

PT vascular tissue, improving the biocompatibility of grafts, or for

PT promoting re-endothelialization at the site of vascular injuries.

XX Claim 9; Page 113-119; 231pp; English.

XX The present invention describes human laminin alpha 5. Also described is

CC an isolated laminin 10. Laminin 10 has vulnarary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell

CC growth and differentiation in tissue repair development. Specifically,

CC laminin 10 can be used for accelerating the healing injuries of vascular

CC tissue, improving the biocompatibility of grafts useful for treating such

CC injuries, for promoting re-endothelialisation at the site of vascular

CC injuries, and promote cell attachment and subsequent cell stasis,

CC proliferation, differentiation, and/or migration. The present sequence

CC represents a second chain protein of laminin 10, from the present

XX invention

SQ Sequence 1786 AA;

Query Match 100.0%; Score 9754; DB 5; Length 1786;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLLQLLAFSPFLALCRARVRAQEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Db 1 MGLLQLLAFSPFLALCRARVRAQEPFYSYCAEGSCYPATGDLIGRAQKLSVTSTCGLHK 60

Qy 61 PEPYCIIVSHLOEDKKCFICNSODPYHETINPDSHLIENAVTTFAFNRLKIWQSENGVEN 120

Db 61 PEPYCIIVSHLOEDKKCFICNSODPYHETINPDSHLIENAVTTFAFNRLKIWQSENGVEN 120

Qy 121 VTIQDLEAEFHTLIMTFTFRPAAMLIERSSDFGKTGWYRYPAYDCEASFPFGISTG 180

Db 121 VTIQDLEAEFHTLIMTFTFRPAAMLIERSSDFGKTGWYRYPAYDCEASFPFGISTG 180

Qy 181 PMKYVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPYSPRIQNLKLTNLRKFKVKL 240

Db 181 PMKYVDDIICDSRYSDIEPSTEGEVIFFALDPAFKIEDPYSPRIQNLKLTNLRKFKVKL 240

Qy 241 HTLGNLLDSRMEIREKYYIAYVDMVRGNCFCYGHASECAPVDGFNEBEVGMVHGWC 300

Db 241 HTLGNLLDSRMEIREKYYIAYVDMVRGNCFCYGHASECAPVDGFNEBEVGMVHGWC 300

Qy 301 RHNTKGLNCELWDFVHDLPMWPAEGRNSNACKCNCHESISCHDFMAVILATGNVSG 360

Db 301 RHNTKGLNCELWDFVHDLPMWPAEGRNSNACKCNCHESISCHDFMAVILATGNVSG 360

Qy 361 VDDCQHNTMGRNCEQCKPFYYQHPERDIRDPNFCERCTCDPAGSQNREGICDSYTFSTG 420

Db 361 VDDCQHNTMGRNCEQCKPFYYQHPERDIRDPNFCERCTCDPAGSQNREGICDSYTFSTG 420

Qy 421 LIAQCRCKLNVGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGNPCDSETHCY 480

Db 421 LIAQCRCKLNVGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGNPCDSETHCY 480

Qy 481 CKRLVTGQRCDOCLPEHWGLSNDLDGCRPCDCLDGLGALNNSCFABSGQSCSRPHMIGRC 540

Db 481 CKRLVTGQRCDOCLPEHWGLSNDLDGCRPCDCLDGLGALNNSCFABSGQSCSRPHMIGRC 540

Qy 541 NEVEPGYYPATLDHYLYABEANLQPGVSIIVERQIQRIPSWTCAGFVRPEGAYLFF 600

Db 541 NEVEPGYYPATLDHYLYABEANLQPGVSIIVERQIQRIPSWTCAGFVRPEGAYLFF 600

Qy 601 IDNIPYSMEYDILIRVEPOLPDHWEKAVITVORPORIPTSRGCGNTIPDDNQVLSLPG 660

Db 601 IDNIPYSMEYDILIRVEPOLPDHWEKAVITVORPORIPTSRGCGNTIPDDNQVLSLPG 660

Qy 661 SRYVVLPRPVCPEKGTNTVRLLEPQYTSDDVESPYTLIDSLVLMPCYCKSLDIFTVGG 720

Db 661 SRYVVLPRPVCPEKGTNTVRLLEPQYTSDDVESPYTLIDSLVLMPCYCKSLDIFTVGG 720

Qy 721 SGGVVWTSAMETFORVRCLENSRSVVTPTMDVCRNIIFISALLHOTGLACEDPOGS 780

Db 721 SGGVVWTSAMETFORVRCLENSRSVVTPTMDVCRNIIFISALLHOTGLACEDPOGS 780

Qy 781 LSSVCDPNGGQCCQCRPNVVGRITCNRCAPGTFTGFGSPGCKPCECHLQGSVNAFCNPVTQC 840

Db 781 LSSVCDPNGGQCCQCRPNVVGRITCNRCAPGTFTGFGSPGCKPCECHLQGSVNAFCNPVTQC 840

Qy 841 HCFQGYARQDRCLPWHGFPSCQPCQCNHADDPCDVTGECNLCQDVTWGHNCERCLA 900

Db 841 HCFQGYARQDRCLPWHGFPSCQPCQCNHADDPCDVTGECNLCQDVTWGHNCERCLA 900

Qy 901 GYVGDPPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960

Db 901 GYVGDPPIIGSGDHCRPCPCPDGSDSGRQFARSCYQDPVTQLACVCDPGYIGSRCDDCAS 960

Qy 961 GYFNGPSEVGGSCQPCQCHNNITDTPBACDKETGRCLKCLYHTEGEHCQFCRFGYGDA 1020

Db 961 GYFNGPSEVGGSCQPCQCHNNITDTPBACDKETGRCLKCLYHTEGEHCQFCRFGYGDA 1020

Qy 1021 LRQDCRKVCNYLGTVOEHGNCSDCCQDKATGQCLCLPNVIGNQNCRCRAPNTWLASGTG 1080

Db 1021 LRQDCRKVCNYLGTVOEHGNCSDCCQDKATGQCLCLPNVIGNQNCRCRAPNTWLASGTG 1080

Qy 1081 CDPNCNAAHSFGPSCNFTGQCCMPFGGHTCSQCELFWDGDPDVECRACDCDPRGIE 1140

Db 1081 CDPNCNAAHSFGPSCNFTGQCCMPFGGHTCSQCELFWDGDPDVECRACDCDPRGIE 1140

QY 1141 TPOCDOSTGCVGVGEGPRCDKTRGYSGVFPDCTPCHOCFALMDVIIAELTNRTRF 1200  
DB 1141 TPOCDOSTGCVGVGEGPRCDKTRGYSGVFPDCTPCHOCFALMDVIIAELTNRTRF 1200  
QY 1201 LEKAKALKISGVTPRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNFPERAEKLIKDV 1260  
DB 1201 LEKAKALKISGVTPRETVDVSVERKVSSEIKDILAQSPAAPLKNIGNFPERAEKLIKDV 1260  
QY 1261 TENMAQVEVKLSDTTSGNSTAKELDSLOTEAESLNTVKELAEQLEFIKNSDIRGALDS 1320  
DB 1261 TENMAQVEVKLSDTTSGNSTAKELDSLOTEAESLNTVKELAEQLEFIKNSDIRGALDS 1320  
QY 1321 ITKYFQMSLEAEERVAENASTTEPNSTVEQSALMDRVEDVMVERESQFKSQBEQARLLDE 1380  
DB 1321 ITKYFQMSLEAEERVAENASTTEPNSTVEQSALMDRVEDVMVERESQFKSQBEQARLLDE 1380  
QY 1381 LAGKLOSLLSAAAEWTCGTPPGASCSETECGPNCRTDEGERKCGPGCGGLVTVAHNA 1440  
DB 1381 LAGKLOSLLSAAAEWTCGTPPGASCSETECGPNCRTDEGERKCGPGCGGLVTVAHNA 1440  
QY 1441 WQKAMDLDDQVLSALAEVEQLSRWSEAKLRADAEAKQSAEDILLKTNATKERMKDSNEEL 1500  
DB 1441 WQKAMDLDDQVLSALAEVEQLSRWSEAKLRADAEAKQSAEDILLKTNATKERMKDSNEEL 1500  
QY 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKWEFSTPQOLNLTEDIRERVESLSQVEVI 1560  
DB 1501 RNLIKQIRNFLTQDSADLDSIEAVANEVLKWEFSTPQOLNLTEDIRERVESLSQVEVI 1560  
QY 1561 LQHSADIAEAEMLEBEAKKASATDKVTADWKEALEEAEKAAQAAEKAKQADEDI 1620  
DB 1561 LQHSADIAEAEMLEBEAKKASATDKVTADWKEALEEAEKAAQAAEKAKQADEDI 1620  
QY 1621 QGTQNLTSIESTASEETLFNASQRISELENNVELKRAAQNQGEAEYIEKVYTVK 1680  
DB 1621 QGTQNLTSIESTASEETLFNASQRISELENNVELKRAAQNQGEAEYIEKVYTVK 1680  
QY 1681 QSAEDVKTLDGELDEKYYKVENLIAKTEESADARKAEMLQNEAKTLLAQANSKLQLL 1740  
DB 1681 QSAEDVKTLDGELDEKYYKVENLIAKTEESADARKAEMLQNEAKTLLAQANSKLQLL 1740  
QY 1741 KDLERYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786  
DB 1741 KDLERYEDNQRYLEDKAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

RESULT 7  
AAM48896  
ID AAM48896 standard; protein; 1786 AA.  
XX AC AAM48896;  
XX DT 04-APR-2002 (first entry)  
XX DE Laminin protein.  
XX Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;  
KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;  
KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;  
KW gene therapy; angiostatin antagonist; endostatin antagonist;  
KW antiangiogenic; cycostatic; antiarthritic; endostatin; antiinflammatory;  
KW cerebroprotective; antidiabetic; virucide; antipretic; vulnerary;  
KW gynaecological; cat scratch fever.  
XX OS Unidentified.  
XX PN WO200193897-A2.  
XX PD 13-DEC-2001.  
XX PF 04-JUN-2001; 2001WO-US017947.  
XX PR 02-JUN-2000; 2000US-0209065P.

PR 08-MAY-2001; 2001US-0289387P.  
PA (ENTR-) ENTREMED INC.  
PI Sim KL, Macdonald NJ;  
XX WPI; 2002-130569/17.  
DR N-PSDB; ABA97525.  
XX Regulating angiogenesis and treatment of angiogenesis-mediated diseases,  
e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding  
compound or actin disrupting compound.  
PS Example 11; Fig 6A; 95pp; English.  
XX The present invention relates to methods of regulating angiogenesis in an  
individual by administering an angiogenesis regulating composition  
comprising a tropomyosin binding compound or an actin disrupting  
compound. The compositions are useful for treating diseases and processes  
mediated by angiogenesis including haemangioma, solid tumours, blood  
borne tumours, leukaemia, metastasis, Crohn's disease, coronary or  
cerebral collateral, arthritis, diabetic neovascularisation, macular  
degeneration, wound healing, Helicobacter related diseases, ovulation,  
menstruation, and cat scratch fever. The present sequence is a protein  
described in the exemplification of the invention  
SQ Sequence 1786 AA;  
Query Match 99.8%; Score 9738; DB 5; Length 1786;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGLIQLLAFSLACRAVRVRAQEPFSGYCAEGSCYPATGDLITGRAQKLSVTSTCGLHK 60  
DB 1 MGLIQLLAFSLACRAVRVRAQEPFSGYCAEGSCYPATGDLITGRAQKLSVTSTCGLHK 60  
QY 61 PEPTCYVSHLQEDKKCTICNSQDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVEN 120  
DB 61 PEPTCYVSHLQEDKKCTICNSQDPYHETLNPDSHLIENVVTTTAPNRLKIWWQSENGVEN 120  
QY 121 VTIOQLDEAEFPHFTHLIMTKTPPAAMLIERSDDPKTWGVYRYFAYDCEASPPGISTG 180  
DB 121 VTIOQLDEAEFPHFTHLIMTKTPPAAMLIERSDDPKTWGVYRYFAYDCEASPPGISTG 180  
QY 181 PMKKVDDIICDSRYSDIEPSTEGERVIIFRALDPAPKIEDPSPRIQNLKLTNLRKIKVKL 240  
DB 181 PMKKVDDIICDSRYSDIEPSTEGERVIIFRALDPAPKIEDPSPRIQNLKLTNLRKIKVKL 240  
QY 241 HTLGNLILDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGFEVEGVMVHGCMC 300  
DB 241 HTLGNLILDSRMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGFEVEGVMVHGCMC 300  
QY 301 RHNTKGLNCELMDPFYHDLPMRPAEGNSNACKKCNCHSHISCHFDMAVYLATGNVSGG 360  
DB 301 RHNTKGLNCELMDPFYHDLPMRPAEGNSNACKKCNCHSHISCHFDMAVYLATGNVSGG 360  
QY 361 VCDQCQHNMTGRNCEQCKPFYVQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420  
DB 361 VCDQCQHNMTGRNCEQCKPFYVQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG 420  
QY 421 LIAQCRCRLNVEGEHCDVCKEGDYDLSSEDPFGCKSCACNPLGTIPGNPCDSETHCY 480  
DB 421 LIAQCRCRLNVEGEHCDVCKEGDYDLSSEDPFGCKSCACNPLGTIPGNPCDSETHCY 480  
QY 481 CKRLVTGQHCDCQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESQCSRCRPHMIGRQC 540  
DB 481 CKRLVTGQHCDCQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFAESQCSRCRPHMIGRQC 540  
QY 541 NEVEPGYFFATLDHYLYEAEANLPGVSIYEROYIQDRIPSWTACGVRVPEGAYLEFF 600  
DB 541 NEVEPGYFFATLDHYLYEAEANLPGVSIYEROYIQDRIPSWTACGVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEYDILIRYEPQLPDHWEKAVITVQRGRIPTSSRCQNTTIPDDDNQVVSLSGP 660





241 HTLGNLLDLSMEIREKYYAYVDMVVRGNCFCYGHASECAPVDGPNFEEVGMVGHGMC 300  
301 RNTKGLNCELMDFYHDLPRPABGRNSNAKCKCNHSHSISCHDFMAVYLATGNVSGG 360  
301 RNTKGLNCELMDFYHDLPRPABGRNSNAKCKCNHSHSISCHDFMAVYLATGNVSGG 360  
361 VDDCOHNTMGRNCQCKPFYYQHPERDIRDNFNCERTCTCDPAGSQNEGICDSYDFSTG 420  
361 VDDCOHNTMGRNCQCKPFYYQHPERDIRDNFNCERTCTCDPAGSQNEGICDSYDFSTG 420  
421 LIAGCRCKLVNVEGHCDCVKEGFFYDLSSDPFGCKSCACNPLGTIPGNCDCSETGHCY 480  
421 LIAGCRCKLVNVEGHCDCVKEGFFYDLSSDPFGCKSCACNPLGTIPGNCDCSETGHCY 480  
481 CKRLVTGHCDCQLPEHMGSLNDLDCRCPDCDLGGALNNSCFABSGQSCSRPHMIGRQC 540  
481 CKRLVTGHCDCQLPEHMGSLNDLDCRCPDCDLGGALNNSCFABSGQSCSRPHMIGRQC 540  
541 NEVEGYYPATLDHYLYEAEANLPGVSIIVERQIQRIPSWTCAAGFVRPEGAYLEFF 600  
541 NEVEGYYPATLDHYLYEAEANLPGVSIIVERQIQRIPSWTCAAGFVRPEGAYLEFF 600  
601 IDNIPYSMEYDLIRYEPOLPDHWEKAVITVORPGRIPTSRRCGNTIPDDNQVVSLSPG 660  
601 IDNIPYSMEYDLIRYEPOLPDHWEKAVITVORPGRIPTSRRCGNTIPDDNQVVSLSPG 660  
661 SRYVLPVPCEKGTNTVRLLEPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
661 SRYVLPVPCEKGTNTVRLLEPQYTSDDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
721 SDGVVTSNAWTFORYRCLNSRSVVKTPMTDVCNIIIFSALLHOTGLACEDCPGGS 780  
721 SDGVVTSNAWTFORYRCLNSRSVVKTPMTDVCNIIIFSALLHOTGLACEDCPGGS 780  
781 LSSVCDPNGGQCQCPNPNVVRGTCNRCAPGTGFGSPGCKPCBCHLQGSVNAFCNPVTQC 840  
781 LSSVCDPNGGQCQCPNPNVVRGTCNRCAPGTGFGSPGCKPCBCHLQGSVNAFCNPVTQC 840  
841 HCFQGVYARQCDRLCPGHWFPSQPCQCNHADDPCDPTGECNCDQYTWGHCNRCCLA 900  
841 HCFQGVYARQCDRLCPGHWFPSQPCQCNHADDPCDPTGECNCDQYTWGHCNRCCLA 900  
901 GYIGDPFIIGSGDHCRPCPCPDGDFSGRQFARSQYQDPVTQLACVCDPFGYIGSRCDCCAS 960  
901 GYIGDPFIIGSGDHCRPCPCPDGDFSGRQFARSQYQDPVTQLACVCDPFGYIGSRCDCCAS 960  
961 GYFGPSPVGGSCQPCQCHNITDTPDACDKETGRCLKCLYHTEGEHCQCRFGYIGDA 1020  
961 GYFGPSPVGGSCQPCQCHNITDTPDACDKETGRCLKCLYHTEGEHCQCRFGYIGDA 1020  
1021 LRQDCRKCVCNLYGTVEHCNGSDCQCKATGQCLCLPNVIGQNCDCRCAPTNTWQLASGTG 1080  
1021 LRQDCRKCVCNLYGTVEHCNGSDCQCKATGQCLCLPNVIGQNCDCRCAPTNTWQLASGTG 1080  
1081 CDPNCNAHSPGSCNFTGQCQMPGFGGTCSECCQLFWGDDPVECRACDCDPRGIE 1140  
1081 CDPNCNAHSPGSCNFTGQCQMPGFGGTCSECCQLFWGDDPVECRACDCDPRGIE 1140  
1141 TPQCQOSTGQCVGVGVEGRCDKTRGYSGVFPDCTPCHOCFALWDVYIABLNTNRHRF 1200  
1141 TPQCQOSTGQCVGVGVEGRCDKTRGYSGVFPDCTPCHOCFALWDVYIABLNTNRHRF 1200  
1201 LEKAKALKISGIVGYRETVDSEVERKVEIKDILAQSPAABPLKNIKNLFEAEKLIKDV 1260  
1201 LEKAKALKISGIVGYRETVDSEVERKVEIKDILAQSPAABPLKNIKNLFEAEKLIKDV 1260  
1261 TEMMAQVEVKLSDDTTQSNSSTAKELDSLQTEAESLDNTVKELAEOLFEIKNSDIRGALDS 1320  
1261 TEMMAQVEVKLSDDTTQSNSSTAKELDSLQTEAESLDNTVKELAEOLFEIKNSDIRGALDS 1320  
1321 ITKYFQMSLEAERNVASTPENSTNVEQSALMRDRVEDVMMERE-SQFKQEQAQRLLD 1379  
1321 ITKYFQMSLEAERNVASTPENSTNVEQSALMRDRVEDVMMERE-SQFKQEQAQRLLD 1380

1380 ELAGKLQSLDLSAAAEWTCCTPPGASCSETCGPNCRITDEGERKCGGPGCGGLVTVAHN 1439  
1381 ELAGKLQSLDLSAAAEWTCCTPPGASCSETCGPNCRITDEGERKCGGPGCGGLVTVAHN 1440  
1440 AWQKAMDLDODVLSALAEVQOLSKMVSSEAKLRADAEAKQSAEDILLKTNATKERKWDKSNEE 1499  
1441 AWQKAMDLDODVLSALAEVQOLSKMVSSEAKLRADAEAKQSAEDILLKTNATKERKWDKSNEE 1500  
1500 LRNLIKQIRNFLTQDSADLDSIEAVANEVLKXEMPTSTPOQLNLTEDIRERVESLSQVEV 1559  
1501 LRNLIKQIRNFLTQDSADLDSIEAVANEVLKXEMPTSTPOQLNLTEDIRERVESLSQVEV 1560  
1560 ILQHSADITARAEMILBEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQKOADED 1619  
1561 ILQHSADITARAEMILBEAKRASKSATDVKVTADMVKEALEEAEKAQVAEKAQKOADED 1620  
1620 IQGTQNLTSISETAASBETLFNASQRISELERNVVEELKRAAQNSEAEYIEKVYVTV 1679  
1621 IQGTQNLTSISETAASBETLFNASQRISELERNVVEELKRAAQNSEAEYIEKVYVTV 1680  
1680 QSAEDVKTLDGELDEKVKYKVENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQ 1739  
1681 QSAEDVKTLDGELDEKVKYKVENLIAKTTESADARRKAEMLQNEAKTLLAQANSKLQ 1740  
1740 LKDLERYEDNQRYLEDKQELARLEGEVRSLLKDISQKVAVYST 1784  
1741 LKDLERYEDNQRYLEDKQELARLEGEVRSLLKDISQKVAVYST 1785

RESULT 9  
AAB19798  
ID AAB19798 standard; protein; 1765 AA.  
XX AAB19798;  
AC AAB19798;  
DT 05-MAR-2001 (first entry)  
XX Human laminin 2 mature beta-1 chain.  
DE Laminin 2: human; nerve regeneration; angiogenic; cell adhesion;  
KW degenerative muscle disorder; muscular dystrophy; cell therapy.  
XX Homo sapiens.  
OS WO2000066730-A2.  
XX 09-NOV-2000.  
XX 28-APR-2000; 2000WO-US011378.  
XX 30-APR-1999; 99US-0131720P.  
XX 15-JUN-1999; 99US-0139198P.  
XX 12-JUL-1999; 99US-0143289P.  
XX 24-SEP-1999; 99US-0155945P.  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX Yurchenco P;  
XX MPI: 2000-687537/67.  
XX N-PSDB; AAA88898.  
XX Purified laminin 2 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX Claim 5; Page 199-204; 305pp; English.  
XX The present sequence is that of the human laminin 2 beta-1 chain mature  
CC protein. Laminin 2 is composed of alpha-2 (400 kDa), beta-1 (100 kDa) and  
CC gamma-1 (100 kDa) chains. It is thought to be specifically required for  
CC stabilizing myotubes during skeletal muscle development, and for

CC preventing apoptosis. Genetic defects in its structure or expression are  
CC associated with a major type of congenital muscular dystrophy. Laminin 2  
CC is also thought to be important in Schwann cell/basal lamina  
CC interactions. The invention provides laminin 2, alpha-2, beta-1 and gamma-  
CC 1 chain polypeptides (see AAB19791-806) and the polynucleotides encoding  
CC them (see AAB8891-906), methods for making recombinant laminin 2, cells  
CC that express recombinant laminin 2, and methods for using purified  
CC laminin 2 for research and therapeutic purposes including peripheral  
CC nerve regeneration, treatment of degenerative muscle disorders,  
CC angiogenesis regulation, promoting cell attachment and migration, ex vivo  
CC cell therapy, improving the take of grafts, improving the  
CC biocompatibility of medical devices and preparing improved culture  
CC devices and media  
XX  
SQ Sequence 1765 AA;

Query Match 99.0%; Score 9654; DB 3; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSCGLHKPEPYCIVSHLOEDKKFCICNS 81  
DB 1 QEPFSGYCAEGSCYPATGDLIGRAQKLSVTSCGLHKPEPYCIVSHLOEDKKFCICNS 60

QY 82 QDPYHETLNPDSHLIENVTTPAPNRLKIWMQSENGVENVTIQDLEAEFHTLIMTK 141  
DB 61 QDPYHETLNPDSHLIENVTTPAPNRLKIWMQSENGVENVTIQDLEAEFHTLIMTK 120

QY 142 TFRPAMLIERSDFGKTGWYRVFAVDCEASFPGISGTGPMKVVDDIICDSRYSDIEPST 201  
DB 121 TFRPAMLIERSDFGKTGWYRVFAVDCEASFPGISGTGPMKVVDDIICDSRYSDIEPST 180

QY 202 EGEVIFRALDPAFKIEDPYSRIQNLKIKTNLRKFKVHLTLGNLDSMEIREKYVA 261  
DB 181 EGEVIFRALDPAFKIEDPYSRIQNLKIKTNLRKFKVHLTLGNLDSMEIREKYVA 240

QY 262 VYDMVRGNCFCYGHASCAPVDGFNEVEGWHGCHMRNTHKGLNCELMDPFYHDLPM 321  
DB 241 VYDMVRGNCFCYGHASCAPVDGFNEVEGWHGCHMRNTHKGLNCELMDPFYHDLPM 300

QY 322 RPAEGRNNAKCKNCNHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPPY 381  
DB 301 RPAEGRNNAKCKNCNHSISCHFDMAVYLATGNVSGVCDCCQHNMTGRNCEQCKPPY 360

QY 382 YQHPERDTRDNFCERCTCDPAGSQNREGICDSYDFSTGLIAGQCKLNVEGEHCDVCK 441  
DB 361 YQHPERDTRDNFCERCTCDPAGSQNREGICDSYDFSTGLIAGQCKLNVEGEHCDVCK 420

QY 442 EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSTGHYCKRLVTOQHCDQCLPEHWGLS 501  
DB 421 EGFYDLSSDPFGCKSCACNPLGTIPGPNPCDSTGHYCKRLVTOQHCDQCLPEHWGLS 480

QY 502 NDLDCRCPDCDILGALNNSCFASGQSCRPMMIGRQCNEVPBGYYFATLDHLYEAE 561  
DB 481 NDLDCRCPDCDILGALNNSCFASGQSCRPMMIGRQCNEVPBGYYFATLDHLYEAE 540

QY 562 ANLGGVSIIVRQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNTPYSNEVDILIRYEPQLP 621  
DB 541 ANLGGVSIIVRQYIQDRIPSWTGAGFVRVPEGAYLEFFIDNTPYSNEVDILIRYEPQLP 600

QY 622 DHWEKAVITVORPGRIPITSSRCGNTIIPDDNQVVSLSFGSRYYVLPVPCFEKGTNYVR 681  
DB 601 DHWEKAVITVORPGRIPITSSRCGNTIIPDDNQVVSLSFGSRYYVLPVPCFEKGTNYVR 660

QY 682 LELPQYTSDDSPVSLPYLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 741  
DB 661 LELPQYTSDDSPVSLPYLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720

QY 742 NSRSVVKTPMTDVCNRIIFSIALLHQTGLACEDCDPOGSLSSVCDPNGGQCCQCPNVCGR 801  
DB 721 NSRSVVKTPMTDVCNRIIFSIALLHQTGLACEDCDPOGSLSSVCDPNGGQCCQCPNVCGR 780

QY 802 TCNRCAPGTFGFGSGCKPCECHLQGSVNAPCNPTVQCHCFQGVYARQCDRCLPGHWGF 861

DB 781 TCNRCAPGTFGFGSGCKPCECHLQGSVNAPCNPTVQCHCFQGVYARQCDRCLPGHWGF 840  
QY 862 PSCQPCQCNHADDCCDFVTGSCINCCDYTWGNCERCLAGYVGPDIIGSDHDCRCPCCPD 921  
DB 841 PSCQPCQCNHADDCCDFVTGSCINCCDYTWGNCERCLAGYVGPDIIGSDHDCRCPCCPD 900

QY 922 GPDGSRFASRCYQDPVTLQACVDPGYTGSRCDDCAGYFQNPSEVGSQCPQCHNN 981  
DB 901 GPDGSRFASRCYQDPVTLQACVDPGYTGSRCDDCAGYFQNPSEVGSQCPQCHNN 960

QY 982 IDTTDPACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLTGVEHCN 1041  
DB 961 IDTTDPACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNLYLTGVEHCN 1020

QY 1042 GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTNQLASGTGDCPCNCNAHSPGSCNEFTG 1101  
DB 1021 GSDCCQDKATGQCLCLPNVIGQNCDCRCAPTNQLASGTGDCPCNCNAHSPGSCNEFTG 1080

QY 1102 QCQWMPFGGRTSECCQELFWGDPDVECRACDDPRGIETPQCDQSTGOCVCEGVEGPR 1161  
DB 1081 QCQWMPFGGRTSECCQELFWGDPDVECRACDDPRGIETPQCDQSTGOCVCEGVEGPR 1140

QY 1162 CDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1221  
DB 1141 CDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIQPYRETVD 1200

QY 1222 SVBRKVSIEIKDIIAQSAPAAEPLKNIKNLPEEAEKLIKDVTEMAQVEVLSLDTTSOSNST 1281  
DB 1201 SVBRKVSIEIKDIIAQSAPAAEPLKNIKNLPEEAEKLIKDVTEMAQVEVLSLDTTSOSNST 1260

QY 1282 AKELDSIQTBASIDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABEVRNASTTE 1341  
DB 1261 AKELDSIQTBASIDNTVKELAEQLEFIKNSDIRGALDSITKYFQMSLEABEVRNASTTE 1320

QY 1342 PNSTVESALMRDRVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAEMTCGTP 1401  
DB 1321 PNSTVESALMRDRVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAEMTCGTP 1380

QY 1402 PGASCSSTEGCGNCRITDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLASALAEVOL 1461  
DB 1381 PGASCSSTEGCGNCRITDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLASALAEVOL 1440

QY 1462 SKWVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521  
DB 1441 SKWVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500

QY 1522 EAVANEVLKXMPSTPQOLQNLTFEDIRERVESLSQVEVILQHSAAADIAEAEMLEAKRA 1581  
DB 1501 EAVANEVLKXMPSTPQOLQNLTFEDIRERVESLSQVEVILQHSAAADIAEAEMLEAKRA 1560

QY 1582 SKSATDVKVTADVMVKEALBEAKAQAQVAAEKAKIQAQDEDIQGTQNLITSISETAASEETL 1641  
DB 1561 SKSATDVKVTADVMVKEALBEAKAQAQVAAEKAKIQAQDEDIQGTQNLITSISETAASEETL 1620

QY 1642 FNASQRISELERNVBELKRAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKVKY 1701  
DB 1621 FNASQRISELERNVBELKRAQAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKVKY 1680

QY 1702 ENLIATKTESADARAKAEMLQNEAKTLLAQANSKLQLLQKLERKYEDNQRYLEDAQBL 1761  
DB 1681 ENLIATKTESADARAKAEMLQNEAKTLLAQANSKLQLLQKLERKYEDNQRYLEDAQBL 1740

QY 1762 ARLEGEVRSLLKDISQKAVYSTCL 1786  
DB 1741 ARLEGEVRSLLKDISQKAVYSTCL 1765

RESULT 10  
AAB48449  
TD AAB48449 standard; protein; 1765 AA.  
XX  
AC AAB48449;

XX 02-MAR-2001 (first entry)  
 XX Human laminin 8 polypeptide, SEQ ID NO: 16.  
 XX Human; laminin 8; neuroprotective; angiogenic; osteopathic;  
 KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
 KW vascular tissue injury; neural injury; angiogenesis regulation.  
 XX *Homo sapiens*.  
 OS  
 XX WO2000066732-A2.  
 PN  
 XX 09-NOV-2000.  
 PD  
 XX 28-APR-2000; 2000WO-US011543.  
 PF  
 XX 30-APR-1999; 99US-0131720P.  
 PR  
 XX 21-AUG-1999; 99US-0149738P.  
 PR  
 XX 24-SEP-1999; 99US-0155945P.  
 PR  
 XX 11-FEB-2000; 2000US-0182012P.  
 PR  
 XX (BIOS-) BIOSTRATUM INC.  
 PA  
 XX Kortessmaa J, Tryggvason K;  
 PI  
 XX WPI: 2000-687539/67.  
 DR N-PSDB; AAC83710.  
 XX  
 XX Purified laminin 8 protein, useful for research and therapeutic purposes  
 PT including peripheral nerve regeneration, treatment of degenerative muscle  
 PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
 PT  
 XX Claim 5; Page 163-168; 245pp; English.  
 PS  
 XX The present sequence is a laminin 8 polypeptide chain. Laminins are a  
 CC family of heterotrimeric glycoproteins that function via binding  
 CC interactions with neighbouring cell receptors and by forming laminin  
 CC networks. They are signalling molecules which influence cellular  
 CC function. Laminin 8 is useful for treating injuries to tissue of  
 CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,  
 CC treating injuries to vascular tissue, promoting cell attachment and  
 CC migration, ex vivo cell therapy, improving the biocompatibility of  
 CC medical devices, and preparing improved cell culture devices and media.  
 CC Laminin 8 is also useful for promoting re-endothelialisation at the site  
 CC of vascular injuries, improving the take of grafts, improving the  
 CC biocompatibility of medical devices, treating neural injuries (neural  
 CC regeneration), regulating angiogenesis, and promoting cell attachment and  
 CC migration  
 CC  
 XX Sequence 1765 AA;  
 SQ  
 Query Match 99.0%; Score 9654; DB 3; Length 1765;  
 Best Local Similarity 100.0%; Pred. NO. 0;  
 Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps - 0;  
 22 QPEPSYCAEGSCVPATGDLII GRAQKLSVTSTGLHKPEPYCIYSHLQEDKKCFICNS 81  
 1 QPEPSYCAEGSCVPATGDLII GRAQKLSVTSTGLHKPEPYCIYSHLQEDKKCFICNS 60  
 82 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDEAFHFTHLIMTPK 141  
 61 QDPYHETLNPDSHLIENVTTFAPNRLKIWQSENGVENVTIQLDEAFHFTHLIMTPK 120  
 142 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFFGISTGPMKVVDDIIICDSRYSDIEPST 201  
 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCEASFFGISTGPMKVVDDIIICDSRYSDIEPST 180  
 202 EGEVIFRALDPAFKIEDPYSPRIQNLKTIINLAIKFKVLHTLGDNLDSRMIREKYIYA 261  
 181 EGEVIFRALDPAFKIEDPYSPRIQNLKTIINLAIKFKVLHTLGDNLDSRMIREKYIYA 240  
 262 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVHGHCMCRHNTKGLNCELCLMDFYHDLFW 321

241 VYDMVVRGNCFCYGHASECAPVDGFNEVEGVHGHCMCRHNTKGLNCELCLMDFYHDLFW 300  
 322 RPAEGRNSACKKCNCHHSISCHFDNAVYLATGNTSGGVCDCCOHNMTGRNCEOCKPFY 381  
 301 RPAEGRNSACKKCNCHHSISCHFDNAVYLATGNTSGGVCDCCOHNMTGRNCEOCKPFY 360  
 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHECHDVCK 441  
 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSTGLIAGQCRCKLNVEGHECHDVCK 420  
 442 EGFYDLSSEDPFGCKSCACNPLGTIPGNEPCDSETHCYCKRLVTHGCHDOCLPEHWGLS 501  
 421 EGFYDLSSEDPFGCKSCACNPLGTIPGNEPCDSETHCYCKRLVTHGCHDOCLPEHWGLS 480  
 502 NDLDCRCPDCDLGGALNNSCFAESGQSCRPMMIGRQCNEVEPGYVFATLDHYLAEAE 561  
 481 NDLDCRCPDCDLGGALNNSCFAESGQSCRPMMIGRQCNEVEPGYVFATLDHYLAEAE 540  
 562 ANLPGVSIIVERQYIQDRIPSWTGAGVRVPEGAYLEFFIDNIPYSMEVDILIRYEPOLP 621  
 541 ANLPGVSIIVERQYIQDRIPSWTGAGVRVPEGAYLEFFIDNIPYSMEVDILIRYEPOLP 600  
 622 DHWEKAVITVQRPGRIPTSRCGNITIPDDNQVVSLSPGSKRYVVLPRPVCFEKGNTYTVR 681  
 601 DHWEKAVITVQRPGRIPTSRCGNITIPDDNQVVSLSPGSKRYVVLPRPVCFEKGNTYTVR 660  
 682 LELPYTSSDSVESPYTLDSILVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 741  
 661 LELPYTSSDSVESPYTLDSILVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720  
 742 NSRVVKTPTMTDVCRNIIIFSISALLHQTGLACBDCPQGSLSVCDPENGQCCQCRPNVGR 801  
 721 NSRVVKTPTMTDVCRNIIIFSISALLHQTGLACBDCPQGSLSVCDPENGQCCQCRPNVGR 780  
 802 TCNECAGTGFPGSGCKPCCEHLQGSVNAFNPVTGQCHCQGVYAROCDCCLPGHWGF 861  
 781 TCNECAGTGFPGSGCKPCCEHLQGSVNAFNPVTGQCHCQGVYAROCDCCLPGHWGF 840  
 862 PSCQPCQCNHADDPVTGCECLNCQDYMTHNCERCCLAGYTGDPITIGSGDHCRCPCPD 921  
 841 PSCQPCQCNHADDPVTGCECLNCQDYMTHNCERCCLAGYTGDPITIGSGDHCRCPCPD 900  
 922 GPDGRFASQYQDPVTLQACVDPGYTGSRCDDCASGYFGNPSVEVSGSCQPCOCHNN 981  
 901 GPDGRFASQYQDPVTLQACVDPGYTGSRCDDCASGYFGNPSVEVSGSCQPCOCHNN 960  
 982 IDTTDPEACDKETGRCLKCLYHTEGHEHCQFCRFYGYGDALRODCRKCVCNLYGTVOEHCN 1041  
 961 IDTTDPEACDKETGRCLKCLYHTEGHEHCQFCRFYGYGDALRODCRKCVCNLYGTVOEHCN 1020  
 1042 GSDCCDKATGQCLCLPNVIGQNCDCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1101  
 1021 GSDCCDKATGQCLCLPNVIGQNCDCAPNTWQLASGTGCDPCNCAHSGFSPSCNEFTG 1080  
 1102 QCQCMFGGRTCSQELFWGDPVECRACDCDPRGIETPQDQSTGQCVCEGVGEPGR 1161  
 1081 QCQCMFGGRTCSQELFWGDPVECRACDCDPRGIETPQDQSTGQCVCEGVGEPGR 1140  
 1162 CDKCTGCGSVGFEDCTPCHOCFALMDVIIAELTNRTHREKAKALKISGVIGPYRETVD 1221  
 1141 CDKCTGCGSVGFEDCTPCHOCFALMDVIIAELTNRTHREKAKALKISGVIGPYRETVD 1200  
 1222 SVERKVSSEIKDILAQSPAAPPLKNIQNLFEAEKLIKDVTEMAQVEVKLSPTTQSNSST 1281  
 1201 SVERKVSSEIKDILAQSPAAPPLKNIQNLFEAEKLIKDVTEMAQVEVKLSPTTQSNSST 1260  
 1282 AKELDSIQTAEBSLNDNTVKELAEQLFEIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1341  
 1261 AKELDSIQTAEBSLNDNTVKELAEQLFEIKNSDIRGALDSITKYFQMSLEAEERVNASTTE 1320  
 1342 PNSTVEQSAALMRDRVEDVMMERESQFKQEBEQARLLDELAKGLQSLDLSAAAEETCGTTP 1401

Db 1321 PNSTVQSALMRDRVEDVMRESOFKEQEQAARLDDELAKLQSLDLSAAAEWTCGTP 1380  
 QY 1402 PGASCETECCGPNCRTEGHERKCGGPGCGGLVTVAHNAWOKAMDDODVLSALAEVEQL 1461  
 Db 1381 PGASCETECCGPNCRTEGHERKCGGPGCGGLVTVAHNAWOKAMDDODVLSALAEVEQL 1440  
 QY 1462 SKMVSAAKLRADEAKQASADILLKTNATKEMKDKNEELRNLIKOIRNFLTQDSADLDSI 1521  
 Db 1441 SKMVSAAKLRADEAKQASADILLKTNATKEMKDKNEELRNLIKOIRNFLTQDSADLDSI 1500  
 QY 1522 EAVANEVLKWEFSTPQQLQNLTEDIRRVESLSQVEVILQHSAAADIARAEMLEEAKRA 1581  
 Db 1501 EAVANEVLKWEFSTPQQLQNLTEDIRRVESLSQVEVILQHSAAADIARAEMLEEAKRA 1560  
 QY 1582 SKSATDVKTADWKEALEEAAKAQVAAKAQKQADEDIQTONLLTSISSETAASBETL 1641  
 Db 1561 SKSATDVKTADWKEALEEAAKAQVAAKAQKQADEDIQTONLLTSISSETAASBETL 1620  
 QY 1642 FNASQRISELRNVBELKKAQNSGEAEYIEKVYTVKQSAEDVKTLDGELDEKVKV 1701  
 Db 1621 FNASQRISELRNVBELKKAQNSGEAEYIEKVYTVKQSAEDVKTLDGELDEKVKV 1680  
 QY 1702 ENLIAKTTEESADARRKAEMLQNEAKTLLAQANSKLQLLKOLERYSDNORYLEDKAQEL 1761  
 Db 1681 ENLIAKTTEESADARRKAEMLQNEAKTLLAQANSKLQLLKOLERYSDNORYLEDKAQEL 1740  
 QY 1762 ARLEGEVRSLLKDISOKVAVYSTCL 1786  
 Db 1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765

## RESULT 11

ABB81591

ID ABB81591 standard; protein; 1765 AA.

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CC useful in maintaining cell/tissue phenotype as well as promoting cell  
 CC growth and differentiation in tissue repair development. Specifically,  
 CC laminin 10 can be used for accelerating the healing injuries of vascular  
 CC tissue, improving the biocompatibility of grafts useful for treating such  
 CC injuries, for promoting re-endothelialisation at the site of vascular  
 CC proliferation, and promote cell attachment and subsequent cell stasis,  
 CC proliferation, differentiation, and/or migration. The present sequence  
 CC represents a second chain protein of laminin 10, from the present  
 CC invention  
 XX SQ Sequence 1765 AA;

Query Match 99.0%; Score 9654; DB 5; Length 1765;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 QEPFYSYCAAGSCVPATGDLIGRAOKLSVTSTGCHKEPEYCIVSHLOEDKKCFICNS 81  
 Db 1 QEPFYSYCAAGSCVPATGDLIGRAOKLSVTSTGCHKEPEYCIVSHLOEDKKCFICNS 60  
 QY 82 QDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVENTIQLDLAEAFHFLIMTFK 141  
 Db 61 QDPYHETLNPDHSHLIENVTTFAPNRLKIWQSENGVENTIQLDLAEAFHFLIMTFK 120  
 QY 142 TFRPAAMLIERSDFGKTGWVRYFYAYDCBASPPGISTGPMKVVDDIICDSRYSDIEPST 201  
 Db 121 TFRPAAMLIERSDFGKTGWVRYFYAYDCBASPPGISTGPMKVVDDIICDSRYSDIEPST 180  
 QY 202 EGEVIFRALDPAFKIEDPYSPRIQNLKLTWLRKFKVLTGLDNLDSMEIREKYFA 261  
 Db 181 EGEVIFRALDPAFKIEDPYSPRIQNLKLTWLRKFKVLTGLDNLDSMEIREKYFA 240  
 QY 262 VYDMVVRGNCFCYGHASECAPVDGFNEEVGVMVGHGCMCRHNTKGLNCELCLMDFYHDLPW 321  
 Db 241 VYDMVVRGNCFCYGHASECAPVDGFNEEVGVMVGHGCMCRHNTKGLNCELCLMDFYHDLPW 300  
 QY 322 RPAGRNSNACKKCNCHESISCHFDMAVYLATONVSGVCGVDDCQNTWGRNCEQCKPFY 381  
 Db 301 RPAGRNSNACKKCNCHESISCHFDMAVYLATONVSGVCGVDDCQNTWGRNCEQCKPFY 360  
 QY 382 YQHPERDIRDNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGCCCKLNVEGHEHCDVCK 441  
 Db 361 YQHPERDIRDNFCERCTCDPAGSQNEGICDSTYDFSTGLIAGCCCKLNVEGHEHCDVCK 420  
 QY 442 EGFYDLSEDDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGCHDQCLPEHWGLS 501  
 Db 421 EGFYDLSEDDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGCHDQCLPEHWGLS 480  
 QY 502 NDLGCRPCDCDLGGALNNSCFAESGQSCRPWHIGRQCNEVEPFGYFATLDHYLAEAE 561  
 Db 481 NDLGCRPCDCDLGGALNNSCFAESGQSCRPWHIGRQCNEVEPFGYFATLDHYLAEAE 540  
 QY 562 ANLGGVSIIVERQYIQDRIPSWTGAGRVVRPBGAYLEFFIDNIPYSMEYDILIRYEPOLP 621  
 Db 541 ANLGGVSIIVERQYIQDRIPSWTGAGRVVRPBGAYLEFFIDNIPYSMEYDILIRYEPOLP 600  
 QY 622 DHWEKAVITVQRCRIPRTSSRCNGTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNTYVR 681  
 Db 601 DHWEKAVITVQRCRIPRTSSRCNGTIPDDDNQVVSLSPGSRVYVLPVPCFEKGTNTYVR 660  
 QY 682 LELPYTSSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVWVNSAWETFORVCL 741  
 Db 661 LELPYTSSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVWVNSAWETFORVCL 720  
 QY 742 NSRSVVTPTMTDVCNRIIFSISALLHQTGLACEDCDPQGLSSVCDPNQGCQCRPNVGR 801  
 Db 721 NSRSVVTPTMTDVCNRIIFSISALLHQTGLACEDCDPQGLSSVCDPNQGCQCRPNVGR 780  
 QY 802 TCNRCAGTGFPGSPGCKPCECHLQGSVNAFCNPTVQCHCQGVYARCCDCLPCHWGF 861  
 Db 781 TCNRCAGTGFPGSPGCKPCECHLQGSVNAFCNPTVQCHCQGVYARCCDCLPCHWGF 840  
 QY 862 PSQFCQCNHADDCCDPTVGTGCLNCDYTMGHNCERCLAGYVGDPIIGSGDHCRPCPCPD 921

New human laminin-10 proteins, useful for accelerating the healing of  
 PT vascular tissue, improving the biocompatibility of grafts, or for  
 PT promoting re-endothelialization at the site of vascular injuries.

Claim 9; Page 126-132; 231pp; English.

The present invention describes human laminin alpha 5. Also described is  
 CC an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are

Db	841	PSQPCQCNHGADD	DPVTGECINLCQDYTWGHNCE	CLAGYTGDP	1IGSGDHCRCPCPD	900			
Qy	922	GPDSGRQPARSCYQD	PVTLQLACVDPGYIGSRCD	CASGYFGNPN	EVGSGSQPCQCHNN	981			
Db	901	GPDSGRQPARSCYQD	PVTLQLACVDPGYIGSRCD	CASGYFGNPN	EVGSGSQPCQCHNN	960			
Qy	982	IDTTDPEACD	KETGRCLKCLYHTEG	SHCQCFRFGYYGD	ALRODCRKCVCNYLGTVOEH	1041			
Db	961	IDTTDPEACD	KETGRCLKCLYHTEG	SHCQCFRFGYYGD	ALRODCRKCVCNYLGTVOEH	1020			
Qy	1042	GSDQCQDKATG	QCLCLPNVIGQNC	DCAPNTWOLAS	TGDCPCNCNAHSAF	GPSNCNEFTG 1101			
Db	1021	GSDQCQDKATG	QCLCLPNVIGQNC	DCAPNTWOLAS	TGDCPCNCNAHSAF	GPSNCNEFTG 1080			
Qy	1102	QCQCMFGFG	GRTCSCEQLFWG	DDPECRACD	CDPRGIETPQCDQSTG	QCVGVGVGGR 1161			
Db	1081	QCQCMFGFG	GRTCSCEQLFWG	DDPECRACD	CDPRGIETPQCDQSTG	QCVGVGVGGR 1140			
Qy	1162	CDKCTRGYS	GVFPDCTPCHOC	FFALMDVYIAEL	TNTRHFL	EKAALIKISGVIGPYRETVD 1221			
Db	1141	CDKCTRGYS	GVFPDCTPCHOC	FFALMDVYIAEL	TNTRHFL	EKAALIKISGVIGPYRETVD 1200			
Qy	1222	SVERKVS	EIKDIIILAQSPA	APLNIGNLFEAE	KLKDVTEMAQ	VEVKLSDTTSQSNST 1281			
Db	1201	SVERKVS	EIKDIIILAQSPA	APLNIGNLFEAE	KLKDVTEMAQ	VEVKLSDTTSQSNST 1260			
Qy	1282	AKELDSIQ	TAESLDNTVK	ELAQLEPIKNSD	IRGALDSITKYFQMS	LEAEBERNASTTE 1341			
Db	1261	AKELDSIQ	TAESLDNTVK	ELAQLEPIKNSD	IRGALDSITKYFQMS	LEAEBERNASTTE 1320			
Qy	1342	PNSVTEQ	SALMRDVEDVM	MERESQFEKEQ	BEQARILDEL	AGLQSLDLSAAAE	MTCGTP 1401		
Db	1321	PNSVTEQ	SALMRDVEDVM	MERESQFEKEQ	BEQARILDEL	AGLQSLDLSAAAE	MTCGTP 1380		
Qy	1402	PGASCS	TECGGPNCR	TDEGERKCGG	PGCGGLVTVAHNA	WKAMDLDQDVL	SALAEVQL 1461		
Db	1381	PGASCS	TECGGPNCR	TDEGERKCGG	PGCGGLVTVAHNA	WKAMDLDQDVL	SALAEVQL 1440		
Qy	1462	SKMYS	EAKLRAD	EAKQSAED	ILLKTNATKE	WDKSNEELNL	IKQIRNFLTQDSAD	LSI 1521	
Db	1441	SKMYS	EAKLRAD	EAKQSAED	ILLKTNATKE	WDKSNEELNL	IKQIRNFLTQDSAD	LSI 1500	
Qy	1522	EAVANEVL	KWEMPSTP	QOLQNL	TEDIR	ERVESLSQVE	VILQHSADITARA	EMLLBEAKRA 1581	
Db	1501	EAVANEVL	KWEMPSTP	QOLQNL	TEDIR	ERVESLSQVE	VILQHSADITARA	EMLLBEAKRA 1560	
Qy	1582	SKSATD	VKVTAD	MVKEALEE	EAKQVAEAKIKO	ADEDIQGTQ	NLNTSIESETA	ASSETL 1641	
Db	1561	SKSATD	VKVTAD	MVKEALEE	EAKQVAEAKIKO	ADEDIQGTQ	NLNTSIESETA	ASSETL 1620	
Qy	1642	FNASQ	RIS	ELERNVEEL	KRAAQNSGE	AEYIEKVYVY	TKQSAEDVK	TKTDLGELDEK	YKVY 1701
Db	1621	FNASQ	RIS	ELERNVEEL	KRAAQNSGE	AEYIEKVYVY	TKQSAEDVK	TKTDLGELDEK	YKVY 1680
Qy	1702	ENLTA	KTTESAD	ARRKAEML	QNEAKTLLA	QNSKLQ	LLDKLERK	YEDNORYLED	KAQEL 1761
Db	1681	ENLTA	KTTESAD	ARRKAEML	QNEAKTLLA	QNSKLQ	LLDKLERK	YEDNORYLED	KAQEL 1740
Qy	1762	ARLEGE	VSRLK	DI	SQKVAVYSTCL	1786			
Db	1741	ARLEGE	VSRLK	DI	SQKVAVYSTCL	1765			
RESULT 12									
AAB19799									
ID	AAB19799 standard; protein; 1786 AA.								
XX	AC AAB19799;								
XX	05-MAR-2001 (first entry)								
XX	Mouse laminin 2 beta-1 chain.								

181 PMKVVDDIICDSRYSDIEPSTEVEIFRALDPFAKIEDPVSRIQNLKATILNRKIFVKL 240  
241 HTLGDNLDRMEIREKIYAVYDMVVRGNCFCYGHASECAPVDGNGNEVEGWHGCHMC 300  
241 HTLGDNLDRMEIREKIYAVYDMVVRGNCFCYGHASECAPVDGNGNEVEGWHGCHMC 300  
301 RHNTKGLNCELCHDFYHDLRPAEGRNSNACKKCNNEHSISCHPDMAYVILATGNVSGG 360  
301 RHNTKGLNCELCHDFYHDLRPAEGRNSNACKKCNNEHSISCHPDMAYVILATGNVSGG 360  
361 VCDCCQNTWGRNCEQCKPYQHPERDIRDPNFCRCTCDPAGSNGEGICDSTYDFSTG 420  
361 VCDCCQNTWGRNCEQCKPYQHPERDIRDPNFCRCTCDPAGSNGEGICDSTYDFSTG 420  
421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSEDPGCKSCACNPLGTIPGNGPCDSETGHY 480  
421 LIAGQCRKLNVEGEHCDVCKEGFYDLSSEDPGCKSCACNPLGTIPGNGPCDSETGHY 480  
481 CKRLVTQCHQDCLPEHFWGLSNDLDCRCPDCLGGALNNSCPAESGQSCSRPHMIGROC 540  
481 CKRLVTQCHQDCLPEHFWGLSNDLDCRCPDCLGGALNNSCPAESGQSCSRPHMIGROC 540  
541 NEVEPGYFATLDHYLVEAEANLPGVSIYERQYIQRIPSWTGTAGFVRVPEGAYLEPF 600  
541 NEVEPGYFATLDHYLVEAEANLPGVSIYERQYIQRIPSWTGTAGFVRVPEGAYLEPF 600  
601 IDNTPYSMEYDILIRYBPQPDHWEKAVITVQRPRIPTSSRCGNTIPDDDNQVSLSPG 660  
601 IDNTPYSMEYDILIRYBPQPDHWEKAVITVQRPRIPTSSRCGNTIPDDDNQVSLSPG 660  
661 SRYVLPFRPVEFGKTYTVLELIPQYTSDDSVESPYTLIDSLVMPYCKSIDITVGG 720  
661 SRYVLPFRPVEFGKTYTVLELIPQYTSDDSVESPYTLIDSLVMPYCKSIDITVGG 720  
721 SGDGWVNTSAMETQRYVRLNLSNVKTPMTDTCRNIIIFSIALLHQTGLACECPQGS 780  
721 SGDGWVNTSAMETQRYVRLNLSNVKTPMTDTCRNIIIFSIALLHQTGLACECPQGS 780  
781 LSSVCDPNNGQCCQRPNNVGRTCNRCAPGIFGFGSPGCKCECHLQGSVNAFCNPVTGOC 840  
781 LSSVCDPNNGQCCQRPNNVGRTCNRCAPGIFGFGSPGCKCECHLQGSVNAFCNPVTGOC 840  
841 HCFQGVYARQDRCLPGHWGFPSCQPCQCNHADDCTPVTECLNCQDYMTHGNCERCLA 900  
841 HCFQGVYARQDRCLPGHWGFPSCQPCQCNHADDCTPVTECLNCQDYMTHGNCERCLA 900  
901 GYGDPIIGSGDHCRPCPCPDGSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDDCAS 960  
901 GYGDPIIGSGDHCRPCPCPDGSGRQFARSCYQDPVTQLACVCDPFGYIGSRCDDCAS 960  
961 GYFGNPSVGVSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGHEHCQFCRFGYVGA 1020  
961 GYFGNPSVGVSCQPCQCHNIDITDPEACDKETGRCLKCLYHTEGHEHCQFCRFGYVGA 1020  
1021 LRQCDRCVCNVYLTGVQEHNGSCQCDKATGQCLCLPNVIGQNCDCRCAPNWOLASGTG 1080  
1021 LRQCDRCVCNVYLTGVQEHNGSCQCDKATGQCLCLPNVIGQNCDCRCAPNWOLASGTG 1080  
1081 CDPNCNAAHFGPSCNFTGQCQCPGFGRTGSECOELFWGDPDVECRACDPRGIE 1140  
1081 CDPNCNAAHFGPSCNFTGQCQCPGFGRTGSECOELFWGDPDVECRACDPRGIE 1140  
1141 TPQCDQSTGQCVGVGVGPRCDKTRGYSVGFPPDCTPCHQCFCALWVILAEFLNTRHRF 1200  
1141 TPQCDQSTGQCVGVGVGPRCDKTRGYSVGFPPDCTPCHQCFCALWVILAEFLNTRHRF 1200  
1201 LEKALKIKISGVIGYRFTVDSVERKVEIKDILAQSPAAPLKNIGLFEAEKLIKDV 1260  
1201 LEKALKIKISGVIGYRFTVDSVERKVEIKDILAQSPAAPLKNIGLFEAEKLIKDV 1260  
1261 TEMAQVEVKLSDTTQSQNSTAKELDSLQTEASLNTVXELAQLEFIKNSDIRGALDS 1320

1261 TEMAQVEVKLSDTTQSQNSTAGELQALQAEBSLDTVKELAEQLEFIKNSDIQOALDS 1320  
1321 ITKTFQMSLEAEERVNASTTTEPNSTVEQSALMRDRVEDVNVVERESQPKQEBOARLLDE 1380  
1321 ITKTFQMSLEAEERVNASTTTEPNSTVEQSALMRDRVEDVNVVERESQPKQEBOARLLDE 1380  
1381 LAGKLOSLDLGAAAEAMTCGTPPGASCSETCEGCGNCRDTEGERKCGGCGGLVTVAHNA 1440  
1381 LAGKLOSLDLGAAAEAMTCGTPPGASCSETCEGCGNCRDTEGERKCGGCGGLVTVAHNA 1440  
1441 WQKAMDLDODVLSALAEVEQLSKMVSEAKLRADBAKQSAEDILLKTNTATKEMDKSNEEL 1500  
1441 WQKAMDLDODVLSALAEVEQLSKMVSEAKLRADBAKQSAEDILLKTNTATKEMDKSNEEL 1500  
1501 RNLKIQINFTQDSADLDSIEAVANEVLKMEPSTPOOLQNLTEDIRERVESISOVEVI 1560  
1501 RNLKIQINFTQDSADLDSIEAVANEVLKMEPSTPOOLQNLTEDIRERVESISOVEVI 1560  
1561 LOHSAADITARAEMLEAEKASKATDVKVTADMVKEALEAEAKQAAEAKAIQOADEDI 1620  
1561 LOHSAADITARAEMLEAEKASKATDVKVTADMVKEALEAEAKQAAEAKAIQOADEDI 1620  
1621 QGTQNLTSISETAASEETLFPNASQRISELERVVEELKRKAAQNSGEAEYIEKVYTVK 1680  
1621 QGTQNLTSISETAASEETLFPNASQRISELERVVEELKRKAAQNSGEAEYIEKVYTVK 1680  
1681 QSAEDVKKTLQDELDEKVKYVENLIAKKTSSADARRKAEMLQNEAKTLLAQANSKLQLL 1740  
1681 QSAEDVKKTLQDELDEKVKYVENLIAKKTSSADARRKAEMLQNEAKTLLAQANSKLQLL 1740  
1741 KDLERKYNEDNQRYLEDKAEQELARLEGEVRSLLKDIISQKAVYSTCL 1786  
1741 KDLERKYNEDNQRYLEDKAEQELARLEGEVRSLLKDIISQKAVYSTCL 1786  
RESULT 13  
AAB48450  
ID AAB48450 standard; protein; 1786 AA.  
XX  
AC AAB48450;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Mouse laminin 8 polypeptide, SEQ ID NO: 18.  
XX  
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;  
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;  
KW vascular tissue injury; neural injury; angiogenesis regulation.  
XX  
OS Mus musculus.  
XX  
PN WO200066732-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011543.  
XX  
PR 30-APR-1999; 99US-0134720P.  
PR 21-AUG-1999; 99US-0149738P.  
PR 24-SEP-1999; 99US-0155945P.  
PR 11-FEB-2000; 2000US-0182012P.  
XX  
PA (BIOS-) BIOSTRATUM INC.  
XX  
XX Kortessmaa J, Tryggvason K;  
PI WPI; 2000-687539/67.  
XX  
DR N-PSDB; AAC83711.  
XX  
XX Purified laminin 8 protein, useful for research and therapeutic purposes  
PT including peripheral nerve regeneration, treatment of degenerative muscle  
PT disorders, angiogenesis regulation, and ex vivo cell therapy.  
XX



PS Claim 5; Page 176-182; 245pp; English.

XX The present sequence is a laminin 8 polypeptide chain. Laminins are a family of heterotrimeric glycoproteins that function via binding interactions with neighbouring cell receptors and by forming laminin networks. They are signalling molecules which influence cellular function. Laminin 8 is useful for treating injuries to tissue of mesenchymal origin, such as bone, cartilage, tendon, and ligament, treating injuries to vascular tissue, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, and preparing improved cell culture devices and media. Laminin 8 is also useful for promoting re-endothelialisation at the site of vascular injuries, improving the take of grafts, improving the biocompatibility of medical devices, treating neural injuries (neural regeneration), regulating angiogenesis, and promoting cell attachment and migration

QY Sequence 1786 AA;

Best Local Similarity 93.7%; Score 9144; DB 3; Length 1786;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLQLLAPFLACRARVAQPEPSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60

DB 1 MGLQLVPAFGVLALWTRVCAQPEPSYGCAGSCYPATGDLIGRAQKLSVTSTCGLHK 60

QY 61 PEYCIYVSHLOEKKQFICNSQDPYHETLNPDSHLLENVVTTPAPNRLKIWQSENGVEN 120

DB 61 PEYCIYVSHLOEKKQFICNSQDPYHETLNPDSHLLENVVTTPAPNRLKIWQSENGVEN 120

QY 121 VTQLDLAEAFPHFTHLIMTKTFRPAMLLIERSDFGKTVGVYRYPAYDCEASFPGISTG 180

DB 121 VTQLDLAEAFPHFTHLIMTKTFRPAMLLIERSDFGKTVGVYRYPAYDCEASFPGISTG 180

QY 181 PMKQVDDIIICDSYSDIEPTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVL 240

DB 181 PMKQVDDIIICDSYSDIEPTEGEVIFRALDPAFKIEDPSPRIQNLKITNLRIKFKVL 240

QY 241 HTLGNLLDSMEIREKYIYAVDMVVRGFCVGHASECAPVDGNEEVGVHGHCMC 300

DB 241 HTLGNLLDSMEIREKYIYAVDMVVRGFCVGHASECAPVDGNEEVGVHGHCMC 300

QY 301 RHNTKGLNCELAMDYHDLPMRPAEGRNSNACKKCNHESISCHDFDMAVLATGNVSG 360

DB 301 RHNTKGLNCELAMDYHDLPMRPAEGRNSNACKKCNHESISCHDFDMAVLATGNVSG 360

QY 361 VCDQCQHTWGRNCEQCKPFYQHPERDIRDPNFCERTCDPAGSNEGICDSYTDFTSG 420

DB 361 VCDQCQHTWGRNCEQCKPFYQHPERDIRDPNFCERTCDPAGSNEGICDSYTDFTSG 420

QY 421 LIAGQCRCKLNVGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETGHCY 480

DB 421 LIAGQCRCKLNVGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETGHCY 480

QY 481 CKRLVTGQCHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABESQCSRPHMIGROC 540

DB 481 CKRLVTGQCHCDQCLPEHWGLSNDLDGCRPCDCLGGALNNSCFABESQCSRPHMIGROC 540

QY 541 NEVPGYVFAFLDHYLVEAEANLPGVSVIYEROYIQRIPSWTGAQFVRVPEGAYLEFF 600

DB 541 NEVPGYVFAFLDHYLVEAEANLPGVSVIYEROYIQRIPSWTGAQFVRVPEGAYLEFF 600

QY 601 IDNTPYSMEYDILIRYBPQPDHWEKAVITVQRPGRIPTSRCGNTIIPDDNQVSLSPG 660

DB 601 IDNTPYSMEYDILIRYBPQPDHWEKAVITVQRPGRIPTSRCGNTIIPDDNQVSLSPG 660

QY 661 SRYVLPKPCFEGKNTYVLELPQYTSDDSVESPVTLIDSLVMPYCKSLDIFTVGG 720

DB 661 SRYVLPKPCFEGKNTYVLELPQYTSDDSVESPVTLIDSLVMPYCKSLDIFTVGG 720

QY 721 SGDGWNTNSAWETPQRYRCLENSRSVVKTPMTDVCNRNIIFSISALIHQTGLACECDPQGS 780

DB 721 SGDGWNTNSAWETPQRYRCLENSRSVVKTPMTDVCNRNIIFSISALIHQTGLACECDPQGS 780

QY 781 LSSVCDNNGGQCQCRPNVVGRTNRCAPGTGFGPSPCKPCECHLQGSVNAFCNPVTGQC 840

DB 781 LSSVCDNNGGQCQCRPNVVGRTNRCAPGTGFGPSPCKPCECHLQGSVNAFCNPVTGQC 840

QY 841 HCFQGVVARQCDRLCPGHGWPSPQPCQCNHADDCCPVTGECILNCODYTGHNCERCLA 900

DB 841 HCFQGVVARQCDRLCPGHGWPSPQPCQCNHADDCCPVTGECILNCODYTGHNCERCLA 900

QY 901 GYGDPIIGSDHCRPCPDGPDGSPGSRQFARSCYQDPVTIQLACVCPGPGVIGSRCDCCAS 960

DB 901 GYGDPIIGSDHCRPCPDGPDGSPGSRQFARSCYQDPVTIQLACVCPGPGVIGSRCDCCAS 960

QY 961 GYFNGPSEVGSQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQFCRGYGYGDA 1020

DB 961 GYFNGPSEVGSQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHCQFCRGYGYGDA 1020

QY 1021 LRQCRKVCNLYGTVOEHNGSDCQCDKATGQCCLPENVIGQNCDCRCAPTNWLASGTG 1080

DB 1021 LRQCRKVCNLYGTVOEHNGSDCQCDKATGQCCLPENVIGQNCDCRCAPTNWLASGTG 1080

QY 1081 CDPNCNNAHSGFSGSCNEFTGQCOCYMGFGGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140

DB 1081 CDPNCNNAHSGFSGSCNEFTGQCOCYMGFGGRTCSCEQLFWGDPDVECRACDCDPRGIE 1140

QY 1141 TPQCDQSTGQCVGVGEGPRCDKCTRGYSGVFPDCTPCHQCFALMDVIIAELNTRTHRF 1200

DB 1141 TPQCDQSTGQCVGVGEGPRCDKCTRGYSGVFPDCTPCHQCFALMDVIIAELNTRTHRF 1200

QY 1201 LEKAKALKISGVIQPYRBTVDVSVERKSEIKDIIAQSPAAPLKNIGNLPEAEKLIKDV 1260

DB 1201 LEKAKALKISGVIQPYRBTVDVSVERKSEIKDIIAQSPAAPLKNIGNLPEAEKLIKDV 1260

QY 1261 TEMMAQVEVKLSDDTTSSOSNSTAKELDSIQTEAESLDNTVKELAEQLEFINKSDIRGALDS 1320

DB 1261 TEMMAQVEVKLSDDTTSSOSNSTAKELDSIQTEAESLDNTVKELAEQLEFINKSDIRGALDS 1320

QY 1321 ITKYPQMSLEAEERNVASTPSTNTEOSALMRDRVEDVMMERESQFKKEQEQEARILDE 1380

DB 1321 ITKYPQMSLEAEERNVASTPSTNTEOSALMRDRVEDVMMERESQFKKEQEQEARILDE 1380

QY 1381 LAGKLSLDLSAAABMTCTGTPPGASCSETECGGNCRTDEGERKCGGCGGLVTVAHNA 1440

DB 1381 LAGKLSLDLSAAABMTCTGTPPGASCSETECGGNCRTDEGERKCGGCGGLVTVAHNA 1440

QY 1441 WQKAMDLDQDVLASALAEVEQLSKMVSSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEEL 1500

DB 1441 WQKAMDLDQDVLASALAEVEQLSKMVSSEAKLRADAEAKQSAEDILLKTNATKEMDKSNEEL 1500

QY 1501 RNLIKQIRNFLTQDSADILDSIEAVANEVTKWEMPTPOOLNLTEDIRERVESLSQVEVI 1560

DB 1501 RNLIKQIRNFLTQDSADILDSIEAVANEVTKWEMPTPOOLNLTEDIRERVESLSQVEVI 1560

QY 1561 LQHSADIAARAEMLEAEAKRASKATDVKVTADVMKEALEAEAKQAAEAKAIKQADEDI 1620

DB 1561 LQHSADIAARAEMLEAEAKRASKATDVKVTADVMKEALEAEAKQAAEAKAIKQADEDI 1620

QY 1621 QCTQNLTSISSETAASSETIFNASQRISELERNVVEELKRYAAQNSGAEYIEKVVIVTK 1680

DB 1621 QCTQNLTSISSETAASSETIFNASQRISELERNVVEELKRYAAQNSGAEYIEKVVIVTK 1680

QY 1681 QSAEDVKTKLDGELDEKVKYVENLIAKKTSSADARRKAEMLONEAKTLLAQANSKLQLL 1740

DB 1681 QSAEDVKTKLDGELDEKVKYVENLIAKKTSSADARRKAEMLONEAKTLLAQANSKLQLL 1740

QY 1741 KDLERKYEDNQYLEDKAEQELARLEGEVRSLLKDIQSKVAVYSTCL 1786

DB 1741 KDLERKYEDNQYLEDKAEQELARLEGEVRSLLKDIQSKVAVYSTCL 1786

RESULT 14

ABB61592

ID	AB881592 standard; protein; 1786 AA.	QY	181	PMKKVDDII	CD	SRYS	DI	EP	ST	EG	EV	I	FR	AL	D	P	AP	K	IE	D	P	S	R	I	O	N	L	L	K	I	T	N	L	R	I	K	F	V	K	L	240																		
XX	AB881592;	DB	181	PMKKVDDII	CD	SRYS	DI	EP	ST	EG	EV	I	FR	AL	D	P	AP	K	IE	D	P	S	R	I	O	N	L	L	K	I	T	N	L	R	I	K	F	V	K	L	240																		
XX	19-SEP-2002 (first entry)	QY	241	HTLGDNLL	DS	RE	IR	E	K	Y	V	A	V	D	M	V	R	G	N	C	F	C	Y	G	H	A	S	E	C	A	P	V	D	G	N	E	E	V	E	G	M	V	H	G	M	C	300												
XX	Mouse laminin 10 second chain protein sequence SEQ ID NO:10.	DB	241	HTLGDNLL	DS	RE	IR	E	K	Y	V	A	V	D	M	V	R	G	N	C	F	C	Y	G	H	A	S	E	C	A	P	V	D	G	N	E	E	V	E	G	M	V	H	G	M	C	300												
XX	Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation; tissue repair development; laminin; healing; vascular tissue; re-endothelialisation; vascular injury; cell attachment; cell stasis; proliferation; migration.	QY	301	RHNTKGLN	C	E	L	C	M	D	F	Y	H	D	L	P	M	R	P	A	E	R	N	S	N	A	K	C	N	C	N	E	H	S	I	S	C	H	F	D	M	A	V	L	A	T	N	V	S	G	360								
KW		DB	301	RHNTKGLN	C	E	L	C	M	D	F	Y	H	D	L	P	M	R	P	A	E	R	N	S	N	A	K	C	N	C	N	E	H	S	I	S	C	H	F	D	M	A	V	L	A	T	N	V	S	G	360								
KW		QY	361	VCDDCOHNT	M	G	N	C	E	O	C	K	P	F	Y	Y	Q	H	P	E	R	D	I	R	P	N	E	C	E	R	C	T	C	D	P	A	G	S	Q	N	E	G	I	C	D	S	T	D	F	S	T	G	420						
OS	Mus musculus.	DB	361	VCDDCOHNT	M	G	N	C	E	O	C	K	P	F	Y	Y	Q	H	P	E	R	D	I	R	P	N	E	C	E	R	C	T	C	D	P	A	G	S	Q	N	E	G	I	C	D	S	T	D	F	S	T	G	420						
XX		QY	421	LIAGCQCR	K	L	N	V	E	G	H	C	D	V	C	K	E	G	F	Y	D	L	S	S	E	D	P	F	C	K	S	C	A	C	N	P	L	T	I	P	G	G	N	P	C	D	S	E	T	H	C	Y	480						
FT		DB	421	LIAGCQCR	K	L	N	V	E	G	H	C	D	V	C	K	E	G	F	Y	D	L	S	S	E	D	P	F	C	K	S	C	A	C	N	P	L	T	I	P	G	G	N	P	C	D	S	E	T	H	C	Y	480						
FT		QY	481	CKRLVTG	O	H	C	D	O	C	L	P	E	H	W	G	L	S	N	D	L	D	G	C	R	P	C	D	C	D	I	G	G	A	L	N	N	S	C	P	A	E	S	G	G	C	S	C	R	P	H	M	I	G	R	Q	540		
XX	W0200250111-A2.	DB	481	CKRLVTG	O	H	C	D	O	C	L	P	E	H	W	G	L	S	N	D	L	D	G	C	R	P	C	D	C	D	I	G	G	A	L	N	N	S	C	P	A	E	S	G	G	C	S	C	R	P	H	M	I	G	R	Q	540		
XX	27-JUN-2002.	QY	541	NEVEGYYF	A	T	I	D	H	L	Y	E	A	E	A	N	L	G	P	G	V	S	I	V	E	R	Q	I	O	R	I	P	S	W	T	G	A	G	F	V	R	P	E	G	A	Y	E	F	600										
XX	21-DEC-2001; 2001WO-US051035.	DB	541	NEVEGYYF	A	T	I	D	H	L	Y	E	A	E	A	N	L	G	P	G	V	S	I	V	E	R	Q	I	O	R	I	P	S	W	T	G	A	G	F	V	R	P	E	G	A	Y	E	F	600										
XX	21-DEC-2000; 2000US-0257449P.	QY	601	IDNIPYS	M	E	Y	D	I	L	R	Y	E	P	O	L	P	D	H	E	K	A	V	I	T	V	O	R	E	G	R	I	P	T	S	R	C	G	T	I	P	D	D	N	Q	V	V	S	L	S	P	G	660						
PR	28-MAR-2001; 2001US-0279282P.	DB	601	IDNIPYS	M	E	Y	D	I	L	R	Y	E	P	O	L	P	D	H	E	K	A	V	I	T	V	O	R	E	G	R	I	P	T	S	R	C	G	T	I	P	D	D	N	Q	V	V	S	L	S	P	G	660						
PR	13-NOV-2001; 2001US-00279282.	QY	661	SRYVVL	P	R	P	V	C	F	E	K	G	T	N	T	V	R	L	E	L	P	Q	T	S	D	S	D	V	E	S	P	T	L	I	D	S	L	V	L	M	P	Y	C	K	S	L	I	F	T	V	G	720						
XX	(BIOS-) BIOSTRATUM INC.	DB	661	SRYVVL	P	R	P	V	C	F	E	K	G	T	N	T	V	R	L	E	L	P	Q	T	S	D	S	D	V	E	S	P	T	L	I	D	S	L	V	L	M	P	Y	C	K	S	L	I	F	T	V	G	720						
XX	Tryggvason K, Doi M, Thyboll J;	QY	721	SGDGVV	T	S	A	N	E	T	F	O	R	Y	E	C	L	S	R	S	V	V	K	T	M	D	V	C	R	N	I	I	F	S	I	A	L	L	H	O	T	G	L	A	C	D	P	G	S	780									
DR	WPI; 2002-557650/59.	DB	721	SGDGVV	T	S	A	N	E	T	F	O	R	Y	E	C	L	S	R	S	V	V	K	T	M	D	V	C	R	N	I	I	F	S	I	A	L	L	H	O	T	G	L	A	C	D	P	G	S	780									
XX	N-PSDB; ABQ72910.	QY	781	LSSVCD	P	N	G	G	O	C	R	P	N	V	V	G	T	C	N	R	C	A	P	T	G	F	G	P	S	G	K	P	C	E	H	L	Q	S	V	N	A	F	C	N	P	V	T	G	840										
PT	New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.	DB	781	LSSVCD	P	N	G	G	O	C	R	P	N	V	V	G	T	C	N	R	C	A	P	T	G	F	G	P	S	G	K	P	C	E	H	L	Q	S	V	N	A	F	C	N	P	V	T	G	840										
XX	Claim 9; Page 140-145; 231pp; English.	QY	841	HCFOG	V	I	A	R	O	C	D	R	C	L	P	H	W	G	F	P	S	C	O	C	N	G	H	A	D	D	C	P	V	T	G	E	C	L	N	C	O	D	T	Y	H	G	N	C	E	R	L	A	900						
CC	The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence encodes a second chain protein of laminin 10, from the present invention	DB	841	HCFOG	V	I	A	R	O	C	D	R	C	L	P	H	W	G	F	P	S	C	O	C	N	G	H	A	D	D	C	P	V	T	G	E	C	L	N	C	O	D	T	Y	H	G	N	C	E	R	L	A	900						
CC		QY	901	GYGDP	I	I	G	S	G	D	H	C	R	P	C	P	D	P	S	G	R	O	F	A	R	S	C	Y	Q	D	P	V	T	L	Q	A	C	V	D	P	G	I	G	S	R	C	D	C	A	S	960								
CC		DB	901	GYGDP	I	I	G	S	G	D	H	C	R	P	C	P	D	P	S	G	R	O	F	A	R	S	C	Y	Q	D	P	V	T	L	Q	A	C	V	D	P	G	I	G	S	R	C	D	C	A	S	960								
CC		QY	961	GYFGN	P	S	V	E	G	S	C	O	P	C	O	C	H	N	I	D	T	D	P	E	A	C	K	E	T	G	R	C	L	K	C	L	Y	H	T	E	G	E	K	O	F	C	R	E	G	Y	G	D	A	1020					
CC		DB	961	GYFGN	P	S	V	E	G	S	C	O	P	C	O	C	H	N	I	D	T	D	P	E	A	C	K	E	T	G	R	C	L	K	C	L	Y	H	T	E	G	E	K	O	F	C	R	E	G	Y	G	D	A	1020					
XX		QY	1021	LRQD	C	R	K	C	V	N	L	G	T	V	O	E	H	C	N	G	S	D	C	O	C	K	A	T	G	Q	L	C	L	P	N	V	I	G	O	N	C	D	R	C	A	P	N	T	W	L	A	S	G	T	1080				
XX		DB	1021	LRQD	C	R	K	C	V	N	L	G	T	V	O	E	H	C	N	G	S	D	C	O	C	K	A	T	G	Q	L	C	L	P	N	V	I	G	O	N	C	D	R	C	A	P	N	T	W	L	A	S	G	T	1080				
XX		QY	1081	CDPCN	C	N	A	H	S	F	G	S	C	N	E	F	T	G	O	C	C	M	P	O	F	G	G	R	T	S	E	C	O	E	L	F	W	G	D	P	D	V	E	C	R	A	C	D	C	P	R	G	I	E	1140				
XX		DB	1081	CDPCN	C	N	A	H	S	F	G	S	C	N	E	F	T	G	O	C	C	M	P	O	F	G	G	R	T	S	E	C	O	E	L	F	W	G	D	P	D	V	E	C	R	A	C	D	C	P	R	G	I	E	1140				
XX		QY	1141	TPQCD	O	S	T	G	O	S	T	G	C	V	C	V	E	G	V	E	G	P	R	C	D	K	T	R	G	Y	S	G	V	F	P	D	C	T	P	C	H	O	C	F	A	L	W	D	V	I	A	E	L	N	T	R	H	F	1200
XX		DB	1141	TPQCD	O	S	T	G	O	S	T	G	C	V	C	V	E	G	V	E	G	P	R	C	D	K	T	R	G	Y	S	G	V	F	P	D	C	T	P	C	H	O	C	F	A	L	W	D	V	I	A	E	L	N	T	R	H	F	1200
XX		QY	1201	LEKAK	A	L	K	I	S	G	V	I	G	P	R	E	T	V	D	S	V	E	K	V	S	E	I	K	D	I	L	A	Q	S	P	A	A	B	P	L	K	N	I	G	N	I	F	E	A	E	K	L	I	K	D	V	1260		
XX		DB	1201	LEKAK	A	L	K	I	S	G	V	I	G	P	R	E	T	V	D	S	V	E	K	V	S	E	I	K	D	I	L	A	Q	S	P	A	A	B	P	L	K	N	I	G	N	I	F	E	A	E	K	L	I	K	D	V	1260		
XX		QY	1261	TEWMA	Q	V	E	K	L	S	D	T	T	S	Q	S	N	S	T	A	K	E	L																																				

Db	1261	TEKAAVEVKLTDTASQSNSTAGELGALQAEESLDKTVKELAEQLERIKNSDIQGLDS	1320
Qy	1321	ITKYFOMSLAEERNVASTENSTVEQSGALMRDVEDVMERESQPKQKQBOEARLIDE	1380
Db	1321	ITKYFOMSLAEERKVNASTTDFNSTVEQSGALTRDVEDMLERESPFKEQEQBOEARLIDE	1380
Qy	1381	LAGKQSLDLAAAEMTCCTPPGASGSETECGGPNCRITDEGRKCGGPGCGGLVTVAHNA	1440
Db	1381	LAGKQSLDLAAAQWTCCTPPGADCSSECGGPNCRITDEGEKCGGPGCGGLVTVAHSA	1440
Qy	1441	WQKAMDLDQDVTLSALAEVQSLSNVSEAKIRADEAKQSAEDILLTNATKERMOKSNEEL	1500
Db	1441	WQKAMDFDRDLVSALAEVQSLSNVSEAKVRADAKQNAQDVLTKTNATKERVDSNEDL	1500
Qy	1501	RNLIKQIRNFTQDSADLDSIEAVANEVLKMWPSSTPQOLQNLITDIERVESLSQVEVI	1560
Db	1501	RNLIKQIRNFTQDSADLDSIEAVANEVLKSGNASTPQOLQNLITDIERVESLTSQVEVI	1560
Qy	1561	LQHSAAIDARAEMLEAEAKRASKSATDVTADMYKEALAEAKQVAEKAQKQADSDI	1620
Db	1561	LQSAADIDARAELLAEAKRASKSATDVTADMYKEALEAEAKQVAEKAQKQADSDI	1620
Qy	1621	QGTQNLITSESTASSETLTFNASORISELERNVEELKRAQNSGEAEYIEKVVTYVK	1680
Db	1621	QGTQNLITSESTASSETLTFNASORISELERNVEELKRAQNSGEAEYIEKVYISVK	1680
Qy	1681	QSAEDVYKTLTGELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQLL	1740
Db	1681	QNAEDVYKTLTGELDEKYYKVENLIAKTEESADARRKAEMLQNEAKTLQAQNSKLQLL	1740
Qy	1741	KDLERKVEDNORYLEDKAQELARLEGEVRSLLKDISOKVANVYSTCL	1786
Db	1741	EDLERKVEDNORYLEDKAQELVRLGEVRSLLKDISERVANVYSTCL	1786

PT	XX	Query Match	93.2%;	Score 9087;	DB 2;	Length 1776;
PS	XX	Best Local Similarity	92.5%;	Pred. No. 0;		
CC	XX	Matches 1647;	Conservative	70;	Mismatches	59;
CC	XX				Indels	4;
CC	XX				Gaps	1;
CC	XX	1	MGLLOLAFSPFALCRARVRAQEPFSGYGAEGSCYPATGDLIGRAQKLSVTSGLHK	60		
CC	XX	1	MGLLQVAFGVLALWGTRVCAQEPFSGYGAEGSCYPATGDLIGRAQKLSVTSGLHK	60		
CC	XX	61	PEPVCIVSHLOEDKKCFICNSQDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVEN	120		
CC	XX	61	PEPVCIVSHLOEDKKCFICNSQDPYHETLNPDSHLIENVVTTAPNRLKIWQSENGVEN	120		
CC	XX	121	VTIQLDEAEFPHFTLIMTKTFRPAAMLIERSSDPKKTGWVYRYFAYDCEASFPFGISTG	180		
CC	XX	121	VTIQLDEAEFPHFTLIMTKTFRPAAMLIERSSDPKKTGWVYRYFAYDCEASFPFGISTG	180		
CC	XX	181	PMKQVDDIICDSRYSDIEPSTEGEVI FRALDPAPFKIEDPYSRIQNLKLTNLRKEVKL	240		
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CC	XX	301	RHNTKGLNCELQCMDFYHDLFWPAPAGNSNACKKCNCHSISCHFDPMAYLATGNVSGG	360		
CC	XX	301	RHNTKGLNCELQCMDFYHDLFWPAPAGNSNACKKCNCHSISCHFDPMAYLATGNVSGG	360		
CC	XX	361	VCDDCQNTWGRNCEOCKPFYVQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTG	420		
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CC	XX	421	LIAGQCRCKLVNVEHCDVCKEGBFYDLSSDDPFCCKSCACNPLGTIPGGNPDSETHCY	480		
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CJD.

Claim 15; Page 90-93; 132pp; English.

This is the amino acid sequence of the mouse laminin B1 chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidosis. The laminin products (see AAW50888-98) may include mouse or human laminin A or A1 chain, laminin B1 or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidosis such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis). the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler syndrome, kuru and animal scrapie (Prp amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin).

Sequence 1776 AA;

QY 481 CKELVTCQHQDQCLPEHMGSLNDLDCRCPDCLGGALNNSCPAESGQCSRPHMIGRQC 540  
DB 481 CKELVTCQHQDQCLPEHMGSLNDLDCRCPDCLGGALNNSCEDSGQCSCLPHMIGRQC 540  
QY 541 NEVEPGYFATLDHYLYEAEANLPGVSVIYERQYQIDRIPSWTGAQFVRVPEGAYLEFF 600  
DB 541 NEVEPGYFATLDHYLYEAEANLPGVSVIYERQYQIDRIPSWTGAQFVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEYDIILIRVEPQLPDHWEKAVITVQRPGRIPPTSSRCGNITPDDDNQVSLSPG 660  
DB 601 IDNIPYSMEYDIILIRVEPQLPDHWEKAVITVQRPGRIPPTSSRCGNITPDDDNQVSLSPG 660  
QY 661 SRYVLPVPVCFKGTNYVRLLELPQVTSDDSVESPYTLIDSLVMPYCKSLDIITVGG 720  
DB 661 SRYVLPVPVCFKGTNYVRLLELPQVTSDDSVESPYTLIDSLVMPYCKSLDIITVGG 720  
QY 721 SGDVNTNSAWETFORVRCLENRSVVKTPMTDVCNIIIFSIISALLHQTGLACEDPQGS 780  
DB 721 SGDVNTNSAWETFORVRCLENRSVVKTPMTDVCNIIIFSIISALLHQTGLACEDPQGS 780  
QY 781 LSSVCDPNGQCCQCRPNVVGRTNRCAPGTGFGPGCKPCBCHLOGSVNAFCNPTVTC 840  
DB 781 LSSVCDPNGQCCQCRPNVVGRTNRCAPGTGFGPGCKPCBCHLOGSVNAFCNPTVTC 840  
QY 841 HCFQGYVAROCDRLPGHMGFPSCOPCCNGHADDCTVTEGLNCQDYTMHNCERCLA 900  
DB 841 HCFQGYVAROCDRLPGHMGFPSCOPCCNGHADDCTVTEGLNCQDYTMHNCERCLA 900  
QY 901 GYGDPIIGSDGHCRCPCDPDPSGRQFARSCYQDPVTQLQACVCDPGYIGSRCDCCAS 960  
DB 901 GYGDPIIGSDGHCRCPCDPDPSGRQFARSCYQDPVTQLQACVCDPGYIGSRCDCCAS 960  
QY 961 GYFNPSEVGSCOPCOCHNIIITDPEACDKETGRCLKCLYHTEGHCQFCRFGYVGA 1020  
DB 961 GYFNPSEVGSCOPCOCHNIIITDPEACDKETGRCLKCLYHTEGHCQFCRFGYVGA 1020  
QY 1021 LRQDCRKCVCNYLGTVEHCNCSQCDKATGQCLCLPNVIGQCRCAPNTWQLASGTG 1080  
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DB 1081 CDPNCNNAHSFGSCNEFTGQCCMPGFGRTSCBCELFWDGPDVECRACDCDPRGIE 1140  
QY 1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSVFPDCTFCHQCFCALMDVIIAELTNTRHF 1200  
DB 1141 TPQCDQSTGQCVCEGVEGPRCDKTRGYSVFPDCTFCHQCFCALMDVIIAELTNTRHF 1200  
QY 1201 LEKAKALKISGIVGYRETVDVSVERKVEIKDILAQSPAAEPLKIGNLFEAEKLIKDV 1260  
DB 1201 LEKAKALKISGIVGYRETVDVSVERKVEIKDILAQSPAAEPLKIGNLFEAEKLIKDV 1260  
QY 1261 TEMMAQVEVKLSDTTSGSNSTAKELDSLQTEAESLDNTVKELABQLEFIKNSDIRGALDS 1320  
DB 1261 TEMMAQVEVKLSDTTSGSNSTAKELDSLQTEAESLDNTVKELABQLEFIKNSDIRGALDS 1320  
QY 1321 ITKYPQMSLEAEERVNASTTSPNSTVGSALMRDRVEDVMRESQPKQEQEQAALLDE 1380  
DB 1321 ITKYPQMSLEAEERVNASTTSPNSTVGSALMRDRVEDVMRESQPKQEQEQAALLDE 1380  
QY 1381 LAGKLOSLDLAAAEWTCGTPPGACSETECGGPNCRITDEGERKCGGCGGLVTVAHNA 1440  
DB 1381 LAGKLOSLDLAAAEWTCGTPPGACSETECGGPNCRITDEGERKCGGCGGLVTVAHNA 1440  
QY 1441 WOKAMDLDDQVLSALAEVQLSKMVEAKLRADSAEDILKTATKEKMDKSNEDL 1500  
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QY 1681 QSAEDVKKTLDGELDEKYYKKVENLIKAKTESADARBAEMLQNEAKTLAQANSKLQLL 1740  
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QY 1741 KDLERKYEDNORYLEDAQELARLEGEVRSLLKDISQKVA 1780  
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DB 1781 EDLERKYEDNORYLEDAQELARLEGEVRSLLKDISQKVA 1780

Search completed: May 18, 2004, 14:41:53  
Job time : 55.5494 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:10:58 ; Search time 13.5107 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-6  
Perfect score: 9754  
Sequence: 1 MGLQLLAFSLALCRARVR.....EVRSLKDISQKAVYSTCL 1786

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/2/aa/5B\_COMB.pep: \*  
3: /cgn2\_6/prodata/2/aa/6A\_COMB.pep: \*  
4: /cgn2\_6/prodata/2/aa/6B\_COMB.pep: \*  
5: /cgn2\_6/prodata/2/aa/PCITUS\_COMB.pep: \*  
6: /cgn2\_6/prodata/2/aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9754	100.0	1786	4	US-09-562-702A-14
2	9754	100.0	1786	4	US-09-561-818A-14
3	9754	100.0	1786	4	US-09-561-709B-9
4	9654	99.0	1765	4	US-09-562-702A-16
5	9654	99.0	1765	4	US-09-561-818A-16
6	9144	93.7	1786	4	US-09-562-702A-18
7	9144	93.7	1786	4	US-09-561-818A-18
8	8873	91.0	1725	4	US-09-562-702A-20
9	8873	91.0	1725	4	US-09-561-818A-20
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11	6051.5	62.0	1196	2	US-08-735-893-4
12	5051.5	51.8	1799	4	US-09-845-583A-6
13	4926.5	50.5	1798	4	US-09-561-709B-11
14	4921.5	50.5	1798	4	US-09-845-583A-8
15	3832.5	39.3	1761	4	US-09-561-709B-1
16	3076.5	31.5	1101	4	US-09-561-709B-5
17	2940.5	30.1	1342	4	US-09-561-709B-13
18	1682	17.2	1605	4	US-09-562-702A-30
19	1682	17.2	1605	4	US-09-561-818A-26
20	1680.5	17.2	1609	4	US-09-562-702A-22
21	1680.5	17.2	1609	4	US-09-561-818A-22
22	1680.5	17.2	1617	4	US-09-562-702A-26
23	1677	17.2	1572	4	US-09-562-702A-32
24	1677	17.2	1572	4	US-09-561-818A-28
25	1673	17.2	279	1	US-08-152-019A-29
26	1673	17.2	1576	4	US-09-562-702A-24
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28	1673	17.2	1584	4	US-09-562-702A-28
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41	1539	15.8	3106	4	US-09-562-702A-10
42	1534.5	15.7	3084	4	US-09-562-702A-12
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45	1515.5	15.5	1587	4	US-09-845-583A-10

ALIGNMENTS

RESULT 1  
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; Sequence 14, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 89-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-14

Query Match 100.0%; Score 9754; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-561-818A-14  
; Sequence 14, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99/274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-14

Query Match 100.0%; Score 9754; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 RENTKGLNCELWDFYHDL.PWRPASEGRNSNACKCKNCNEHSISCHFDMAVYLATGNVSGG 360  
Qy 361 VCDCCOHNMTGRNCQCKPFFYQHBERDIRDNFNCERCTCDPAGSQNEGI CDSYTDFTSG 420  
Db 361 VCDCCOHNMTGRNCQCKPFFYQHBERDIRDNFNCERCTCDPAGSQNEGI CDSYTDFTSG 420  
Qy 421 LIAGQCRKLVNVEGHCDCVKEGFFYDLSDSEDFGCKSCACNPLGTIPGNGPCDSETHCY 480  
Db 421 LIAGQCRKLVNVEGHCDCVKEGFFYDLSDSEDFGCKSCACNPLGTIPGNGPCDSETHCY 480  
Qy 481 CKRLVTGQHCDCQLPEHNGLSNDLDCRCPDCLDGLGALNNSCFABSGQSCSRPHMIGRQC 540  
Db 481 CKRLVTGQHCDCQLPEHNGLSNDLDCRCPDCLDGLGALNNSCFABSGQSCSRPHMIGRQC 540  
Qy 541 NEVEGYYPATLDHVLVYAEAEANLPGVSVISVERQVIQDRIPSWTCAGFVRVPEGAYLEFF 600  
Db 541 NEVEGYYPATLDHVLVYAEAEANLPGVSVISVERQVIQDRIPSWTCAGFVRVPEGAYLEFF 600  
Qy 601 IDNIPYSMEYDILIRYEPOLPHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPG 660  
Db 601 IDNIPYSMEYDILIRYEPOLPHWEKAVITVQRPGRIPTSRRCGNTIPDDNQVVSLSPG 660  
Qy 661 SRYVVLPRPVCPEKGTNYVRLLELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
Db 661 SRYVVLPRPVCPEKGTNYVRLLELPOYTSSDSVESPYTLIDSLVMPYCKSLDIFTVGG 720  
Qy 721 SGDGVVTSASWETFQRYRCLNSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPOGS 780  
Db 721 SGDGVVTSASWETFQRYRCLNSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPOGS 780  
Qy 781 LSVCDPNGGQCCQCPNPNVGRVTCNRCAPGTFFGSPGCKPCBCHLOGSVNAFCNVTQC 840  
Db 781 LSVCDPNGGQCCQCPNPNVGRVTCNRCAPGTFFGSPGCKPCBCHLOGSVNAFCNVTQC 840  
Qy 841 HCFQGYVYARQDRCLPLPHMGFFSPCCQCNHADDPCDPTVTECLNCQDYTMGNHCERCLA 900  
Db 841 HCFQGYVYARQDRCLPLPHMGFFSPCCQCNHADDPCDPTVTECLNCQDYTMGNHCERCLA 900  
Qy 901 GYGGDPIIGSGDHCRPCPCPDGDSGRQPARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
Db 901 GYGGDPIIGSGDHCRPCPCPDGDSGRQPARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
Qy 961 GYFGNPSVGGSCQPCQCHNNIDTTPDCAKDETGRCLKCLVHTGEHCQCFRFGYDGA 1020  
Db 961 GYFGNPSVGGSCQPCQCHNNIDTTPDCAKDETGRCLKCLVHTGEHCQCFRFGYDGA 1020  
Qy 1021 LRQDCKVCNYLGTVQEHNCNGSDCCDKATCQCLCLPNVIGQNCDCRCAPTWQLASGTG 1080  
Db 1021 LRQDCKVCNYLGTVQEHNCNGSDCCDKATCQCLCLPNVIGQNCDCRCAPTWQLASGTG 1080  
Qy 1081 CDPNCNAHSGPSCNFTGOCQMPGFGRTCSCEQLFWGDPDVECRACDDCPRGIE 1140  
Db 1081 CDPNCNAHSGPSCNFTGOCQMPGFGRTCSCEQLFWGDPDVECRACDDCPRGIE 1140  
Qy 1141 TPQCDQSTQCVCVEGVEPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIIAELTNRTHRF 1200  
Db 1141 TPQCDQSTQCVCVEGVEPRCDKCTRGYSGVFPDCTPCHQCFCALWDVIIAELTNRTHRF 1200  
Qy 1201 LEKAKALKISGVIGPYREFVDSVERKVSIEKDILAQSPAAPLKNIGNLFEAEKLIKDV 1260  
Db 1201 LEKAKALKISGVIGPYREFVDSVERKVSIEKDILAQSPAAPLKNIGNLFEAEKLIKDV 1260  
Qy 1261 TENMAQVEVKLSDTTSSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
Db 1261 TENMAQVEVKLSDTTSSQSNSTAKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
Qy 1321 ITKYFOMSLAEERVNASTTENSIVQESALMRDVEDVMMERESQFKEQEQARILDE 1380  
Db 1321 ITKYFOMSLAEERVNASTTENSIVQESALMRDVEDVMMERESQFKEQEQARILDE 1380  
Qy 1381 LAGKQLQSLDLAAAEWTCCTPPGASCSETECGGPNCRDTDEGRKCGGCGGLVTVAHNA 1440  
Db 1381 LAGKQLQSLDLAAAEWTCCTPPGASCSETECGGPNCRDTDEGRKCGGCGGLVTVAHNA 1440

## RESULT 3

US-09-561-709B-9  
; Sequence 9, Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; CURRENT FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-9

Query Match 100.0%; Score 9754; DB 4; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGLLQLLAFSFLALCRARVAAQEPFSYCAEGSCYPATGDLIIGRAQKLSVTSCGLHK 60  
Db 1 MGLLQLLAFSFLALCRARVAAQEPFSYCAEGSCYPATGDLIIGRAQKLSVTSCGLHK 60  
Qy 61 PEPYCVISHVQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
Db 61 PEPYCVISHVQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
Qy 121 VTQDLDEAEFHHTHLIMTFKTRPAAMLIERSDFGKTWGVYRFAYDCEASFPGISTG 180  
Db 121 VTQDLDEAEFHHTHLIMTFKTRPAAMLIERSDFGKTWGVYRFAYDCEASFPGISTG 180  
Qy 181 PMKVKVDIIICDSYSOIEPSTEGEVIIPRALDPAFKIEDPYSPIQNLKITNRIKFKVL 240  
Db 181 PMKVKVDIIICDSYSOIEPSTEGEVIIPRALDPAFKIEDPYSPIQNLKITNRIKFKVL 240  
Qy 241 HTLGDNLDSRMEIREKYYVAVYDMVVRGNCFCYGHASECAPVDGFFNEVEGVHGHCMC 300



Db 241 HTLGDNLLDSEIREYKYYAVYDMVVRGNCFYGHASECAPVDGFNEEVEGVHGHCMC 300  
QY 301 RHNTKGLNCLCMDFYHDLFWRPAEGRNSNACKKCNBHSISCHFDMAVYLATGNVSGG 360  
Db 301 RHNTKGLNCLCMDFYHDLFWRPAEGRNSNACKKCNBHSISCHFDMAVYLATGNVSGG 360  
QY 361 VCDQCQNTVGRNCEQCKPYYOHPERDIRDPNFCRCCTCDPAGSQNEGICSYTDFSTG 420  
Db 361 VCDQCQNTVGRNCEQCKPYYOHPERDIRDPNFCRCCTCDPAGSQNEGICSYTDFSTG 420  
QY 421 LIAQCRCKLVNGEHCDVCKEGFYDLSSDPGCKSCAPNPLGTIPGGNCPDSETHGY 480  
Db 421 LIAQCRCKLVNGEHCDVCKEGFYDLSSDPGCKSCAPNPLGTIPGGNCPDSETHGY 480  
QY 481 CKRLVTGQHCQDCLPEHGWLSNLDGCRPCDCLGGALNNSCPAESGCSCRPHMIGRQC 540  
Db 481 CKRLVTGQHCQDCLPEHGWLSNLDGCRPCDCLGGALNNSCPAESGCSCRPHMIGRQC 540  
QY 541 NEVEPGYFATLHYLYEAEANLGPVSVIRQYIQRIPSWTGAFTVRVPEGAYLEFF 600  
Db 541 NEVEPGYFATLHYLYEAEANLGPVSVIRQYIQRIPSWTGAFTVRVPEGAYLEFF 600  
QY 601 IDNIPYMEYDILIRYBPQLPDHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVWLSFG 660  
Db 601 IDNIPYMEYDILIRYBPQLPDHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVWLSFG 660  
QY 661 SRYVTLPRPVCFKGTNYTVRLLEPQYTSDDSDVESPYTLIDSLVMPYCKSLDIETVGG 720  
Db 661 SRYVTLPRPVCFKGTNYTVRLLEPQYTSDDSDVESPYTLIDSLVMPYCKSLDIETVGG 720  
QY 721 SGDGVTNSAWETFORVRCLENSRSVVKPMTDVCNIIIPSIALLHQTLGACEDPQGS 780  
Db 721 SGDGVTNSAWETFORVRCLENSRSVVKPMTDVCNIIIPSIALLHQTLGACEDPQGS 780  
QY 781 LSSVCDPNQGCQCRPNVGRNTNRCAPTGFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840  
Db 781 LSSVCDPNQGCQCRPNVGRNTNRCAPTGFGPGSGCKPCECHLQGSVNAFCNPVTGQC 840  
QY 841 HCFQGVVAROCDRLCPGHWFPSPOCQCNHADDQDPTVTECLNQDVTMGNHCERCLA 900  
Db 841 HCFQGVVAROCDRLCPGHWFPSPOCQCNHADDQDPTVTECLNQDVTMGNHCERCLA 900  
QY 901 GYVGDPIIGSDHCRPCPCPDGPDGSGRFARSQYQDPTVTLQACVCDPGYIGSRCDCCAS 960  
Db 901 GYVGDPIIGSDHCRPCPCPDGPDGSGRFARSQYQDPTVTLQACVCDPGYIGSRCDCCAS 960  
QY 961 GYFNPSEVGSQPCQCHNIDITDPEACDKETGRCKLKYHTEGHCQCFRFGYIGDA 1020  
Db 961 GYFNPSEVGSQPCQCHNIDITDPEACDKETGRCKLKYHTEGHCQCFRFGYIGDA 1020  
QY 1021 LRQDCRCVCNLYLTQVQHCNCGSDCQCDKATGQCLCLPNVIGQNCDCRCAFNPTWQLASGTG 1080  
Db 1021 LRQDCRCVCNLYLTQVQHCNCGSDCQCDKATGQCLCLPNVIGQNCDCRCAFNPTWQLASGTG 1080  
QY 1081 CDPNCNAAHSFPGSCNEFTGQCCMPFGGRTCSQCELFWDGDPDVECRACDDPRGIE 1140  
Db 1081 CDPNCNAAHSFPGSCNEFTGQCCMPFGGRTCSQCELFWDGDPDVECRACDDPRGIE 1140  
QY 1141 TPQCDQSTGQCVGVEGPRCDKTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHRF 1200  
Db 1141 TPQCDQSTGQCVGVEGPRCDKTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHRF 1200  
QY 1201 LEKAKALKISGVIGPYHETVDSVERKVSSEIKDILASPAAPLKNIGNLFEAEKLIKDV 1260  
Db 1201 LEKAKALKISGVIGPYHETVDSVERKVSSEIKDILASPAAPLKNIGNLFEAEKLIKDV 1260  
QY 1261 TEMMAQVEVKLSDDTSSNSTAKELDSLOTAEASLNTVKELAEQLEFKNSDIRGALDS 1320  
Db 1261 TEMMAQVEVKLSDDTSSNSTAKELDSLOTAEASLNTVKELAEQLEFKNSDIRGALDS 1320  
QY 1321 ITKYFQMSLEABERNASTTEPNSTVQSAALMRDRVEDVNMVERESQFKEQSEQARLLDE 1380

Db 1381 ITKYFQMSLEABERNASTTEPNSTVQSAALMRDRVEDVNMVERESQFKEQSEQARLLDE 1380  
QY 1381 LAGKLOSLDLSAAAEAMTCGTPPGASCSETBEGGPNCRITDEGERKCGGPGGGLYVAHNA 1440  
Db 1381 LAGKLOSLDLSAAAEAMTCGTPPGASCSETBEGGPNCRITDEGERKCGGPGGGLYVAHNA 1440  
QY 1441 WQKAMDLDDQVLSALAEVEQLSKVSEAKURADBAKQSAEDILLKTNATKEKMDKNEEL 1500  
Db 1441 WQKAMDLDDQVLSALAEVEQLSKVSEAKURADBAKQSAEDILLKTNATKEKMDKNEEL 1500  
QY 1501 RNLIKQIRNFUTQDSADLDSIEAVANEVLKXMEMESTPQQLQNLTEDIRERVESLSQVEVI 1560  
Db 1501 RNLIKQIRNFUTQDSADLDSIEAVANEVLKXMEMESTPQQLQNLTEDIRERVESLSQVEVI 1560  
QY 1561 LQHSAAADTARAEMLLEBAKASKSATDVKTADVMKEALBEAEKAQVAAEKAIQOADEDI 1620  
Db 1561 LQHSAAADTARAEMLLEBAKASKSATDVKTADVMKEALBEAEKAQVAAEKAIQOADEDI 1620  
QY 1621 QGTQNLTSISETAASEETLFNASQRISELRNVEELKRKAQNSGEAEYIEKVVYTVK 1680  
Db 1621 QGTQNLTSISETAASEETLFNASQRISELRNVEELKRKAQNSGEAEYIEKVVYTVK 1680  
QY 1681 QSAEDVKTLDGELDEKYYKVENLIKKTBSADARRKAEMLQNEAKTLAQANSKLQLL 1740  
Db 1681 QSAEDVKTLDGELDEKYYKVENLIKKTBSADARRKAEMLQNEAKTLAQANSKLQLL 1740  
QY 1741 KDLERKYEDNORYLEDKQAQELARLEGEVRSLLKDISQKVAVYSTCL 1786  
Db 1741 KDLERKYEDNORYLEDKQAQELARLEGEVRSLLKDISQKVAVYSTCL 1786

## RESULT 4

US-09-562-702A-16  
; Sequence 16, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: furchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-562-702A-16

Query Match 99.0%; Score 9654; DB 4; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QBPFFSYGCAAGSCVPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 81  
Db 1 QBPFFSYGCAAGSCVPATGDLIIIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKCFICNS 60  
QY 82 QDPVHETLNPSHILIENVTTFAPNRLKIWWQSGENVNTIQLDLAEAFHFLIMTFK 141  
Db 61 QDPVHETLNPSHILIENVTTFAPNRLKIWWQSGENVNTIQLDLAEAFHFLIMTFK 120  
QY 142 TFRPAAMLIERSSDFGKTGWYRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 201  
Db 121 TFRPAAMLIERSSDFGKTGWYRYPAYDCEASFPGISTGPMKKVDDIICDSRYSDIEPST 180

QY 202 EGEVIFRALDPFAKIEDPYSPIRIONLLKITNLRKIFVKLHTLGDNLDSRMEIREKYYA 261  
Db 181 EGEVIFRALDPFAKIEDPYSPIRIONLLKITNLRKIFVKLHTLGDNLDSRMEIREKYYA 240  
QY 262 VYDMVVRGNCFCYGHASECAPVDGNEVEGVMHGHCMCRNTKGLNCELWDFYHDLPW 321  
Db 241 VYDMVVRGNCFCYGHASECAPVDGNEVEGVMHGHCMCRNTKGLNCELWDFYHDLPW 300  
QY 322 RPAEGRNSNACKKNCNNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTMGRNCEOCKPFY 381  
Db 301 RPAEGRNSNACKKNCNNEHSISCHFDMAVYLATGNVSGVCDCCOHNMTMGRNCEOCKPFY 360  
QY 382 YQHPERDIRDPNFCRCTCDPAGSQNEGICSDYTDFTSTGLIAGQCRCKLANVEGHCDCVCK 441  
Db 361 YQHPERDIRDPNFCRCTCDPAGSQNEGICSDYTDFTSTGLIAGQCRCKLANVEGHCDCVCK 420  
QY 442 EGFYDLSSDDPGCKSCACNPJGTTIPGNGPCDSETHCYCKELVTGQCHDQCLPHEHGLS 501  
Db 421 EGFYDLSSDDPGCKSCACNPJGTTIPGNGPCDSETHCYCKELVTGQCHDQCLPHEHGLS 480  
QY 502 NDLGCRPCDCLGALANNSCFEAGSCQSCRPHEMIGROCNEVEPGYYFATLDHYLYEABE 561  
Db 481 NDLGCRPCDCLGALANNSCFEAGSCQSCRPHEMIGROCNEVEPGYYFATLDHYLYEABE 540  
QY 562 ANLGPQVSIYERQYIQRDIPSWTGAQFVRVPGAVILEPFDINIPYSMEYDILIRYEPOLP 621  
Db 541 ANLGPQVSIYERQYIQRDIPSWTGAQFVRVPGAVILEPFDINIPYSMEYDILIRYEPOLP 600  
QY 622 DHWEKAVITVQRPGRIPTSRRGNTIPDDNDQVSLSPGSRVYVLPVPCFEKGTNYTVR 681  
Db 601 DHWEKAVITVQRPGRIPTSRRGNTIPDDNDQVSLSPGSRVYVLPVPCFEKGTNYTVR 660  
QY 682 LELPQVTSDDSVESPYTLIDSLVMPYCKSLDIFTVGSGDGUVVNSAWETFFQYRCLE 741  
Db 661 LELPQVTSDDSVESPYTLIDSLVMPYCKSLDIFTVGSGDGUVVNSAWETFFQYRCLE 720  
QY 742 NSRSVVKTPMTDVCNRIIFSI SALLHOTGLACECPDQGLSSVCDPNGGQCCQCRNVVGR 801  
Db 721 NSRSVVKTPMTDVCNRIIFSI SALLHOTGLACECPDQGLSSVCDPNGGQCCQCRNVVGR 780  
QY 802 TNCRCAPGTFGRGSPCKPCBCHLQGSVNAFCNPVTVGQCHQCGVYARQCDRCLPWHGP 861  
Db 781 TNCRCAPGTFGRGSPCKPCBCHLQGSVNAFCNPVTVGQCHQCGVYARQCDRCLPWHGP 840  
QY 862 PSQPCQCHGADCDPVTGECNCDQYTMGNCRCLAGYGGDPIIGSGDHCRCPD 921  
Db 841 PSQPCQCHGADCDPVTGECNCDQYTMGNCRCLAGYGGDPIIGSGDHCRCPD 900  
QY 922 GPDGSRQFARSCYQDPVTIQLACVCDPVGIGSRCDCCASGYFGNPSVGGSCQPCQCHN 981  
Db 901 GPDGSRQFARSCYQDPVTIQLACVCDPVGIGSRCDCCASGYFGNPSVGGSCQPCQCHN 960  
QY 982 IDTTDPEACDKETGRCLKCLYHTEGHCOPCFRFGYGGDALRODCRKCVCNLYGTVOEHCN 1041  
Db 961 IDTTDPEACDKETGRCLKCLYHTEGHCOPCFRFGYGGDALRODCRKCVCNLYGTVOEHCN 1020  
QY 1042 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTCDPCNCNAAHSGFSCNEFTG 1101  
Db 1021 GSDCQCDKATGQCLCLPNVIGQNCRCAPNTWQLASGTCDPCNCNAAHSGFSCNEFTG 1080  
QY 1102 QCCMFPGGRTCSQCEQLFWGDDPVECRACDPRGIEPTQCDQSTGQCVCVEGVEGR 1161  
Db 1081 QCCMFPGGRTCSQCEQLFWGDDPVECRACDPRGIEPTQCDQSTGQCVCVEGVEGR 1140  
QY 1162 CDKCTRGYSVFPDCTPCHQCQFALMDVIIAELTNTRTHRELEKAKALKISGVIGPYRETVD 1221  
Db 1141 CDKCTRGYSVFPDCTPCHQCQFALMDVIIAELTNTRTHRELEKAKALKISGVIGPYRETVD 1200  
QY 1222 SVBRKVSIEKIDILAQSPAAEPLKNIGNLFEAEKLIKOVTEMAQVEVKLSDTTSCSNST 1281  
Db 1201 SVBRKVSIEKIDILAQSPAAEPLKNIGNLFEAEKLIKOVTEMAQVEVKLSDTTSCSNST 1260  
QY 1282 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITIKYFQMSLEAEERVNASTTE 1341

Db 1261 AKELDSLQTEAESLDNTVKELAEQLEFIKNSDIRGALDSITIKYFQMSLEAEERVNASTTE 1320  
QY 1342 PNSTVQCSALMRDRVEDVMMERESQFKEQEQEARLLDLBLAGKQLSLDLSSAAAEVTCGTP 1401  
Db 1321 PNSTVQCSALMRDRVEDVMMERESQFKEQEQEARLLDLBLAGKQLSLDLSSAAAEVTCGTP 1380  
QY 1402 PGASCSETCGGPNCRITDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1461  
Db 1381 PGASCSETCGGPNCRITDEGERKCGGPGCGGLVTVVAHNAWQKAMDLDQDVLSALAEVQL 1440  
QY 1462 SKMVSEAKLRADAEAKQSAEDILLKTNAKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1521  
Db 1441 SKMVSEAKLRADAEAKQSAEDILLKTNAKEMKDSNEELRNLIKQIRNFLTQDSADLDSI 1500  
QY 1522 EAVANEVLMKEMESTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAMLEAEKRA 1581  
Db 1501 EAVANEVLMKEMESTPQQLQNLTEDIRERVESLSQVEVILQHSAAADIAEAMLEAEKRA 1560  
QY 1582 SKGATDVKTADVMVKEALEAEAKQAQVAAKAIKQADEDIQGTQNLTLTSESETAASEETL 1641  
Db 1561 SKGATDVKTADVMVKEALEAEAKQAQVAAKAIKQADEDIQGTQNLTLTSESETAASEETL 1620  
QY 1642 FNASQRISELERNVEELKRAAQSAGEAEYIEKVVTYVTKQSAEDVKKTLDGELDERYKKV 1701  
Db 1621 FNASQRISELERNVEELKRAAQSAGEAEYIEKVVTYVTKQSAEDVKKTLDGELDERYKKV 1680  
QY 1702 ENLIAKTTESADARRKAEMLQNEAKTLQAANSKLOLLKDIERYEDNQRYLEDKAQEL 1761  
Db 1681 ENLIAKTTESADARRKAEMLQNEAKTLQAANSKLOLLKDIERYEDNQRYLEDKAQEL 1740  
QY 1762 ARLEGEVRSLLKDISOKVAVYSTCL 1786  
Db 1741 ARLEGEVRSLLKDISOKVAVYSTCL 1765

RESULT 5  
US-09-561-818A-16  
; Sequence 16, Application US/09561818A  
; Patent No. 5638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,2V4-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1765  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-818A-16

Query Match 99.0%; Score 9654; DB 4; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEPFSGVGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKFCICNS 81  
Db 1 QEPFSGVGCAGSCYPATGDLILIGRAQKLSVTSTCGLHKPEPYCIVSHLOEDKKFCICNS 60  
QY 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSGENVENVTIQLDLAEAFHFLHMTFK 141  
Db 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWQSGENVENVTIQLDLAEAFHFLHMTFK 120  
QY 142 TFRPAAMLIERSSDFGKTGWYRYFAYDCASFPFSTGPMKKVDDIICDSRYSDIEPST 201  
Db 121 TFRPAAMLIERSSDFGKTGWYRYFAYDCASFPFSTGPMKKVDDIICDSRYSDIEPST 180  
QY 202 EGEVIFRALDPFAKIEDPYSPIRIONLLKITNLRKIFVKLHTLGDNLDSRMEIREKYYA 261

Db 181 EGEVIFRALDPAFKIEDPYSPRIQNLKIITNLRIKFKVLHTLGDNLDDSRMEIREKYVYA 240  
Qy 262 VYDMVVRGNCFCYGHASECAPVDGNEEVGMVGHCMCHNTKGLNCELQMDFYHDLPW 321  
Db 241 VYDMVVRGNCFCYGHASECAPVDGNEEVGMVGHCMCHNTKGLNCELQMDFYHDLPW 300  
Qy 322 RPAEGRNSACKKCNCKNEHSTISCFDNVAVLATGNTSGVGVCDCCOHNMTGRNCEQCKPFY 381  
Db 301 RPAEGRNSACKKCNCKNEHSTISCFDNVAVLATGNTSGVGVCDCCOHNMTGRNCEQCKPFY 360  
Qy 382 YQHPERDIRDNFCERCTCDPAGSQNEGI CDSYTFSTGLIAGQCRCKLNVGEHCDVCK 441  
Db 361 YQHPERDIRDNFCERCTCDPAGSQNEGI CDSYTFSTGLIAGQCRCKLNVGEHCDVCK 420  
Qy 442 EGFYDLSSDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCDCCLPEHWGLS 501  
Db 421 EGFYDLSSDPFGCKSCACNPLGTIPGNCPCDSETHCYCKRLVTGQHCDCCLPEHWGLS 480  
Qy 502 NDLGCRPCDDLGALNNSCFABSGQSCRPIMIGRQCNEVEFGYYFATLDHYLYEAE 561  
Db 481 NDLGCRPCDDLGALNNSCFABSGQSCRPIMIGRQCNEVEFGYYFATLDHYLYEAE 540  
Qy 562 ANLGFYSIVVERQIVQIRIPSWTGAQFVRVPEGAYLEFFIDNIPYSNEYDILIRYBOLP 621  
Db 541 ANLGFYSIVVERQIVQIRIPSWTGAQFVRVPEGAYLEFFIDNIPYSNEYDILIRYBOLP 600  
Qy 622 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPVPVCFEKGNTYTVR 681  
Db 601 DHWEKAVITVORPGRIPTSSRCGNTIPDDNQVVSLSFGSRVYVLPVPVCFEKGNTYTVR 660  
Qy 682 LELPQYSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 741  
Db 661 LELPQYSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNTNSAWETFORVRCLE 720  
Qy 742 NSRSVVKTPMTDVCERNIIFISALLHOTGLACEDCPGSSLSVCDPNGGQCCQRPNVVGR 801  
Db 721 NSRSVVKTPMTDVCERNIIFISALLHOTGLACEDCPGSSLSVCDPNGGQCCQRPNVVGR 780  
Qy 802 TCNRCAPGTGFGSGCKPCHECHLOGSVNAPCNVPTGCHCFQGVYARQCDRCPLGHGWF 861  
Db 781 TCNRCAPGTGFGSGCKPCHECHLOGSVNAPCNVPTGCHCFQGVYARQCDRCPLGHGWF 840  
Qy 862 PSCQPCQNGHADDPCDPTVTEGLNCDQVTMGHCNRCERCLAGYGDPIIGSGDHCRPCPCPD 921  
Db 841 PSCQPCQNGHADDPCDPTVTEGLNCDQVTMGHCNRCERCLAGYGDPIIGSGDHCRPCPCPD 900  
Qy 922 GPDGSRQFARSCYQDPVTLQACVDCPGYIGSRDCCDCAAGYFGNPSVGGSCQPCQCHNN 981  
Db 901 GPDGSRQFARSCYQDPVTLQACVDCPGYIGSRDCCDCAAGYFGNPSVGGSCQPCQCHNN 960  
Qy 982 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNVLGTQVQHCN 1041  
Db 961 IDTTDPEACDKETGRCLKLYHTEGHCQFCRFGYGDALRQDCRKCVCNVLGTQVQHCN 1020  
Qy 1042 GSDCCDCKATGQCLCPNVIQONCDRCAPNTWQLASGTGDCPCNCAAHSGFSGSCNEFTG 1101  
Db 1021 GSDCCDCKATGQCLCPNVIQONCDRCAPNTWQLASGTGDCPCNCAAHSGFSGSCNEFTG 1080  
Qy 1102 QCCMPFGGRTSCBQCLFWDGPDVECRACDPCRGLETQPCDQSTQCCVCEVGEVGR 1161  
Db 1081 QCCMPFGGRTSCBQCLFWDGPDVECRACDPCRGLETQPCDQSTQCCVCEVGEVGR 1140  
Qy 1162 CDKCTRGVGVFPDCTPCQCFALMDVIIAELTNRTHRFLEKAKALISGVIQYRFTVD 1221  
Db 1141 CDKCTRGVGVFPDCTPCQCFALMDVIIAELTNRTHRFLEKAKALISGVIQYRFTVD 1200  
Qy 1222 SVERRKVSITKOILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVEVKLSDTTQSNS 1281  
Db 1201 SVERRKVSITKOILAQSPAAPLKNIGNLFEBAEKLIKDVTEMAQVEVKLSDTTQSNS 1260  
Qy 1282 AKELSLQTEABSLDNTYKELAEQLEFKNSDIGNALDSITKYFQMSLEAERNVASTTE 1341  
Db 1261 AKELSLQTEABSLDNTYKELAEQLEFKNSDIGNALDSITKYFQMSLEAERNVASTTE 1320

Qy 1342 PNSTVQSALMRDVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1401  
Db 1321 PNSTVQSALMRDVEDVMMERESQFKEQBEQARLLDELAKGLQSLDLSAAAEWTCGTP 1380  
Qy 1402 PGASCESETCGPNCRTDEGERKCGGPGCGGLVTVVAHNAMQKAMDLDQDVLALAEVEQL 1461  
Db 1381 PGASCESETCGPNCRTDEGERKCGGPGCGGLVTVVAHNAMQKAMDLDQDVLALAEVEQL 1440  
Qy 1462 SKMVSBAKLRADEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1521  
Db 1441 SKMVSBAKLRADEAKQSAEDILLKTNATKEMDKSNEELRNLIKQIRNFLTQDSADLDSI 1500  
Qy 1522 EAVANEVLKMEPSTPQOLQNLITEDIRERVSLSQVEVILQHSAAADIAAEMLLEAKRA 1581  
Db 1501 EAVANEVLKMEPSTPQOLQNLITEDIRERVSLSQVEVILQHSAAADIAAEMLLEAKRA 1560  
Qy 1582 SKSATDVKTADMKVEALBEBAKQAAEKAKQADEDIQGTQNLITSISETAASEETL 1641  
Db 1561 SKSATDVKTADMKVEALBEBAKQAAEKAKQADEDIQGTQNLITSISETAASEETL 1620  
Qy 1642 FNASORISELERNVBEELKRAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYKV 1701  
Db 1621 FNASORISELERNVBEELKRAQNSGEAEYIEKVYVTVKQSAEDVKKTLDGELDEKYKV 1680  
Qy 1702 ENLIAKTEESADARRKAEMLQNEAKTLLAQAANSKQLQLKLERKYEDNORYLEDAQEL 1761  
Db 1681 ENLIAKTEESADARRKAEMLQNEAKTLLAQAANSKQLQLKLERKYEDNORYLEDAQEL 1740  
Qy 1762 ARLEGEVRSLLKDISQKAVYVSTCL 1786  
Db 1741 ARLEGEVRSLLKDISQKAVYVSTCL 1765

## RESULT 6

US-09-562-702A-18  
; Sequence 18, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-18

Query Match 93.7%; Score 9144; DB 4; Length 1786;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGLLQLLAFSLALCRARVRAQEPFSGCAGBSGCPATGDLIGRAQKLSVTSCGLHK 60  
Db 1 MGLLVAFAGVLALWALTRVCAQEPFSGCAGBSGCPATGDLIGRAQKLSVTSCGLHK 60  
Qy 61 PEPYCVIHLQEDKKCFICNSODPHETLNPDSHLIENVVTFAPNRLKIMQSGNGVEN 120  
Db 61 PEPYCVIHLQEDKKCFICDSRDPYHETLNPDSHLIENVVTFAPNRLKIMQSGNGVEN 120  
Qy 121 VTQLDLEAFHFTHLIMTFKTRPAAMLIERSDFGKTGWVYVYFAYDCEASFPFGISTG 180

Db 121 VTIQLDLAEFHTLIMTKTFRPAALIERSSDFGKTWGYRYFAYDCSSPFGISTG 180  
Qy 181 PKMKVDDIICDSRYSDIEPSTEVEVI FPAALDPAFKIEDPYSPRIONLLKIINLRKFKVKL 240  
Db 181 PKMKVDDIICDSRYSDIEPSTEVEVI FPAALDPAFKIEDPYSPRIONLLKIINLRKFKVKL 240  
Qy 241 HTLGNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVDGFNEEVEGVMVGHGMC 300  
Db 241 HTLGNLLDSRMEIREKYYAYVDMVRGNCFCYGHASECAPVDGFNEEVEGVMVGHGMC 300  
Qy 301 RNTKGLNCELWDFYHDLFWPAPGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360  
Db 301 RNTKGLNCELWDFYHDLFWPAPGRNSNACKKNCNEHSISCHFDMAVYLATGNVSGG 360  
Qy 361 VCDCHNTGNCNQCCKPFPYQHPERDIRDNFCERTCTCPAGSONEIGICDSYDFSTG 420  
Db 361 VCDCHNTGNCNQCCKPFPYQHPERDIRDNFCERTCTCPAGSONEIGICDSYDFSTG 420  
Qy 421 LIAGQCRKLNVEGHCVDKSGFVYDLSEDPFGKSCACNPLGTIPGNCPCDSTGHY 480  
Db 421 LIAGQCRKLNVEGHCVDKSGFVYDLSEDPFGKSCACNPLGTIPGNCPCDSTGHY 480  
Qy 481 CKRLVTGQCDQCLPWHGLSNDLDCRCDCLGALNNSCFASGOCSCPHMIGRQC 540  
Db 481 CKRLVTGQCDQCLPWHGLSNDLDCRCDCLGALNNSCFASGOCSCPHMIGRQC 540  
Qy 541 NEVEPYFPATLDHYLAEANLPGVSVIVERQYIQDRIPSWTGAQVVRPEGAYLEFF 600  
Db 541 NEVEPYFPATLDHYLAEANLPGVSVIVERQYIQDRIPSWTGAQVVRPEGAYLEFF 600  
Qy 601 INIPYSMEYDLIRYEPOLPHWEKAVITVORPGRIPTSSRCGNTIPDDNOVLSLPG 660  
Db 601 INIPYSMEYDLIRYEPOLPHWEKAVITVORPGRIPTSSRCGNTIPDDNOVLSLPG 660  
Qy 661 SYVVLPRVPCKEKGNVYVRLPELQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGG 720  
Db 661 SYVVLPRVPCKEKGNVYVRLPELQYTSDDSDVESPYTLIDSLVMPYCKSLDIFTVGG 720  
Qy 721 SGGVVNTNASETQRYRCLNSRSVYKTPMTDVCNIIIFISALLHOTGLACECDPOGS 780  
Db 721 SGGVVNTNASETQRYRCLNSRSVYKTPMTDVCNIIIFISALLHOTGLACECDPOGS 780  
Qy 781 LSSVCDPNGGQCRNVVGRTCNRCAPGTGFGPGCKPCCHLQGSVNAFCNVPVTCQ 840  
Db 781 LSSVCDPNGGQCRNVVGRTCNRCAPGTGFGPGCKPCCHLQGSVNAFCNVPVTCQ 840  
Qy 841 HCFQGYARQCDRLCPGHGFPSCQPCQCNHADDPCDVTGCLNCQDYTMGHNCERCLA 900  
Db 841 HCFQGYARQCDRLCPGHGFPSCQPCQCNHADDPCDVTGCLNCQDYTMGHNCERCLA 900  
Qy 901 GYGDPIIGSGDHCRPCPDGSDGROFARSCYQDPVTLQACVCDPBGYIGSRCDCCAS 960  
Db 901 GYGDPIIGSGDHCRPCPDGSDGROFARSCYQDPVTLQACVCDPBGYIGSRCDCCAS 960  
Qy 961 GYFNPSEVGGSCQPCQCHNITDTPDEACDKETGRCLKLYHTEGECQCFRFGYGDG 1020  
Db 961 GYFNPSEVGGSCQPCQCHNITDTPDEACDKETGRCLKLYHTEGECQCFRFGYGDG 1020  
Qy 1021 LQODCRKVCNVLGTVEHCNCSQCDKATQCLCLPNVIONCDRCAPNTWOLASGTG 1080  
Db 1021 LQODCRKVCNVLGTVEHCNCSQCDKATQCLCLPNVIONCDRCAPNTWOLASGTG 1080  
Qy 1081 CDPNCNAAHSGPSCNEFTGQCQMPFGGRTCSQCBELFWGDPDVECRACDCCDPGIE 1140  
Db 1081 CDPNCNAAHSGPSCNEFTGQCQMPFGGRTCSQCBELFWGDPDVECRACDCCDPGIE 1140  
Qy 1141 TPQCDQSTGQCVCEGVEGPRCKCTRGVSGVFPDCTPCQCHQCFALWDVILNTRHRF 1200  
Db 1141 TPQCDQSTGQCVCEGVEGPRCKCTRGVSGVFPDCTPCQCHQCFALWDVILNTRHRF 1200  
Qy 1201 LKAKALKISGVIQPYRETVDSEKVNBIKILAQSPAAPLKNIGIILFEEAEKUTKOV 1260

Db 1201 LKAKALKISGVIQPYRETVDSEKVNBIKILAQSPAAPLKNIGIILFEEAEKUTKOV 1260  
Qy 1261 TENMAQVEVKLSDTTQSNSSTAKELSLQTEAESLNTVKELAEQLEFIKNDSIRGALDS 1320  
Db 1261 TENMAQVEVKLSDTTQSNSSTAGELGALQAEASLSJTKVKELAEQLEFIKNDSIQGALDS 1320  
Qy 1321 ITKYFQMSLEABERVNASTTPEPNSVTVEQSALMRDRVEDVMVERESQFKQBEQCARLLDE 1380  
Db 1321 ITKYFQMSLEABERVNASTTPEPNSVTVEQSALMRDRVEDVMVERESQFKQBEQCARLLDE 1380  
Qy 1381 LAGKIQSLDLSAAAEWTCGTPPGASCSETCEGPGNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
Db 1381 LAGKIQSLDLSAAAEWTCGTPPGADCESECGPGNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
Qy 1441 WQAMLDQDVLVSALAEVEQLSKWSEAKLRADAEKQSAEDILLKTNATKEMKMDKNEEL 1500  
Db 1441 WQAMLDQDVLVSALAEVEQLSKWSEAKLRADAEKQSAEDILLKTNATKEMKMDKNEEL 1500  
Qy 1501 RNLIKQIRNLTEDSADLSIEAVANVLKWEPESTPOOLQNLTEDIRVERVLSQVEVI 1560  
Db 1501 RNLIKQIRNLTEDSADLSIEAVANVLKWEPESTPOOLQNLTEDIRVERVLSQVEVI 1560  
Qy 1561 LQSAADIAAEMLLEAEKASATDKVTADMKVEALEEAEKQVAAEKAIKQADEDI 1620  
Db 1561 LQSAADIAAEMLLEAEKASATDKVTADMKVEALEEAEKQVAAEKAIKQADEDI 1620  
Qy 1621 QGTQNLTSIESETAASEETLFNASORISELERNVVELKXKAAQNSGEAEYIEKVYVTVK 1680  
Db 1621 QGTQNLTSIESETAASEETLFNASORISELERNVVELKXKAAQNSGEAEYIEKVYVTVK 1680  
Qy 1681 QSAEDVKTLDGELDEKVKVENLIARKTEESADARRKAEMLQNEAKTLIAQANSKLQLL 1740  
Db 1681 QSAEDVKTLDGELDEKVKVENLIARKTEESADARRKAEMLQNEAKTLIAQANSKLQLL 1740  
Qy 1741 KDLERKYEDNQRYLEKQAELEAEVRSLLKXDISQKAVAVYSTCL 1786  
Db 1741 KDLERKYEDNQRYLEKQAELEAEVRSLLKXDISQKAVAVYSTCL 1786

RESULT 7  
US-09-561-818A-18  
; Sequence 18, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmæg, Jarrko  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99/274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-18

Query Match 93.7%; Score 9144; DB 4; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;  
Matches 165; Conservative 72; Mismatches 59; Indels 0; Gaps 0;  
Qy 1 MGLLQLLAFSLACRARVQAQEPFESYGCABSCYPATGDLIIGRAQKLSVTSTCGLHK 60  
Db 1 MGLLQVAFGLALWGTTRVCAQEPFESYGCABSCYPATGDLIIGRAQKLSVTSTCGLHK 60  
Qy 61 PEPYCVISHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWMQSENGVEN 120  
Db 61 PEPYCVISHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWMQSENGVEN 120  
Qy 121 VTIQLDLAEAFHTLIMTKTFRPAALIERSSDFGKTWGYRYFAYDCSSPFGISTG 180  
Db 121 VTIQLDLAEAFHTLIMTKTFRPAALIERSSDFGKTWGYRYFAYDCSSPFGISTG 180

181 PMKXVDDIIICDSYSOIEPTEGEVIFRALDPAPKIEDPYSPRIQNLKILNIRIKFVKL 240  
Db  
181 PMKXVDDIIICDSYSOIEPTEGEVIFRALDPAPKIEDPYSPRIQNLKILNIRIKFVKL 240  
Qy  
241 HTLGDNLDDSRMEIREKYYAVVDMVVRGNCFCYGHASCECAPVDGPNVEEVEGVHGHCMC 300  
Db  
241 HTLGDNLDDSRMEIREKYYAVVDMVVRGNCFCYGHASCECAPVDGPNVEEVEGVHGHCMC 300  
Qy  
301 RHNTKGLNCELMDFYHDLRPAERGRNSNACKKCNNEHSISCHPDMVAVIATGNVSGG 360  
Db  
301 RHNTKGLNCELMDFYHDLRPAERGRNSNACKKCNNEHSISCHPDMVAVIATGNVSGG 360  
Qy  
361 VCDNCOHNTWGRNCEQCKPYVQHPERDIRDPNFCRCTCDPAGSONEGICDSTDFSTG 420  
Db  
361 VCDNCOHNTWGRNCEQCKPYVQHPERDIRDPNFCRCTCDPAGSONEGICDSTDFSTG 420  
Qy  
421 LIAQQRCKLVNVEGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGGNCPDSETGHCY 480  
Db  
421 LIAQQRCKLVNVEGEHCDVCKEGFYDLSSEDPFGCKSCACNPLGTIPGGNCPDSETGHCY 480  
Qy  
481 CKRLVTQHCDCQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFABSGQSCSRPHMIGROC 540  
Db  
481 CKRLVTQHCDCQCLPEHWGLSNDLDGCRPCDCDLGGALNNSCFABSGQSCSRPHMIGROC 540  
Qy  
541 NEVEPGYFFATLHYLYEAEANLPGVSVIVERQYIQRIPSWTGTAGFVRVPEGAYLEFF 600  
Db  
541 NEVEPGYFFATLHYLYEAEANLPGVSVIVERQYIQRIPSWTGTAGFVRVPEGAYLEFF 600  
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601 IDNIPYMEVDILIRYEPQPDHWEKAVITVQRPRIPTSSRCNTIPDDNQVSLSPG 660  
Db  
601 IDNIPYMEVDILIRYEPQPDHWEKAVITVQRPRIPTSSRCNTIPDDNQVSLSPG 660  
Qy  
661 SRYVLPVPCFEKGMVTVRLELPQYTSDDSVESPYTLIDSLVMPYCKSIDIFTVGG 720  
Db  
661 SRYVLPVPCFEKGMVTVRLELPQYTSDDSVESPYTLIDSLVMPYCKSIDIFTVGG 720  
Qy  
721 SGDGVWNSAWETFORVRCLENSSVVKTMTDVCNRNIIFISIALHQTGLACECDPQGS 780  
Db  
721 SGDGVWNSAWETFORVRCLENSSVVKTMTDVCNRNIIFISIALHQTGLACECDPQGS 780  
Qy  
781 LSSVCDNGGOCQCRPNVVGRTNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGOC 840  
Db  
781 LSSVCDNGGOCQCRPNVVGRTNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGOC 840  
Qy  
841 HCFQGVARQCDRLPGHWGPPSCQPCQNGHADDCDPTVTGECNLCODYTMGNHCERCLA 900  
Db  
841 HCFQGVARQCDRLPGHWGPPSCQPCQNGHADDCDPTVTGECNLCODYTMGNHCERCLA 900  
Qy  
901 GYGDPIIGSDGHCRCPCPDGPGSGRQFARSCYQDPVTLQLACVCDPGVIGSRCDDCAS 960  
Db  
901 GYGDPIIGSDGHCRCPCPDGPGSGRQFARSCYQDPVTLQLACVCDPGVIGSRCDDCAS 960  
Qy  
961 GYFNPSEVSGSCQPCQCHNIDITDPEACDKETGRCLKLYHTEGHCQFCRFGYVGA 1020  
Db  
961 GYFNPSEVSGSCQPCQCHNIDITDPEACDKETGRCLKLYHTEGHCQFCRFGYVGA 1020  
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1021 LRQCRKVCNVLGTVEHNGSCQCDKATGQCLCLPNVIGQNCDCAPNTWLASGTG 1080  
Db  
1021 LRQCRKVCNVLGTVEHNGSCQCDKATGQCLCLPNVIGQNCDCAPNTWLASGTG 1080  
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1081 CDPNCNAAHFGSPCNBFTQCCQCMFGGRTCSQCELFWGDPDVECRACDCDPRGIE 1140  
Db  
1081 CDPNCNAAHFGSPCNBFTQCCQCMFGGRTCSQCELFWGDPDVECRACDCDPRGIE 1140  
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1141 TPQCDQSTGQCQVGVGEPGRCCKTRGYSGVFPDCTPCHQCQFALWDVIAELTNRTHRF 1200  
Db  
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Qy  
1201 LEKAKALISGVIGYRVTDSVERKVEIKDILAQSPAAEPKINIGLPEEAKIKDV 1260  
Db  
1201 LEKAKALISGVIGYRVTDSVERKVEIKDILAQSPAAEPKINIGLPEEAKIKDV 1260

1261 TEMMAQVEVKLSDDTTSSOSNSTAKELDSIOTEAESLDNTVKELABQLEFIKNSDIRGALDS 1320  
Db  
1261 TEMMAQVEVKLSDDTTSSOSNSTAKELDSIOTEAESLDNTVKELABQLEFIKNSDIRGALDS 1320  
Qy  
1321 ITKYFQMSLEAEERNVASTTSPNSTVQSSALMRDRVEDVMMERESQFKEQOEQARLLDE 1380  
Db  
1321 ITKYFQMSLEAEERNVASTTSPNSTVQSSALMRDRVEDVMMERESQFKEQOEQARLLDE 1380  
Qy  
1381 LAGKLOSLDLSAAAEAMTCGPPGASCSTECGPGNCRITDEGERKCGGPGCGGLVTVAHNA 1440  
Db  
1381 LAGKLOSLDLSAAAEAMTCGPPGASCSTECGPGNCRITDEGERKCGGPGCGGLVTVAHNA 1440  
Qy  
1441 WQKAMDLDQDYLALAEVEQLSKMVSEAKURADRAKASAEEDILIKTNATKEMDKSNEEL 1500  
Db  
1441 WQKAMDLDQDYLALAEVEQLSKMVSEAKURADRAKASAEEDILIKTNATKEMDKSNEEL 1500  
Qy  
1501 RNLIKQINFLITQSDLDSTAEVANEVLKMEMESTPOQLQNTLTERERVESLSQVEVI 1560  
Db  
1501 RNLIKQINFLITQSDLDSTAEVANEVLKMEMESTPOQLQNTLTERERVESLSQVEVI 1560  
Qy  
1561 LQHSAAADTARAEMLEBAKRAKASKATDVKYTADMVKEALEEAEKAAVAAEKAIKQADEDI 1620  
Db  
1561 LQHSAAADTARAEMLEBAKRAKASKATDVKYTADMVKEALEEAEKAAVAAEKAIKQADEDI 1620  
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1621 QGTQNLITSISETAASEETLFNASORISELERNVEELKRAKAAQNSGEAEYIEKVYTVK 1680  
Db  
1621 QGTQNLITSISETAASEETLFNASORISELERNVEELKRAKAAQNSGEAEYIEKVYTVK 1680  
Qy  
1681 QSAEDVKVTLQGLDEKVKYVENLIATKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740  
Db  
1681 QSAEDVKVTLQGLDEKVKYVENLIATKTESADARRKAEMLQNEAKTLLAQANSKLQLL 1740  
Qy  
1741 KDLERKYEDNORYLEDKAEQELARLEGEVRSLLKDISQKVAIVYSTCL 1786  
Db  
1741 KDLERKYEDNORYLEDKAEQELARLEGEVRSLLKDISQKVAIVYSTCL 1786

## RESULT 8

US-09-562-702A-20  
; Sequence 20, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-20

Query Match 91.0%; Score 8873; DB 4; Length 1725;

Best Local Similarity 92.9%; Pred. No. 0;

Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy 62 EYICVISHLOEKKFCICNSQDPYHETLNPDHSLTENVTTFAPNRLKIWQSENGVNV 121

Db 1 EYICVISHLOEKKFCICNSQDPYHETLNPDHSLTENVTTFAPNRLKIWQSENGVNV 60

Qy 122 TTQOLDLEAFHFHTLIMTFKTPRPAAMLIERSDDFKTGVYRYPAYDCEASFPGISGTP 181

Db 61 TIQDLAEAFHFTLIMTKTFRPAAMLIERSDFGTWGVYRYPAYDCSSFFGISTGP 120  
Qy 182 MKKVDIIICDSYSDIEPSTGEVIFRALDPAFKIEDPYSRIQNLKITNLRKFVKLH 241  
Db 121 MKKVDIIICDSYSDIEPSTGEVIFRALDPAFKIEDPYSRIQNLKITNLRKFVKLH 180  
Qy 242 TLGDNLDSRMEIREKYYAVYDMVVRGNCPCYGHASECAPVDGNEVEGVHGHCMCR 301  
Db 181 TLGDNLDSRMEIREKYYAVYDMVVRGNCPCYGHASECAPVDGNEVEGVHGHCMCR 240  
Qy 302 HNTKGLNCELMDFFVHDLPRWAEGRNSNACKKNCNHSISCHPDMAVILATGNVSGV 361  
Db 241 HNTKGLNCELMDFFVHDLPRWAEGRNSNACKKNCNHSISCHPDMAVILATGNVSGV 300  
Qy 362 CDDCCHNTMGRNCEOCKPFYQHPERDIRDPNFCERTCDPAGSQNEGICDSYDFSTGL 421  
Db 301 CDDCCHNTMGRNCEOCKPFYQHPERDIRDPNFCERTCDPAGSQNEGICDSYDFSTGL 360  
Qy 422 IAGQCRKLVNVEGHCDCVCKEFDYLSBEDPGCKSCACNPLGTIPGNCPCDSETHGVC 481  
Db 361 IAGQCRKLVNVEGHCDCVCKEFDYLSBEDPGCKSCACNPLGTIPGNCPCDSETHGVC 420  
Qy 482 KRLVTHGOHCDQCLPEHGWLSNDLDGCRPCDCLGALANNSCPAESGQSCSRPHMIGRCN 541  
Db 421 KRLVTHGOHCDQCLPEHGWLSNDLDGCRPCDCLGALANNSCPAESGQSCSRPHMIGRCN 480  
Qy 542 EYEPGYFATLDRHLYVEAEANLPGVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFFI 601  
Db 481 EYEPGYFATLDRHLYVEAEANLPGVSVIVERQYIQRIPSWTGAQFVRVPEGAYLEFFI 540  
Qy 602 DNIPISEMEYDILIRYEPQLPDHWEKAVITVQPPGRIPTSRRGNTIPDDNDNOVLSPGS 661  
Db 541 DNIPISEMEYDILIRYEPQLPDHWEKAVITVQPPGRIPTSRRGNTIPDDNDNOVLSPGS 600  
Qy 662 RYVVLPRPVCFEKGTNYTVRLLEPQVTSSDSDVESPYTLIDSLVLMPYCKSLDIFTVGGS 721  
Db 601 RYVVLPRPVCFEKGTNYTVRLLEPQVTSSDSDVESPYTLIDSLVLMPYCKSLDIFTVGGS 660  
Qy 722 GDGVNTNSAWEITFORVCLSENSSVUKTPTMTDVCNRIIFSIALLHOTGLACECPQSSL 781  
Db 661 GDGVNTNSAWEITFORVCLSENSSVUKTPTMTDVCNRIIFSIALLHOTGLACECPQSSL 720  
Qy 782 SSVCDPENGQCCQPRNVVGRTCNRCAPGTFTGPGSCCKPCBCHLOGSVNAPCNVPTGQCH 841  
Db 721 SSVCDPENGQCCQPRNVVGRTCNRCAPGTFTGPGSCCKPCBCHLOGSVNAPCNVPTGQCH 780  
Qy 842 CPGVVARQCDRLCPGHWFPPSCQPCQNGHADDCTPVTGCLNCDYTMHNCRCCLAG 901  
Db 781 CPGVVARQCDRLCPGHWFPPSCQPCQNGHADDCTPVTGCLNCDYTMHNCRCCLAG 840  
Qy 902 YGDPPIIGSDHCRPCPCPDGDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG 961  
Db 841 YGDPPIIGSDHCRPCPCPDGDSGRQFARSCYQDPVTIQLACVCDPGYIGSRCDDCASG 900  
Qy 962 YFNGNPEVSGSCPCQCHNIDITDDEACDKETGRCLKLYHTEGHCQFCFPYVGDAL 1021  
Db 901 YFNGNPEVSGSCPCQCHNIDITDDEACDKETGRCLKLYHTEGHCQFCFPYVGDAL 960  
Qy 1022 RQCRKVCNLYTVGHEHNGSDCQCDKATGQCLCLPNVIGMCDRCAPNTWQLASGTGC 1081  
Db 961 RQCRKVCNLYTVGHEHNGSDCQCDKATGQCLCLPNVIGMCDRCAPNTWQLASGTGC 1020  
Qy 1082 DPCNNAHSGFPGSCNEFTQCCQCMFPGGRTCSBCEQLFWGDDPVECRACDCDPRGIET 1141  
Db 1021 DPCNNAHSGFPGSCNEFTQCCQCMFPGGRTCSBCEQLFWGDDPVECRACDCDPRGIET 1080  
Qy 1142 PQCDQSTGQCVGVEGPRCDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHREL 1201  
Db 1081 PQCDQSTGQCVGVEGPRCDKCTRGYSVFPDCTPCHQCFALMDVIIAELTNRTHREL 1140  
Qy 1202 EKAKALKISGIVGYRETVDVSRVKSEIKDIIAQSPAAEPLKNIQNLFEAEKLIKDV 1261  
Db 1141 EKAKALKISGIVGYRETVDVSRVKSEIKDIIAQSPAAEPLKNIQNLFEAEKLIKDV 1200

Qy 1262 EMMAQVEVKLSDDTSSOSNSTAKELDSLOTEAESLNTVKELEAEQLEFIKNSDIRGALDSI 1321  
Db 1201 EMMAQVEVKLSDDTSSOSNSTAGELGALQAEASLDTKTVKELEAEQLEFIKNSDIQGALDSI 1260  
Qy 1322 TKYFQMSLEAEERVNASTTTPNSTVBSQALMRDRVEDVMMERESQFKEQEQEARLLDEL 1381  
Db 1261 TKYFQMSLEAEERVNASTTTPNSTVBSQALTRDVEDLMLERESPFKEQEQEARLLDEL 1320  
Qy 1382 AGKLQSLDLSAAAEAMTCGTPPGASCSETBEGGNCRTDSEGRKCGPGCGGLVTVAHNAW 1441  
Db 1321 AGKLQSLDLSAAAEAMTCGTPPGASCSETBEGGNCRTDSEGRKCGPGCGGLVTVAHNAW 1380  
Qy 1442 QKAWDLDODVLSALAEVQQLSKMVSRAKLRADAKOSAEIDILLKTNATKEKMDKSNEELR 1501  
Db 1381 QKAWDLDODVLSALAEVQQLSKMVSRAKLRADAKQNAQDVLKTNATKEKMDKSNEELR 1440  
Qy 1502 NLIKQIRNFLTQPSADLDSIEAVANEVLMEMPTPQQLQNLTFEDIRVERVESQVEVIL 1561  
Db 1441 NLIKQIRNFLTQPSADLDSIEAVANEVLMEMPTPQQLQNLTFEDIRVERVESQVEVIL 1500  
Qy 1562 QHSAADITARAEMLEEAERKASKATDVKTADVMVKEALEBAEAKAQAADDEDIQ 1621  
Db 1501 QHSAADITARAEMLEEAERKASKATDVKTADVMVKEALEBAEAKAQAADDEDIQ 1560  
Qy 1622 GTQNLTSISETAASBETLNFASQRISELERNVVELKXKAAQNSGEAEYIEKVVTYVKQ 1681  
Db 1561 GTQNLTSISETAASBETLNFASQRISELERNVVELKXKAAQNSGEAEYIEKVVTYVKQ 1620  
Qy 1682 SAEDVKTLDELDEKYEKVENLIAKTTESADARRKAEMLONEAKTLAQAANSKLQLLX 1741  
Db 1621 NADDVKTLDELDEKYEKVENLIAKTTESADARRKAEMLONEAKTLAQAANSKLQLLX 1680  
Qy 1742 DLERKYEDNORYLEDKAEQELARLEGEVRSLLKDIQSKVAVYSTCL 1786  
Db 1681 DLERKYEDNORYLEDKAEQELARLEGEVRSLLKDIQSKVAVYSTCL 1725

## RESULT 9

US-09-561-818A-20  
; Sequence 20, Application US/09561818A  
; Patent No. 6638907  
; GENERAL INFORMATION:  
; APPLICANT: Kortessmaa, Jarkko  
; APPLICANT: Tryggvason, Karl  
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use  
; FILE REFERENCE: 99,274-D  
; CURRENT APPLICATION NUMBER: US/09/561,818A  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20:  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-561-818A-20

Query Match 91.0%; Score 8873; DB 4; Length 1725;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 1602; Conservative 71; Mismatches 52; Indels 0; Gaps 0;

Qy 62 EPCYGVSHLQDKKCFICNSQDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 121  
Db 1 EPCYGVSHLQDKKCFICNSQDPVHETLNPDSHLIENVVTFAPNRLKIWWQSENGVENV 60  
Qy 122 TIQDLAEAFHFTLIMTKTFRPAAMLIERSDFGTWGVYRYPAYDCSSFFGISTGP 181  
Db 61 TIQDLAEAFHFTLIMTKTFRPAAMLIERSDFGTWGVYRYPAYDCSSFFGISTGP 120  
Qy 182 MKKVDIIICDSYSDIEPSTGEVIFRALDPAFKIEDPYSRIQNLKITNLRKFVKLH 241  
Db 121 MKKVDIIICDSYSDIEPSTGEVIFRALDPAFKIEDPYSRIQNLKITNLRKFVKLH 180

QY 242 TLGNLLDSMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGFBNEVEGMVGHCMCR 301  
DB 181 TLGNLLDSMEIREKYIYAVYDMVVRGNCFCYGHASECAPVDGFBNEVEGMVGHCMCR 240  
QY 302 HNTKGLNCLCMDYHDLRPAEGRNSNAKCKNCNBSHISCPHDMAYILATGNVSGV 361  
DB 241 HNTKGLNCLCMDYHDLRPAEGRNSNAKCKNCNBSHISCPHDMAYILATGNVSGV 300  
QY 362 CDDCQHTWGRNCEOCQKPFYOHPERDIRDPNFCERCTCDPAGSONEGICDSYTFDFSTGL 421  
DB 301 CDDCQHTWGRNCEOCQKPFYOHPERDIRDPNFCERCTCDPAGSONEGICDSYTFDFSTGL 360  
QY 422 IAGCCKLNVGEHCDVCEGFDYLSDDPGCKSCACNPLGTIPGNCDCDSTGHCYC 481  
DB 361 IAGCCKLNVGEHCDVCEGFDYLSDDPGCKSCACNPLGTIPGNCDCDSTGHCYC 420  
QY 482 KRLVTGQHCDCQCLPEHGWGLSNDLDGCRPCDCLGGALNNSCFABSGQCSRPHMIGRQCN 541  
DB 421 KRLVTGQHCDCQCLPEHGWGLSNDLDGCRPCDCLGGALNNSCFABSGQCSRPHMIGRQCN 540  
QY 542 EYEPGYYPATLDHYLYEAEANLPGQSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 601  
DB 481 EYEPGYYPATLDHYLYEAEANLPGQSVIVERQYIQDRIPSWTGAQFVRVPEGAYLEFFI 540  
QY 602 DNIPIYMEYDILIRYEPQLPDHWKXAVITVQRPGRPTSSRCGNTIPDDNQVVSLSFGS 661  
DB 541 DNIPIYMEYDILIRYEPQLPDHWKXAVITVQRPGRPTSSRCGNTIPDDNQVVSLSFGS 600  
QY 662 RYVVLPRPCFEGKNTYVRLBELPQYTSDDSDVESPYTLIDSLVMPYCKSLDFTVGGG 721  
DB 601 RYVVLPRPCFEGKNTYVRLBELPQYTSDDSDVESPYTLIDSLVMPYCKSLDFTVGGG 660  
QY 722 GDGVVNSAWETFORVRCLENRSVVVKTPTMTDVCNIIIFSALLHOTGLACECDPOGSL 781  
DB 661 GDGVVNSAWETFORVRCLENRSVVVKTPTMTDVCNIIIFSALLHOTGLACECDPOGSL 720  
QY 782 SSVCDPNGCQCRPNVGRNCRNAPGTFFGPGSCPCCHLQGSVNAFCNPTVQCH 841  
DB 721 SSVCDPNGCQCRPNVGRNCRNAPGTFFGPGSCPCCHLQGSVNAFCNPTVQCH 780  
QY 842 CFQGVYARQCDCLPGHGWFPSCQPCQNGHADDCTVGTGCLNCQDYVTHGNCERCLAG 901  
DB 781 CFQGVYARQCDCLPGHGWFPSCQPCQNGHADDCTVGTGCLNCQDYVTHGNCERCLAG 840  
QY 902 YGDPPIIGSGDCHRCPCPDGSDGQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 961  
DB 841 YGDPPIIGSGDCHRCPCPDGSDGQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900  
QY 962 YFQNPSEVGGSCQPCQCHNIDTTPDPEACDRETGRCLKLYHTEGEHCQCFRFGYGGAL 1021  
DB 901 YFQNPSEVGGSCQPCQCHNIDTTPDPEACDRETGRCLKLYHTEGEHCQCFRFGYGGAL 960  
QY 1022 RODCRKVCNLYGTQVBEHNGSDCOCDKATGQCLCPNVIGQCDRCAPNTWOLASGTGC 1081  
DB 961 RODCRKVCNLYGTQVBEHNGSDCOCDKATGQCLCPNVIGQCDRCAPNTWOLASGTGC 1020  
QY 1082 DPCNMAHAFSGPNEFTGQCCQMPFGGRTCECQELFWGDPDVECRACDCCDPRGIE 1141  
DB 1021 DPCNMAHAFSGPNEFTGQCCQMPFGGRTCECQELFWGDPDVECRACDCCDPRGIE 1080  
QY 1142 PQCDQSTGQCVGVEGPRCDKCTRYSVFPDCTPCHQCFALWDVILAEIWNTRHFL 1201  
DB 1081 PQCDQSTGQCVGVEGPRCDKCTRYSVFPDCTPCHQCFALWDVILAEIWNTRHFL 1140  
QY 1202 EKAKALKISGVIGPYRETVDVSVERKVBKIDILAQSPAAPLKNIGLNFEEAKLIKDV 1261  
DB 1141 EKAKALKISGVIGPYRETVDVSVERKVBKIDILAQSPAAPLKNIGLNFEEAKLIKDV 1200  
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DB 1201 EMMAOVEVKLSSTTQSGNSTAKELSLQTEAESIDNTVKELAEOLFIKNSDREGALDSI 1260  
QY 1322 TKYFQMSLEABERNVASTTPEPNSVQSGALMRDRVEDVMMERESQFKEQEQEQLLDEL 1381

DB 1261 TKYFQMSLEABERNVASTTPEPNSVQSGALMRDRVEDVMMERESQFKEQEQEQLLDEL 1320  
QY 1382 AGKLOSLDLASAAEMTCGTPPGASCSETECGGPNCRDDEGRKCGGPGCGGLVTVAHNAW 1441  
DB 1321 AGKLOSLDLASAAEMTCGTPPGADCSECECGGPNCRDDEGRKCGGPGCGGLVTVAHSAW 1380  
QY 1442 QKAMLDODDVLASAAVEOLSKMYSEAKLRADEAKQSAEDILLKTNATKEKMDKSNELR 1501  
DB 1381 QKAMLPDRDVLASAAVEOLSKMYSEAKYRADEAKQADVLLKTNATKEKVDKSNEDLR 1440  
QY 1502 NLIKQIRNPLTQDSADLDSIEAVANVLMKEMPTTPOOLQNLITEDIRREVESISQVEVIL 1561  
DB 1441 NLIKQIRNPLTQDSADLDSIEAVANVLMKEMPTTPOOLQNLITEDIRREVETLSQVEVIL 1500  
QY 1562 QKSAADIARAEMLEAEAKASKSATDVKTADMYKEALEBAEAKQAAEKAIKQADEDIQ 1621  
DB 1501 QKSAADIARAEMLEAEAKASKSATDVKTADMYKEALEBAEAKQAAEKAIKQADEDIQ 1560  
QY 1622 GTQNLITISSETAASEETLFPNASORISELERNVEELKRAAQNAGAEYIEKVYVTVKQ 1681  
DB 1561 GTQNLITISSETAASEETLFPNASORISELERNVEELKRAAQNAGAEYIEKVYVTVKQ 1620  
QY 1682 SAEDVYKTLDELDEKYEKVESLIAQKTESADARRKAEMLONEAKTLLAQANSKLQLE 1741  
DB 1621 NADDVYKTLDELDEKYEKVESLIAQKTESADARRKAEMLONEAKTLLAQANSKLQLE 1680  
QY 1742 DLERKVENQRYLEDKQELARLEGEVRSLLKDISQKAVYVSTCL 1786  
DB 1681 DLERKVENQRYLEDKQELARLEGEVRSLLKDISQKAVYVSTCL 1725

RESULT 10  
US-08-144-121-4  
; Sequence 4, Application US/08144121  
; Patent No. 5610031  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagman, David W.  
; TITLE OF INVENTION: Bk CHAIN OF LAMININ AND METHODS OF USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: BOSTON  
; STATE: Massachusetts  
; COUNTRY: United States  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 27-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Domain



LOCATION:	1..250																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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RESULT 11  
US-08-735-893-4  
; Sequence 4, Application US/08735893  
; Patent No. 5914317  
; GENERAL INFORMATION:  
; APPLICANT: Burgesson, Robert E.

APPLICANT: Wagman, David W.  
TITLE OF INVENTION: B1K CHAIN OF LAMININ AND METHODS OF USE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: BOSTON  
STATE: Massachusetts  
COUNTRY: United States  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/735,893  
FILING DATE: 18-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/144,121  
FILING DATE: 27-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: (MGP-0780.1) MGP-021DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1196 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
NAME/KEY: Domain  
LOCATION: 1..250  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 251..437  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 438..807  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 808..840  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 841..1196

US-08-735-893-4  
Query Match 62.0%; Score 6051.5; DB 2; Length 1196;  
Best Local Similarity 67.7%; Pred. No. 0;  
Matches 1195; Conservative 0; Mismatches 0; Indels 571; Gaps 2;  
QY 22 QBPFSYGCAGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIYVSHLQEDKKCFICN 80  
DB 1 QBPFSYGCAGSCYPATGDLIGRAQKLSVTSITTCGLHKPEPYCIYVSHLQEDKKCFICN 60  
QY 81 SQDPHETLNPSHLIENVVITFAPNRLKIWQSENGVENVTIQLDLAEFPHFTHLIMTF 140  
DB 61 SQDPHETLNPSHLIENVVITFAPNRLKIWQSENGVENVTIQLDLAEFPHFTHLIMTF 120  
QY 141 KTFRPAAMLIERSDFGKTGWYRYFAYDCEASFGISTGPMKKVDDIIICDSRYSDIEPS 200  
DB 121 KTFRPAAMLIERSDFGKTGWYRYFAYDCEASFGISTGPMKKVDDIIICDSRYSDIEPS 180  
QY 201 TEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKFKVLTGDNLLDSRMEIREKYYY 260  
DB 181 TEGEVIFRALDPAFKIEDPYSRIQNLKLTNLRKFKVLTGDNLLDSRMEIREKYYY 240

QY	261	AVYDMVVRGNCFCYGHASECAPVDGFNEEVGMVGHGCMCRHNTKGLNCELAMDFFYHDL	320
DB	241	AVYDMVVRGNCFCYGHASECAPVDGFNEEVGMVGHGCMCRHNTKGLNCELAMDFFYHDL	300
QY	321	WRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNSGGVCCDDCQNTMTGRNCEQCKPF	380
DB	301	WRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGNSGGVCCDDCQNTMTGRNCEQCKPF	360
QY	381	YVQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGOCRCNVEGEHCDVC	440
DB	361	YVQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFSTGLIAGOCRCNVEGEHCDVC	420
QY	441	KGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCQCLPESHGL	500
DB	421	KGFYDLSSEDPFGCKSCACNPLGTIPGPNPCDSETHCYCKRLVTGQHCQCLPESHGL	480
QY	501	SNLDGCRPCDCDLGGLNNSCFABSGQSCRPHMIGRCNEVEPGYVYFATLDHYLAE	560
DB	438	-----	437
QY	561	EAHLFGVSIIVERQYIQRIIPSWTGAQVRVPEGAYLEFFIDNIPYSMEYDILIRYPOL	620
DB	438	-----	437
QY	621	PDHWEKAVITVQRPGRIFTSSRCGNTIPDDDNQVVSLSQSRYSVVLPRPVCFEKGTNTV	680
DB	438	-----	437
QY	681	RLELPQYSSSDVESPYTLIDSLVLPYCKSLDIFTVGGSGDGVVTSNAWETFORICL	740
DB	438	-----	437
QY	741	ENSRVVKTPMTDVCNIIIPISALLHQTGLACECDPQGSILSSVCDPNGGQCCQCPNVVG	800
DB	438	-----	437
QY	801	RTCNRCAPGTFGFGSGGCKPCECHLQSVNAPCNVPTGQCHCFQGVYARQCDRLPGHWG	860
DB	438	-----	437
QY	861	FPSCQFCQNGHADDPCDVTGECNCDQYTMGHNCERCLAGYGDPIIGSDHCRPCPCP	920
DB	438	-----	437
QY	921	DGPDGRQFARSCYQDPVTLQACVDPGVIGSRCDDCASGYFNPSEVSGSQCPQCHN	980
DB	438	-----	437
QY	981	NIDTTDPEACDKETGRCLKCLYHTEGEHCQFCRFGYGDALRQDCKKVCNVLGTVQEH	1040
DB	438	-----CVCNVLGTVQEH	450
QY	1041	NGSDCCQDKATGQCLCLPNVIGQNCDCAPNTWOLASGTGCDPCNCAHSGPSCNEFT	1100
DB	451	NGSDCCQDKATGQCLCLPNVIGQNCDCAPNTWOLASGTGCDPCNCAHSGPSCNEFT	510
QY	1101	GCQCMFGGRTCEQQLFWGDPDVECRACDPRGIETPCDQSTGQCVCEGVEGP	1160
DB	511	GCQCMFGGRTCEQQLFWGDPDVECRACDPRGIETPCDQSTGQCVCEGVEGP	570
QY	1161	RCDKTRGYSQVFPDCTCHQCFALMDVIIAELTNTHRELEKAKIKISGVIGPVRETV	1220
DB	571	RCDKTRGYSQVFPDCTCHQCFALMDVIIAELTNTHRELEKAKIKISGVIGPVRETV	630
QY	1221	DSVERKVSSEIKDILAQSPAAEPLKNIQNLFEAEKLIKDVTEMMAQVVKLSDTTSSQNS	1280
DB	631	DSVERKVSSEIKDILAQSPAAEPLKNIQNLFEAEKLIKDVTEMMAQVVKLSDTTSSQNS	690
QY	1281	TAKELDSLQTEAESLDTNKKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVAST	1340
DB	691	TAKELDSLQTEAESLDTNKKELAEQLEFIKNSDIRGALDSITKYFQMSLEAEERNVAST	750

QY 1341 EPNSTVBSALMRDRVEDVMERESOPKEQEOBARLLDELACKLOSLLSAAEMTCGT 1400  
 DB 751 EPNSTVBSALMRDRVEDVMERESOPKEQEOBARLLDELACKLOSLLSAAEMTCGT 810  
 QY 1401 PPGASCSETECGGNCRTEDEGERKCGGPGCGGLVTVAHNAWQAMOLDQDVL SALAEVQ 1460  
 DB 811 PPGASCSETECGGNCRTEDEGERKCGGPGCGGLVTVAHNAWQAMOLDQDVL SALAEVQ 870  
 QY 1461 LSKMVSBAKLRADEAKOAEEDILLKTATKEKMDKNEELRNLIKQIRNFLTODSADLDS 1520  
 DB 871 LSKMVSBAKLRADEAKOAEEDILLKTATKEKMDKNEELRNLIKQIRNFLTODSADLDS 930  
 QY 1521 IEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEAEKR 1580  
 DB 931 IEAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEAEKR 990  
 QY 1581 ASKATDVKTADVMVKALBEAEKAAQVAEKAIKQADEDIQGTQNLITISSESTAASET 1640  
 DB 991 ASKATDVKTADVMVKALBEAEKAAQVAEKAIKQADEDIQGTQNLITISSESTAASET 1050  
 QY 1641 LFNASQRISELERNVEBELKRAAQNAGEAYIEKVYTVKQSAEDVKYKTLDELDEKYYK 1700  
 DB 1051 LFNASQRISELERNVEBELKRAAQNAGEAYIEKVYTVKQSAEDVKYKTLDELDEKYYK 1110  
 QY 1701 VENLIAKTTESADAREKAEWLQNEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAOE 1760  
 DB 1111 VENLIAKTTESADAREKAEWLQNEAKTLLAQANSKLOLLKDLERKYEDNQRYLEDKAOE 1170  
 QY 1761 LARLEGEVRSLLKDISOKVAVYSTCL 1786  
 DB 1171 LARLEGEVRSLLKDISOKVAVYSTCL 1196

RESULT 12  
 US-09-845-583A-6  
 ; Sequence 6, Application US/09945583A  
 ; Patent No. 6635616  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burgeson, Robert  
 ; APPLICANT: Brunken, William Joseph  
 ; APPLICANT: Champliand, Marie-France  
 ; APPLICANT: Hunter, Dale  
 ; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
 ; FILE REFERENCE: 10287-056001  
 ; CURRENT APPLICATION NUMBER: US/09/845, 583A  
 ; PRIOR FILING DATE: 2001-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/200,863  
 ; PRIOR FILING DATE: 2000-05-01  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1799  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-845-583A-6

Query Match 51.88; Score 5051.5; DB 4; Length 1799;  
 Best Local Similarity 50.84; Pred. No. 1.8e-285;  
 Matches 907; Conservative 304; Mismatches 560; Indels 15; Gaps 8;  
 7 LAFSFLALCRARVRAQPEFSY-GCAEGSCYPATGDLIGRAQKLSVSTCGLHKPEPYC 65  
 21 LRLGLLSVLAATLAQAPSLDVPFCGRGSCYPATGDLVLVGRADRLTASSTCGLHSPQVC 80  
 66 IVSHLQDKKCFICNSODPYHETLNPDSHLIENVTTTAPNRLKIWQSENGVENVTIQL 125  
 81 IVSHLQDKKCFICNSODPYHETLNPDSHLIENVTTTAPNRLKIWQSENGVENVTIQL 140  
 126 DLEAEFHFTLIMFTKTPRPAAMLIRSSDFGKTGWYRYFYADCEASPGISTGPMKKV 185  
 141 DLEAEFHFTLIMFTKTPRPAAMLIRSSDFGKTGWYRYFYADCEASPGISTGPMKKV 200  
 186 DDIIICDSRYSIDIPSTEGEVIIPALOPAFKIEDPYSPRIQNLKLTNLRIRKVLKTLTGD 245

DB 201 DDVVCESRYSEIPESTEGEVIYRVLDPALPIPDYSSRIQNLKLTNLRIRKVLKTLTGD 260  
 QY 246 NLLDSRMEIREKYYAYVDMVVRGNCFCYGHASBECAPVDGFNEVEGMVHGMCHMCHNTK 305  
 DB 261 NLLDPRREIREKYYAYVDMVVRGNCFCYGHASBECAPVDGFNEVEGMVHGMCHMCHNTK 320  
 QY 306 GLNCELMDYFHDLPWRPAEGRNSNACKNCNNEHSISCHFDMAVYVATGNGVGVCDCC 365  
 DB 321 GLNCEQODFYQDLPWPAEDGHTHACRKECNGHCHSCHFDMAVYVATGNGVGVCDCC 380  
 QY 366 QHNTMGNCQCKPFFYQHPEIRDIRPNFCERTCDPAGSQNEGICDSYTDSTGLIAQ 425  
 DB 381 QHNTAGSHCEFCFPFFYQDPTKMDRPAVCRPCDPCDPMGSDGGRCDSDHDPVLGLVSQ 440  
 QY 426 CRCKLVNVEGHCVDCKEGFYDLSSEBDFGCKSCACNPLGTIPGNPCDSETCGCHYCKRLV 485  
 DB 441 CRCKLVNVEGHCVDCKEGFYDLSSEBDFGCKSCACNPLGTIPGNPCDSETCGCHYCKRLV 500  
 QY 486 TGHGDCQCLPEHGLNLDGCRPCDCLGGALNNSCFABSCQSCRPHMIQRQNEVEP 545  
 DB 501 TGHGDCQCLPEHGLNLDGCRPCDCLGGALNNSCFABSCQSCRPHMIQRQNEVEP 560  
 QY 546 GYFATLDHLYVEAEANLPGVSIYVERQYIQDRIPSWTGTAGFVRVPEGAYLEFFIDNIP 605  
 DB 561 GYFATLDHLYVEAEANLPGVSIYVERQYIQDRIPSWTGTAGFVRVPEGAYLEFFIDNIP 619  
 QY 606 YSMEYDILLIRYEPQDPHWEKAVITVQREGRIPTSRQNTIPDDNQVVSLSQSRVYV 665  
 DB 620 RAMDYDILLIRYEPQDPHWEKAVITVQREGRIPTSRQNTIPDDNQVVSLSQSRVYV 679  
 QY 666 LPRPVCPEKGTNTVLELPQYTSDDSVESBYT--LIDSLVLMPCYKSLDIFTVGGSGD 723  
 DB 680 LPRPVCPEKGTNTVLELPQYTSDDSVESBYT--LIDSLVLMPCYKSLDIFTVGGSGD 734  
 QY 724 GVTNSAWETFORYRCLENSRVVTKMTDVCNITIFSIALLHQTGLACBCDPQGSLS 783  
 DB 735 DAAALERRRTTFRYRCHERGLMPSKAPLSETCAPLLISVSALYNGALPCQCDPQGSLS 794  
 QY 784 VCDPMGQCCQCRNVVGRNCRNCPGTGFGPSGCKPCCEHLQGSVNAFCNVPVTCQCHCF 843  
 DB 795 ECSPHGGQCKCKGVVGRRCVCACTGYGFGAGCAQCCSPDGLSALCEGTSQCCPCR 854  
 QY 844 QGVYARQCRCLPGHWGPPSCQPCQCNHADDPCDPTVTECLNCDQYTVGHNCERCLAGY 903  
 DB 855 PGAFGLRCDHCQRGQWGFENCRPCVNCGRADBCDTHTGACLCRDYTGECERCICAGFH 914  
 QY 904 GDPILGSDHCRPCPCDGDGSRGFASRCYQDPVTLQACVCDPQYIGSSRCDCCASGYF 963  
 DB 915 GDPILGSDHCRPCPCDGDGSRGFASRCYQDPVTLQACVCDPQYIGSSRCDCCASGYF 974  
 QY 964 GNPSEVGGSCQPCQCHNNITDTPDCAKGTGRCLKLYHTEGHCQCFRFGYGDALRQ 1023  
 DB 975 GDPSEKPGRCQCLCECSGNIDPMDPADCPHTGQCLRLCHLHNTGPHGCGYCKPFGHQAARQ 1034  
 QY 1024 DCRKVCNVLGTVOEHNGSD--CCDKATGQCLCLPNVIGQNCBCAPNTWQLASGTCD 1082  
 DB 1035 SCHRCNTLLGTDPRECPSTDLCHCDPSTGQPCPLPHVQGLNCDHCAFNWFTSGRCQ 1094  
 QY 1083 PCNCAAHSGFPCSCNEFTQCCQCMFGGRTCEQELFWGDDPVECRACDPCDPRGIETP 1142  
 DB 1095 PCACHPSRARGPCNEFTQCCQCHAGFGRTCEQELFWGDDPVECRACDPCDPRGIETP 1154  
 QY 1143 QCDQSTGQCVVGVGPRCDKCTRGYSVGPDPCTPCHOCFALMDVIIAELTNTHRELE 1202  
 DB 1155 QCHRSTGHSRCPGVSVCDOCAAGFSGVFPACHPCHACFGDWDVVDLARTRELE 1214  
 QY 1203 KAKALKISGVIQYRBTVDVSVERKSEIKDILAQSPAAEPLKINLGNLFEEAKL---TKD 1259  
 DB 1215 WAOELQCTQVGLAFSSFLNMQGLGWQAIMASNAS--AASAKLVEATEGLRHEIGK 1272  
 QY 1260 VTEMMAQVEKLSDDTTSQSNSTAKELDSLQTEAESLNDNTVKELAEQLEFKNSDIRGALD 1319

Db 1273 TTERLTQLEAELTAVQDENFNANHALSGLERDGFALNLTLRQDQHLILKHSNPLGAYD 1332  
QY 1320 SITKYFQMSLEAEERNVASTTBNSTVEQSALMRDRVEDVMRESQFKEQESCARLLD 1379  
Db 1333 SIRHMSQSTEARRANASTFAVPSVNSADTRRTVELMGAKENFNRLHQAQALG 1392  
QY 1380 ELAKGLQSLDLASAAEWTCGTPPGASCSETTECGGNCRTEDEGRKCGPGCGGLVTVVAHN 1439  
Db 1393 RLSAHARTLSLTGINELVCGAPGDAPCATSPCGAGACRDEQPPRCGGLGCGSAAAPADL 1452  
QY 1440 AMOKAMDLOQDVLASALAEVQLSKMVSBAKLRADEAKOSAEIILKTWATKRWKDSNEE 1499  
Db 1453 ALGRARHSQAELOALVEGGILSRVSETRRQAEAAQQAALDKANASGQVEQANQE 1512  
QY 1500 LRLNLIQINFLTQDSADLDSIAVANEVLMKEMSTPQOQNLTEIRERVESLSQVEV 1559  
Db 1513 LRELIQNVKDFLSQEGADPDSIEMVATRVLDISIPASPEIQRLASEIAERVSRLADVDT 1572  
QY 1560 ILQHSADIAARAEMLLEAKRASKSATDVKTADVMKEALEBAEAKAQAQAEKAIQADE 1619  
Db 1573 ILAHTMGDVRAEQLLODAHARSRAEGERQKAEIVQAALEBAQQAQGAQGAIRGAVD 1632  
QY 1620 IQOTQNLTSISETASSETIFNASORISELERNVVELKRAAONSGEABEYIEKVYTV 1679  
Db 1633 TQTEQTLQVQERWAGAEKSLNSAGERARQDALLEALKLRAGNSLAASABETAGSA 1692  
QY 1680 KQSAEDVKTLDGELDEKYYKVENLIAKTBESADARRKAEMLQNEAKTLLAQANSKLQ 1739  
Db 1693 QSRAREAEKQLEQVGDQVQTVYRALAEKAEGLVLAQAARAEQLDEARDILLOAQDKLQ 1752  
QY 1740 LKDLERKYEDNQRYLEDKQAEARLEGEVRSLLKDISOKVAVYTC 1785  
Db 1753 LOELEGTYENERALEGKAAQDGLGLEARMSVLOAINLQVQYNTC 1798

## RESULT 13

US-09-561-709B-11  
; Sequence 11. Application US/09561709B  
; Patent No. 6682911  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Champiaud, Marie-France  
; APPLICANT: Olson, Pamela  
; APPLICANT: Koch, Manuel  
; APPLICANT: Brunken, William  
; TITLE OF INVENTION: LAMININS AND USES THEREOF  
; FILE REFERENCE: 10287-060001  
; CURRENT APPLICATION NUMBER: US/09/561,709B  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 09/168,949  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 60/061,609  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1798  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-709B-11

Query Match 50.5%; Score 4926.5; DB 4; Length 1798;

Best Local Similarity 49.6%; Fred. No. 3.4e-278; Mismatches 309; Indels 15; Gaps 7;

Matches 886; Conservative 309; Mismatches 309; Indels 15; Gaps 7;

7 LAFSFLACRAVRVAQEPFSGYCAEGSCYCPATGDLIGRAQKLSVTSTCGLHKPFPYCI 66

22 LLLSVLAATLAQAPADVP---GCSRGSCYCPATADLLVGRADRLTASSTCGLNGRQFYCI 78

67 VSHLQEDKKCFKCNQDQYHETLPDPSHLIENVTTPAPNRLKRWQSENGVENVTIOLD 126

79 VSHLQEDKKCFKCLDSRRBFSARDNPHTRIQNVVTSFAPORRAAWQSQNGIPAVTIQLD 138

QY 127 LEAEFHFTHLIMTKTPRPAAMLIERSSDFGKWTGVVRYFAYDCEASFPGWISTGPMKKVD 186  
Db 139 LEAEFHFTHLIMTKTPRPAAMLVERADFORTWHVYRFSYDGGADFGVPPLAPPHWD 198  
QY 187 DIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPRIQNLKITNLRKFKVXLHTLGDN 246  
Db 199 DVVCSRYSEIEPSTEGEVIYRVLDPAIPDPDYSSRIQNLKITNLRVNLTRLHTLGDN 258  
QY 247 LIDSMEIREKYYAVYAVDMVVRGNCFCVGHASECAPVDGFGNEEVGVVGHCHWCNRTKG 306  
Db 259 LLDPREIREKYYALVELVVRGNCFCVGHASECAPAPGAPAHAEVMVHGAACICKNTRG 318  
QY 307 LNCELCWDPFYHDLRWRPABGRNSNACKKCNENHSISCHFDMAVYLATNVSGVGVDDCQ 366  
Db 319 LNCEOCQDFYDLRWRPAEDGHSHACKCDRHGHTHSCHFDMAVYLSGNSGVGVDDCQ 378  
QY 367 HNTMGRNCEOCKPFPYOHPERDIRDPNFCBRCCTCDPAGSONEGICDSYTFSTGLIAGOC 426  
Db 379 HNTAYRHCELCPFFYRPTKDLADPAVCRSCDDCPMGSDGGRCDSHDDPALGVSGQC 438  
QY 427 RCKLNVESHCDCVKEGFYDLSSEDPGCKSCACNPLGITIPGNPCDSETGHCYCKRLVT 486  
Db 439 RCKEHWVTRCQQRDGFGLSTSDPSGRCRCQCNARGTVPGSTPCDPNPSGSCYCKRLVT 498  
QY 487 QHCHDCQLPEHGLSNDLDCRCPDCDLGALANNSCFABESGQCSCRPMTIGRCNEVEPG 546  
Db 499 CRGCDRLCPGHGLSLDLGLGCRPCDDVGGALDPQDDEGTGQCHCRQHWGRCEQVQPG 558  
QY 547 YFATLDHLYBAEAMNGVSIYERQYIQDRIPSWTGAGFVRVPEGAVLEFFINIPY 606  
Db 559 YFRFLDHLIWEAENR-GQVLDVVERLVTPGTPTSGTSGFVRVLEGGOTLEFLVASVPN 617  
QY 607 SNEYDILIRPEPOLPDHWEKAVITVORPGRIPRTSSRCGNITPDDNQVVSLSFGSYVYL 666  
Db 618 AMDYDILLRLEFPVPEQWAELELIVQRPGVPAHSLCGHLVPRDDRIQGTLPQPHARYLIF 677  
QY 667 PRVCFEKGNTYTVRLPQYTSDDSDVESPYT----LDSLVLMPYCKSLDIFTVGGSG 722  
Db 678 PNPVCLLEGISYKULHLVLR-TGSSAQPEPTYPGSGPGLLIDSLVLLPRVLVLEMF-----SG 732  
QY 723 DGVVTSNAWETFORYRCLENSRSVTKPTMDVCRNIIFISISALLHOTGLACDCDPOGSL 782  
Db 733 GDAALERQATFERYQCHERGLVPSKTSPEACAPLISLSTLIYNGALPCQCNPOGSL 792  
QY 783 SVCDPNGQCCQCRNVVGRTCNRCAPGTGFGSGCKPCCECHLQGSVNAFCNVPVGOCHC 842  
Db 793 SECNPHGQCLCKPGVVGRCDDTCAPGYTGTGQACQCCQSPRGALSILCBRTSGCCLC 852  
QY 843 PQGYARQCDRLCPGHGWFPSQPCQCNHADDCCDPTVTECLNCQDYTMHNCERCLAGY 902  
Db 853 RTGAFGLRCDACQRGQWGFPSRCPVCNCGHDECNTHTGACLCGRDHTGGEHCERCIAGF 912  
QY 903 YGDP1IGSDHCRPCPCDPSDGRQFARSCYQDPVTLQLAQVCDRPGYIGSRDCCDCCASY 962  
Db 913 HGDPRLPYGAQCRPCPCPEGFGSQRHFAFSCHODEYSQQIVCHCRAGYITGLCEACAPQ 972  
QY 963 FGNPSEYVSGSCQPCQCHNNITDTPDACDKETGRCLKLYHTEGHEHCQCFRFGYVGDALR 1022  
Db 973 FGDPSRPGRCQLCECSGNIDPMDPADCPHPQQLRCLHHTGEPHCAHSKPGFGQAAAR 1032  
QY 1023 QDCEKVCVNLGTQBEHCNGSD-CQCDKATGCLCLPNVIGQNCDCRCAENTWQLASGTCC 1081  
Db 1033 QSHRCTNLNLGTNPQOCPSDDCHCDPSGQPCPLFNVAALAVDRCAFNWLTSGHGC 1092  
QY 1082 DPCNCAHSGFSCNFTQCCQMPFGGRTCSCEQELFWGDDPVECRACDCDPRGIST 1141  
Db 1093 QPCACLPSPBEGPTCNEFTQCHCLCGFGGRTCSCEQELFWGDDPGLQCHACDCDSRGIDT 1152  
QY 1142 PQCDQSTGQCVGVGEGPFCCKTEGYSGVVPRDCTPCQCCFALMDVIIAELTNTHTPL 1201  
Db 1153 PQCHRTGHTCTCPRGVSGVRCOCARGFSGIIPACHPCFACFGDWRVQDLAAATQRL 1212  
QY 1202 EKAKALKISGVIQYRETVDVSVERKVSIEKDIL-AQSPAAEPLKXIGNLFSAEKLIKDV 1260





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us-10-037-182-6.rai

Db 1086 TSQSSHCQLTGQCCKLGYGKRCSECEQENYGDPPGECIPCDNCRAGTQKPCIDPDTG 1145  
QY 1150 QCVCEGVGPRCDKCTRGYGVFPDCTFCHQCFAWVITIAELTNRTHRELEKAKALKI 1209  
Db 1146 MCRCEGVSGQRCDCARGHSGEFTCLQCHLCPQWDHTISSLSKAVQGLMLAAANNE- 1204  
QY 1210 SGVIGPYRETVDVSVER-----KYSEIKDILIAQS--PAABPLKNIGNLFEEAEKLIKDV 1260  
Db 1205 -----DKRETLPVCEADFKDLGNVSEIERILKHPVFGKFLK-----VKDY 1247  
QY 1261 TEMMAQVEVKLSDTTSQSNSTAKELDSLQTEAESLDNTVKELAEQLEF---IKNSDIRGA 1317  
Db 1248 HDSVRRQIMQIAEQLKAVVEFQDLKDTIERAKNEADLLLEDLQEBIDLQSSVLNASIADS 1307  
QY 1318 LDSITKYPQMSLEAEERVNASTTENSTVEQSALMRDRVEDVMMERESQPKKEQEEQARL 1377  
Db 1308 SENIKKYHISSAEKKIN-----ETSSINTSANTRN-----DLITI 1345  
QY 1378 LDELAKG-----LQSL-----DLSAAAEMTCCGTPPGASCSETECGGPNCRDTEGERKCGG 1427  
Db 1346 LDTLTSKGNLSERLKLQIKIPDIQILNEKVCVPGNVCVPLPCGGALCTGRKGHRKCRG 1405  
QY 1428 PCCGGLVTVAHNAWQKAMLDQDVLSALAEVQLSKMVSEAKLRADAEKQSAEDILLKTN 1487  
Db 1406 PGCHGSLTSLTNALQKAEAKSIIRNLDKQVRGLKNQIESISEQAEVSKNNALQREKLG 1465  
QY 1488 ATKEKMDKSEELNRNLIKQIRNFLTQDSADLDSIEAVANEVLKMEMPTPQOLQNLTEDI 1547  
Db 1466 NTRNQSDSEENINLFKVKVFLLEENVPPEIEKVANGVLDIHLPIPSQNLTDLVKI 1525  
QY 1548 RERVESLSQVEVILQHSAAADIAEAEMLLBEAKRASKATDVKVYADMKVEALEEAEKAQV 1607  
Db 1526 QKHMQLCEDYRTDENRSNEADGAQKLLVKAKAAEKAA--NILLNLDKTLNQLQQAQITQG 1584  
QY 1608 AAEKAIQADEDIQGTQNLTLTSETSETAASEBTLFNASORISELERNVEELKRAAQNNG 1667  
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Db 1756 YARC 1759

Search completed: May 18, 2004, 15:01:48  
Job time : 23.5107 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:56:24 ; Search time 45.4374 Seconds  
(without alignments)  
10937.572 Million cell updates/sec

Title: US-10-037-182-6  
Perfect score: 9754  
Sequence: 1 MGLQLLAFSLALCRARVR.....EVRSLKDISQVAVYSTCL 1786

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pdb:  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pdb:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9754	100.0	1786	9	US-09-873-676-113
2	9754	100.0	1786	9	US-09-938-275-6
3	9754	100.0	1786	14	US-10-037-182-6
4	9654	99.0	1765	14	US-10-037-182-8
5	9144	93.7	1786	9	US-09-938-275-7
6	9144	93.7	1786	14	US-10-037-182-10
7	8873	91.0	1725	14	US-10-037-182-12
8	6044.5	62.0	1196	16	US-10-443-349-4
9	5088.5	52.2	1801	9	US-09-938-275-8
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14	3076.5	31.5	1101	12	US-10-287-971-18
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19	1682	17.2	1605	14	US-10-037-182-18
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ALIGNMENTS

RESULT 1  
US-09-873-676-113  
; Sequence 113, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 113  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-873-676-113

Query Match	100.0%;	Score	9754;	DB	9;	Length	1786;
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						Gaps	0;
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RESULT 2  
US-09-938-275-6  
; Sequence 6, Application US/09938275  
; Patent No. US20020111309A1

; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments  
; FILE REFERENCE: PROTEO.P03  
; CURRENT APPLICATION NUMBER: US/09/938.275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P07942  
; DATABASE ENTRY DATE: 1988-08-01  
US-09-938-275-6

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1741 KDLERKVEDNORVLEKQAELEGEVPSLLKDIQKVAVYSTCL 1786

RESULT 3  
US-10-037-182-6  
; Sequence 6, Application US/10037182  
; Publication No. US2003004899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-6

Query Match 100.0%; Score 9754; DB 14; Length 1786;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLLQLLAFSLALCRARVRAQPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCOLHK 60  
Db 1 MGLLQLLAFSLALCRARVRAQPEFSYGCAEGSCYPATGDLIGRAQKLSVTSTCOLHK 60  
Qy 61 PEPYCVISHIQEDKCFICNSQDPYHETLNPDSHLIENVTTTAPNPLKIWOSENGVEN 120

Db 61 PEPYCTVSHLQEDKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWWQSENGVEN 120  
QY 121 VTIQLDLAEAFHFLHIMTFKTRPAAMLIERSDFGKTGWYRYPAYDCEASFPGISTG 180  
Db 121 VTIQLDLAEAFHFLHIMTFKTRPAAMLIERSDFGKTGWYRYPAYDCEASFPGISTG 180  
QY 181 PMKKVDDIICDSRYSIDIEBTEGEVIFRALDPAFKIEDPSRIQNLKILNLRKFKVKL 240  
Db 181 PMKKVDDIICDSRYSIDIEBTEGEVIFRALDPAFKIEDPSRIQNLKILNLRKFKVKL 240  
QY 241 HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCHMC 300  
Db 241 HTLGDNLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGFNEEVEGMVGHCHMC 300  
QY 301 RHTKGLNCELMDPFHDLPRWPAEGRNSACKKCNNEHSISCHFDMAVYLATGNVSGG 360  
Db 301 RHTKGLNCELMDPFHDLPRWPAEGRNSACKKCNNEHSISCHFDMAVYLATGNVSGG 360  
QY 361 VCDCCQNTMGRNCEOCKPYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFSTG 420  
Db 361 VCDCCQNTMGRNCEOCKPYYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYTFDFSTG 420  
QY 421 LIAGQCRCKLNVEGEHCDVCKEFGYDLSSDDPPGCKSCACNPLGITPGNPNCDSETGHY 480  
Db 421 LIAGQCRCKLNVEGEHCDVCKEFGYDLSSDDPPGCKSCACNPLGITPGNPNCDSETGHY 480  
QY 481 CKSLVTGQHCDCQLPEHWGLSNDLDCRCDLGGALNNSCFABSGQCSCHPHMIGROC 540  
Db 481 CKSLVTGQHCDCQLPEHWGLSNDLDCRCDLGGALNNSCFABSGQCSCHPHMIGROC 540  
QY 541 NEVEPGYFATLDHYLYEAEANLPGFVSIVEROYIOPISWTGAGFVRVPEGAYLEFF 600  
Db 541 NEVEPGYFATLDHYLYEAEANLPGFVSIVEROYIOPISWTGAGFVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEVDILIRPEPOLPDHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVWSLSPG 660  
Db 601 IDNIPYSMEVDILIRPEPOLPDHWEKAVITVQRPGRIPITSSRCGNTIPDDNQVWSLSPG 660  
QY 661 SRYVWLPFRPCFEKGTNTYVRLLEPQVTSDDSVESPYTLIDSLVLMPYCKSLDIPTVGG 720  
Db 661 SRYVWLPFRPCFEKGTNTYVRLLEPQVTSDDSVESPYTLIDSLVLMPYCKSLDIPTVGG 720  
QY 721 SGQGVVNSAWETFORVRCLENRSRVVKTMTDVCNRIIPFISALLHOTGLACECDPQGS 780  
Db 721 SGQGVVNSAWETFORVRCLENRSRVVKTMTDVCNRIIPFISALLHOTGLACECDPQGS 780  
QY 781 LSSVCDENGQOCOCRPNVGRICNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840  
Db 781 LSSVCDENGQOCOCRPNVGRICNRCAPGTFGFGPSGCKPCECHLQGSVNAFCNPVTGQC 840  
QY 841 HCFQGVYARQCDRLPGHWGFPSCQPCQNGHADDQDPTGECINQDQYTMGHNCERCLA 900  
Db 841 HCFQGVYARQCDRLPGHWGFPSCQPCQNGHADDQDPTGECINQDQYTMGHNCERCLA 900  
QY 901 GYVGDPIIGSDGHCRCPCPDGDSGRQFARSCVQDPVTIQLACVCDPVGYSRCDCCAS 960  
Db 901 GYVGDPIIGSDGHCRCPCPDGDSGRQFARSCVQDPVTIQLACVCDPVGYSRCDCCAS 960  
QY 961 GYFONPSEVGSCQPCQCHNNIDTTPDCAKCTETGRCLKCLYHTEGEHCQFCFGYVYDA 1020  
Db 961 GYFONPSEVGSCQPCQCHNNIDTTPDCAKCTETGRCLKCLYHTEGEHCQFCFGYVYDA 1020  
QY 1021 LRQDCRKCVCNLYGTVOEHNGSDCCQDKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080  
Db 1021 LRQDCRKCVCNLYGTVOEHNGSDCCQDKATGQCLCLPNVIGQNCRCAPNTWQLASGTG 1080  
QY 1081 CDPCCNNAHSFGPSCNEFTSQCCQMPFGGRTCSCEQLFWGDDPVECRACDCDPRGIE 1140  
Db 1081 CDPCCNNAHSFGPSCNEFTSQCCQMPFGGRTCSCEQLFWGDDPVECRACDCDPRGIE 1140  
QY 1141 TPQCDQSTGQCVCEGVGPRCDKTRGYSVFFPDCCTPCHOCFALMDVIIAELTNTHRF 1200  
Db 1141 TPQCDQSTGQCVCEGVGPRCDKTRGYSVFFPDCCTPCHOCFALMDVIIAELTNTHRF 1200

QY 1201 LEKAKALKISGVIGPYRETVDVSVERKVSSEIKDILASPAEPLKNIKNLGNLFEAEKLIKDV 1260  
Db 1201 LEKAKALKISGVIGPYRETVDVSVERKVSSEIKDILASPAEPLKNIKNLGNLFEAEKLIKDV 1260  
QY 1261 TEMMAQVEVKLSDDTTSQSNSTAKELSLQTEASESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
Db 1261 TEMMAQVEVKLSDDTTSQSNSTAKELSLQTEASESLDNTVKELAEQLEFIKNSDIRGALDS 1320  
QY 1321 ITKYFQMSLAEERVNASTTTPNSTVQESALMDRVEDVNMERESQFKEQOEQARLLDE 1380  
Db 1321 ITKYFQMSLAEERVNASTTTPNSTVQESALMDRVEDVNMERESQFKEQOEQARLLDE 1380  
QY 1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETCCGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
Db 1381 LAGKLSLDLSAAAEAMTCGTPPGASCSETCCGPNCRCTDEGERKCGGPGCGGLVTVAHNA 1440  
QY 1441 WQKAMLDQDVLALAEVEQISKMWSEAKLRADAEKQASADILLKTNATKEKMDKXNEEL 1500  
Db 1441 WQKAMLDQDVLALAEVEQISKMWSEAKLRADAEKQASADILLKTNATKEKMDKXNEEL 1500  
QY 1501 RNLIKQIRNFITQDSADLDSIEAVANEVLKXWEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560  
Db 1501 RNLIKQIRNFITQDSADLDSIEAVANEVLKXWEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560  
QY 1561 LQHSAAADIARAEMLLERAKKASATDVKTADMKVEALBEAKQAQVAEAKAIQADEDI 1620  
Db 1561 LQHSAAADIARAEMLLERAKKASATDVKTADMKVEALBEAKQAQVAEAKAIQADEDI 1620  
QY 1621 QGTQNLTSITSEETAASEETLFNASQRISELRNVEELKKAQNSGEAEYIEKVYTVTK 1680  
Db 1621 QGTQNLTSITSEETAASEETLFNASQRISELRNVEELKKAQNSGEAEYIEKVYTVTK 1680  
QY 1681 QSAEDVKTLDGELDEKVKYKVENLIAKTBESADARKAEMLQNEAKTLAQANSKLQLL 1740  
Db 1681 QSAEDVKTLDGELDEKVKYKVENLIAKTBESADARKAEMLQNEAKTLAQANSKLQLL 1740  
QY 1741 KDLERKVEDNORYLEDKAQELARLEGEVRSLLKDIQKVAVYSTCL 1786  
Db 1741 KDLERKVEDNORYLEDKAQELARLEGEVRSLLKDIQKVAVYSTCL 1786

RESULT 4  
US-10-037-182-8  
; Sequence 8, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Trygsvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1765  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-037-182-8

Query Match 99.0%; Score 9654; DB 14; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QBPFSYCAEGSCYPATGDLIGRAQKLSVTSTGHLHKKPFCYIVSHLQDCKKFCFNS 81  
Db 1 QBPFSYCAEGSCYPATGDLIGRAQKLSVTSTGHLHKKPFCYIVSHLQDCKKFCFNS 60

QY 82 QDPYHETLNPDSHLIENVVTFAPNRLKIWMQSENGVENVTIQDLEAEFFTHLIMTFK 141  
Db 61 QDPYHETLNPDSHLIENVVTFAPNRLKIWMQSENGVENVTIQDLEAEFFTHLIMTFK 120  
QY 142 TFRPAAMLIERSDGKWTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEBST 201  
Db 121 TFRPAAMLIERSDGKWTGVYRYFAYDCEASFPGISTGPMKKVDDIICDSRYSDIEBST 180  
QY 202 EGEVIFRALDPFAFKIEDPSPRIQNLKLTNRIKFVKLHTLGDNLDSRMEIREKYYIA 261  
Db 181 EGEVIFRALDPFAFKIEDPSPRIQNLKLTNRIKFVKLHTLGDNLDSRMEIREKYYIA 240  
QY 262 VYDMVVRGNCFCYGHASECAPVDGNEEVEGVHGHCMCRHNTKGLNCELCHDFHDLPLW 321  
Db 241 VYDMVVRGNCFCYGHASECAPVDGNEEVEGVHGHCMCRHNTKGLNCELCHDFHDLPLW 300  
QY 322 RAEGSNACKKCNKCNHSIISCHFDMAVYLATGNVSGVCDCCOHTWGRNCEOCKPFY 381  
Db 301 RAEGSNACKKCNKCNHSIISCHFDMAVYLATGNVSGVCDCCOHTWGRNCEOCKPFY 360  
QY 382 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTGLIAGQCRCKLNVGEHCDVCK 441  
Db 361 YQHPERDIRDPNFCERCTCDPAGSQNEGICDSTDFSTGLIAGQCRCKLNVGEHCDVCK 420  
QY 442 EGFYDLSSDDPFGCKSCACNPLGTPGNCPCDSETHCYCKELVYTGQHCDOCLPEHWGLS 501  
Db 421 EGFYDLSSDDPFGCKSCACNPLGTPGNCPCDSETHCYCKELVYTGQHCDOCLPEHWGLS 480  
QY 502 NDLGCRPCDCLGALNNSCFPAESQCSRCRPHMIGROCNEVEPGYFATLDHLYEABE 561  
Db 481 NDLGCRPCDCLGALNNSCFPAESQCSRCRPHMIGROCNEVEPGYFATLDHLYEABE 540  
QY 562 ANLGPQSVISVERQYIQRIPSWTGAQVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 621  
Db 541 ANLGPQSVISVERQYIQRIPSWTGAQVRVPEGAYLEFFIDNIPYSMEYDILIRYEPOLP 600  
QY 622 DHWEKAVITVQRGRIPTSRQNTIPDDNOVSLSPGSRVVLPRPVCPEKGNITVVR 681  
Db 601 DHWEKAVITVQRGRIPTSRQNTIPDDNOVSLSPGSRVVLPRPVCPEKGNITVVR 660  
QY 682 LELPQYTSDDSDVESPYTLIDSLVLMYCKSLDIFTVGGSGGVVTVNSAWETFORYRCLE 741  
Db 661 LELPQYTSDDSDVESPYTLIDSLVLMYCKSLDIFTVGGSGGVVTVNSAWETFORYRCLE 720  
QY 742 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGSLSVCDPNGSQCCOCRNWVGR 801  
Db 721 NSRSVVKTPMTDVCNRIIFSISALLHOTGLACECDPQGSLSVCDPNGSQCCOCRNWVGR 780  
QY 802 TCNRCAPGTFGFGSGCKPCECHLQSVNAPCNVPTGQCHCFQGVYARQCDCLFGHWGF 861  
Db 781 TCNRCAPGTFGFGSGCKPCECHLQSVNAPCNVPTGQCHCFQGVYARQCDCLFGHWGF 840  
QY 862 PSQPCQCNHADDPCDPTVTECLNCDQYTMHNCERCLAGYGDPIISGSDHCRCPCPD 921  
Db 841 PSQPCQCNHADDPCDPTVTECLNCDQYTMHNCERCLAGYGDPIISGSDHCRCPCPD 900  
QY 922 GPDGSRQFARSCYQDPVTQLQACVDPGVIGSRCDPCASGYFNGPSEVGSQCPQCHNN 981  
Db 901 GPDGSRQFARSCYQDPVTQLQACVDPGVIGSRCDPCASGYFNGPSEVGSQCPQCHNN 960  
QY 982 IDTTDPEACDKETGRCLKLYHTEGHHOCFRFGYIGDALRDQCRKVCNLYGTVOEHCN 1041  
Db 961 IDTTDPEACDKETGRCLKLYHTEGHHOCFRFGYIGDALRDQCRKVCNLYGTVOEHCN 1020  
QY 1042 GSPCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTGDCPCNCAHSPGSCNEFTG 1101  
Db 1021 GSPCQCDKATGQCLCLPNVIGQNCDCRCAPNWTQLASGTGDCPCNCAHSPGSCNEFTG 1080  
QY 1102 QCQCMFPGFGRTCEQCEQLFWGDDPVEACRACDCCPRGIFTPQCDQSTGQCVVEGVGEP 1161  
Db 1081 QCQCMFPGFGRTCEQCEQLFWGDDPVEACRACDCCPRGIFTPQCDQSTGQCVVEGVGEP 1140

QY 1162 CDKCTRGYSGVPDDCTPCHQCFAIWDVILIAELTNRTHRELEKAKALKISGVIPYRETVD 1221  
Db 1141 CDKCTRGYSGVPDDCTPCHQCFAIWDVILIAELTNRTHRELEKAKALKISGVIPYRETVD 1200  
QY 1222 SVRKVSEIKDIIAQSPAAEPLKNIQNLFEAEKLIKDVTEMAQVEVKLSDTTSSQSNST 1281  
Db 1201 SVRKVSEIKDIIAQSPAAEPLKNIQNLFEAEKLIKDVTEMAQVEVKLSDTTSSQSNST 1260  
QY 1282 AKELDSLQTEAESLDNTVKELABOLFIKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1341  
Db 1261 AKELDSLQTEAESLDNTVKELABOLFIKNSDIRGALDSITKYPQMSLEAEERVNASTTE 1320  
QY 1342 PNSTVEOSALMRVRVEDVMMERESQFKEQEQAARLLDELAKGLQSLDLSAAAEVTCGTP 1401  
Db 1321 PNSTVEOSALMRVRVEDVMMERESQFKEQEQAARLLDELAKGLQSLDLSAAAEVTCGTP 1380  
QY 1402 PGASCSTEGCGPNCRTDEGERKCGPGCGGLVTVVAHNAWQKAMDLDQDVL SALAEVEQL 1461  
Db 1381 PGASCSTEGCGPNCRTDEGERKCGPGCGGLVTVVAHNAWQKAMDLDQDVL SALAEVEQL 1440  
QY 1462 SKMVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFLTQDSADLDSI 1521  
Db 1441 SKMVSEAKLRADAKQSAEDILLKTNATKEMDKSNEELNLIKQIRNFLTQDSADLDSI 1500  
QY 1522 EAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEBAKRA 1581  
Db 1501 EAVANEVLKMEPSTPQOLQNLTEDIRERVESLSQVEVILQHSAAADIAEAEMLEBAKRA 1560  
QY 1582 SKSATDVKVTADVMVKEALEBAKQAAKAIKQADEDIQGTQNLTSIESETAASEETL 1641  
Db 1561 SKSATDVKVTADVMVKEALEBAKQAAKAIKQADEDIQGTQNLTSIESETAASEETL 1620  
QY 1642 FNASORISELERNVEELKRAAQNSGEAEYIEKVYTVTKQSAEDVKTLDELDEKYYKV 1701  
Db 1621 FNASORISELERNVEELKRAAQNSGEAEYIEKVYTVTKQSAEDVKTLDELDEKYYKV 1680  
QY 1702 ENLIAXKTESADARRKAEMLQNEAKTLAQANSKQLQLKDLERKEDNORYLEDKAAQEL 1761  
Db 1681 ENLIAXKTESADARRKAEMLQNEAKTLAQANSKQLQLKDLERKEDNORYLEDKAAQEL 1740  
QY 1762 ARLEGEVRSLLKDISQKVVYVSTCL 1786  
Db 1741 ARLEGEVRSLLKDISQKVVYVSTCL 1765

RESULT 5  
US-09-938-275-7  
; Sequence 7, Application US/09938275  
; Patent No. US20020111309A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerardo Castillo  
; APPLICANT: Alan Snow  
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
; FILE REFERENCE: PROTEO P03  
; CURRENT APPLICATION NUMBER: US/09/938,275  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Swissprot P02469  
; DATABASE ENTRY DATE: 1989-07-01  
US-09-938-275-7

Query Match 93.7%; Score 9144; DB 9; Length 1786;  
Best Local Similarity 92.7%; Pred.No. 0;  
Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;

QY 1 MGLIQLLAFLAFSLALCRARVRAQEFSEFSGCAEGSCYPATGDLIGRAQKLSVTSTGCLGK 60

Dd		Db	1	MGLLQVFAFGVLALWGTRVCQAQEPESYCAEGSCYPATGDLILLGRAQKLSVTSTCGLHK	60
Qy		Qy	61	PEPYCVISHLOEDKKCFICNSQDPYHETLNPDShLIENVVTPAPNRLKIWQSENGVEN	120
Dd		Dd	61	PEPYCVISHLOEDKKCFICDSRDPYHETLNPDShLIENVVTPAPNRLKIWQSENGVEN	120
Qy		Qy	121	VTIQLDLEAEFFHTHLIMFKTFRPAAMLIERSDFKGWTGVVRYPAYDEASFPDGISTG	180
Dd		Dd	121	VTIQLDLEAEFFHTHLIMFKTFRPAAMLIERSDFKGWTGVVRYPAYDESSFPDGISTG	180
Qy		Qy	181	PMKXVDIIICDSRYSDIEPSTEGETEVIFRALDPAFKIEDPYSPIQNLLKITLRKFVKL	240
Dd		Dd	181	PMKXVDIIICDSRYSDIEPSTEGETEVIFRALDPAFKIEDPYSPIQNLLKITLRKFVKL	240
Qy		Qy	241	HTLGDNLLDSRMIREKYIYAVDMVVRGNPCFVGHASBPVDGNEEVEGMVHGCMC	300
Dd		Dd	241	HTLGDNLLDSRMIREKYIYAVDMVVRGNPCFYGHASBPVDGNEEVEGMVHGCMC	300
Qy		Qy	301	RHNTKGLNCBLCMDFYHDLFWRAEGRSNACKKNCNHSISCHFDMAVIYLATNVSGG	360
Dd		Dd	301	RHNTKGLNCBLCMDFYHDLFWRAEGRSNACKKNCNHSISSCHFDMAVFLATNVSGG	360
Qy		Qy	361	VCDDCOHNTWGRNCEOCKPFYIOHPERDIIDPNFCERCCTCDPAGSNEGICDSYTDPSFG	420
Dd		Dd	361	VCDCNQHTWGRNCEOCKPFYIOHPERDIIDPNLCBPCTCDPAGSNGGICDGYTDFSFG	420
Qy		Qy	421	LIAQCRCKLNVGEHCDCVKEGFYDLSSEDPPGCKSCACNPLGTIPGGNPCDSETGHYC	480
Dd		Dd	421	LIAQCRCCLKHVEGERCDVKEGFYDLSAEDPYGCKSCACNPLGTIPGGNPCDSETGYCY	480
Qy		Qy	481	CKRLVTGOHQCDQCLPERHWGLSNDLDGCRPCDCLGGALNNSCFAEGSQGSCRPHMIGROC	540
Dd		Dd	481	CKRLVTGORCDQCLPQHWWGLSNDLDGCRPCDCLGGALNNSCSDSGQCSCLPHMTIGROC	540
Qy		Qy	541	NEVPYGVYEATLDHYLYEAEEANLPGCVSIYERYIODRIPSWTGAGFVRVPEGAYLEFF	600
Dd		Dd	541	NEVESGYFTFLDHYYTYEAEEANLPGVVVERIQYIODRIPSWTGFGFVRVPEGAYLEFF	600
Qy		Qy	601	IDNI PYSMEYDILIRYEPQLPDHWEKAVITVQRPRIPTSSRCGNTIPDDNOVVSLSPG	660
Dd		Dd	601	IDNI PYSMEYELLIRYEPQLPDHWEKAVITVQRPKIPASSRCGNTVPDDNOVWSLSPG	660
Qy		Qy	661	SRYVTLRPVCFEKGTYNVRLELPQYTSDDSDESPTYLIDSILVMPLYCKSLDIFTVGG	720
Dd		Dd	661	SRYVTLRPVCFEKGMYNVRLELPQTASGSDESPTYTIDSILVMPLYCKSLDIFTVGG	720
Qy		Qy	721	SGDGVWINSAMETFORVRCLENSSVVKTPMTDVCRNIIIFSISALLHOTGLACECPQGS	780
Dd		Dd	721	SGDEVINSAMETFORVRCLENSSVVKTPMTDVCRNIIIFSISALIHOTGLACECPQGS	780
Qy		Qy	781	LSSVCDPNNGGOCQCRPNVVGRTCNRCAPGTFFGPSPGCKPCBECHLOQSNAFCNPVTGC	840
Dd		Dd	781	LSSVCDPNNGGOCQCRPNVVGRTCNRCAPGTFFGPNCGKPCDCHLOQSASAFCDATIGCC	840
Qy		Qy	841	HCFQGIVARQCDRLCPGHGWGPSQPCQCNHADDCDPTVTECLNCDQYTWGHNCRCLA	900
Dd		Dd	841	HCFQGIYARQCDRLCPGWGWGPSQPCQCNHALDCTVTVTECLSCDYTTGHNCRCLA	900
Qy		Qy	901	GXYGDPIIGSDHCRPCPCPDGPGSGRFARSICYQDPVTILOLACVDPGYIGSRCDPCAS	960
Dd		Dd	901	GXYGDPIIGSDHCRPCPCPDGPGSGRFARSICYQDPVTILOLACVDPGYIGSRCDPCAS	960
Qy		Qy	961	GYFGNPSVEGSGSQPCQCHNNDITDPEACDKETGRCLKCLYHTEGHEHCFCRGYVGDA	1020
Dd		Dd	961	GFFGNPSPDFGSGSQPCQCHNNDITDPEACDKUIGRCLKCLYHTEGHDHCOLQYGYVGDA	1020
Qy		Qy	1021	LRQDCKKVCVNYLTGVQEHNGSGSCQCDKATGQCLCLPNVITGONCDRCAPNWTOLASGTG	1080
Dd		Dd	1021	LRQDCKKVCVNYLTGVKEHNGSGDCHDKATGQCSCLPNVITGONCDRCAPNWTOLASGTG	1080
Qy		Qy	1081	CDPCNNAHAHSPGSCNFCTGCCOMPGFGETSCBOELPWGPDVVECRACDCDPRGIE	1140

1081	CGPCNCVAHSPGFCNSNETGQCQCMPGFGGRTSCSQBLFWGDDPVECRACDCDPRGIE	1144
1141	TPQCDOSTGQCVCEGVGPRCDKCTRGISGVGFDPDCTPCHQCQFALMDVIAELTNRTHRF	1200
1141	TPQCDOSTGQCVCEGVGPRCDKCTRGISGVGFDPDCTPCHQCQFALMDALIGELTNRTHKF	1200
1201	LEKAKALKISGVLGPYRETVDISVERKVSSEIKDILAQSPAAEPUNKTGNLFEEAEKLIKDV	1260
1201	LEKAKALKISGVLGPYRETVDISVEKKVNEIKDILAQSPAAEPUNKTGNILFEEAEKLIKDV	1260
1261	TEMAQVEVKLSPTTTSQSNSTAKELBSLOSLOTEAESLNTVKLEAQLFEFKNSDIRGALDS	1320
1261	TERMAQVEVKLTDTSQSNSTAGELGALQABAESLDTVKLEAQLFEFKNSDIQAGALDS	1320
1321	ITKYFQMSLEAEBRVNASITPEPNSITVEQSAIMDRVEDVNMVERESQFKQEEQEARLLDE	1380
1321	ITKYFQMSLEAEBRVNASITDPNSTVEQSALTDRVEDLMLERESPFEQOEQEQARLLDE	1380
1381	LAKGLQSLDLSAAAEWTCGTPPGASCSETECGGPNCTDEGERKCGGPGCGGLVTVAHNA	1440
1381	LAKGLQSLDLSAAAOQTCGTPPGADCSSECGGPNCTDEGERKCGGPGCGGLVTVAHSA	1440
1441	WQAMDDQDVLVSALAAEVEQLSKWVSEAKLDEADKQSAEDIIILKTNATKEKMDKSNBEL	1500
1441	WQAMDPDRDVLVSALAAEVEQLSKWVSEAKVRADKQNAQDVLILKTNATKEKVDKSNEDL	1500
1501	RNLIKQIRNFLTCOSADLDSIEAVANEVLKQWEPSTPQOLQNLNLTEDIRERVESLSQVEVI	1560
1501	RNLIKQIRNFLTEDSADLDSIEAVANEVLKSGNASITPQOLQNLNLTEDIRERVETLSQVEVI	1560
1561	LQHSADIAAPAEMLLEBAKQASKSATDKVYTDWMVKEALBEAEKAQVAABKAIKQADEDI	1620
1561	LQSSADIAAPAEMLLEBAKQASKSATDKVYTDWMVKEALEEBAKQVAABKAIKQADEDI	1620
1621	QGTQNLILTSISETAASEETLFNASORISELERNVBEELKTKAAQNSGEAEYIEKVVYTVK	1680
1621	QGTQNLILTSISETAASEETLTNASQRIKLERNVBEELKTKAAQNSGEAEYIEKVVYSVK	1680
1681	QSAEDVKVTKLDGELDEKVKVVENLIAAKTTESADARKAEMLONEAKTLAQAQNSKLQLL	1740
1681	QNAEDVKVTKLDGELDEKVKVVENLIAQTTESADARKAEMLONEAKTLAQAQNSKLQLL	1740
1741	KDLERKYEDNQRYLDEKQAEALRLEGEVRSLIKDISOQVAVYSTCL	1786
1741	FILERKYEDNQRYLDEKQAEALRLEGEVRSLIKDISEKVAVYSTCL	1786

```

RESULT 6
US/10-037-182-10
/ Sequence 10, Application US/10037182
/ Publication No. US20030044899A1
/ GENERAL INFORMATION:
/ APPLICANT: Tryggvason, Karl
/ APPLICANT: Doi, Masayuki
/ APPLICANT: Tryboll, Jill
/ TITLE OF INVENTION: Recombinant Laminin 10
/ FILE REFERENCE: 98-274-P
/ CURRENT APPLICATION NUMBER: US/10/037,182
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/257,449
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/279,282
/ PRIOR FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 1786
/ TYPE: PRT
/ ORGANISM: Mus musculus
US/10-037-182-10

```

Query Match 93.7%; Score 9144; DB 14; Length 1786;  
Best Local Similarity 92.7%; Pred. No. 0;

Matches 1655; Conservative 72; Mismatches 59; Indels 0; Gaps 0;			
QY	1	MGLLQALAFSLALCARVAQEPESYGCABGSCVPATGDLILIGRAQKLSVTSCGLHK	60
DB	1	MGLLQVAFGLVLAALWGLTRVCAQEPESYGCABGSCVPATGDLILIGRAQKLSVTSCGLHK	60
QY	61	PEPYCTVSHLOEDKCFI CNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN	120
DB	61	PEPYCTVSHLOEDKCFI CDSRDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN	120
QY	121	VTIQLDLAEAFHFTLIMTFKTPRPAAMLIERSDFGKTGVVRYPAYDCEASFPGISTG	180
DB	121	VTIQLDLAEAFHFTLIMTFKTPRPAAMLIERSDFGKTGVVRYPAYDCEASFPGISTG	180
QY	181	PMKVVDDIICDSYSDIESTEGEVIFRALDPFAKIEDPSRIQNLKITNLRIKFVKL	240
DB	181	PMKVVDDIICDSYSDIESTEGEVIFRALDPFAKIEDPSRIQNLKITNLRIKFVKL	240
QY	241	HTLGDNLLDSRMEIREKIYAVYDMVRGNCFCYGHASECAPVDGNEEVEGVHGHCMC	300
DB	241	HTLGDNLLDSRMEIREKIYAVYDMVRGNCFCYGHASECAPVDGNEEVEGVHGHCMC	300
QY	301	RHNTKGLNCLCWDYHDLPLWRPAEGRNSNACKKNCNEHSISCHEDMAVYLATGNVSGG	360
DB	301	RHNTKGLNCLCWDYHDLPLWRPAEGRNSNACKKNCNEHSISCHEDMAVYLATGNVSGG	360
QY	361	VCDDCOHNTWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTG	420
DB	361	VCDDCOHNTWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYDFSTG	420
QY	421	LIAGQCRCKLVNGEHCDCVKEGYDLSDDPFGCKSCACNPLGTTPGNCPCDSETHCY	480
DB	421	LIAGQCRCKLVNGEHCDCVKEGYDLSADPDYCKSCACNPLGTTPGNCPCDSETHCY	480
QY	481	CKRLVTCQHCQDCLPEHMGISNDLDGCRPCDCLGGALNNSCFAGSGQSCSRPHMIGROC	540
DB	481	CKRLVTCQHCQDCLPQHWGLSNDLDGCRPCDCLGGALNNSCEDSGQSCCLPHMIGROC	540
QY	541	NEVEPGYFATLDHYLYEAEANLPGVSIYERQYIQDRIPSWTGAFTVRVPEGAYLEFF	600
DB	541	NEVEPGYFATLDHYLYEAEANLPGVSVVVERQYIQDRIPSWTGPVVRVPEGAYLEFF	600
QY	601	IDNIPYSMEVDILIRYEPOLPDHWEKAVITVQRPRIPTSSRCGNTIPDDNNOVSLSPG	660
DB	601	IDNIPYSMEVDILIRYEPOLPDHWEKAVITVQRPKIPASSRCGNTIPDDNNOVSLSPG	660
QY	661	SRVVLPRPCVFEKGTNTYVRLLEPOYTSSDSDVESPYTLIDSLVLMFYCKSLDIFTVG	720
DB	661	SRVVLPRPCVFEKGMNTYVRLLEPOYTASGSDVESPYTLIDSLVLMFYCKSLDIFTVG	720
QY	721	SGDGVNTNSAWETFORVRCLENSRSVKTPTMTDVCNRIIFSI SALLHOTGLACECDPQGS	780
DB	721	SGDGVNTNSAWETFORVRCLENSRSVKTPTMTDVCNRIIFSI SALLHOTGLACECDPQGS	780
QY	781	LSSVCDPENGQCCRPNNVGRTCNRCAPGTGFGPSPCKPCBCHLOGSVNAPCNVPTGQC	840
DB	781	LSSVCDPENGQCCRPNNVGRTCNRCAPGTGFGPSPCKPCDCHLOGSASAFDAITGQC	840
QY	841	HCPOGVVARQCDRLCPGHWGPPSCQPCQCNHADDCTPVTGECINCDODYTMGNHCERCLA	900
DB	841	HCPOGVVARQCDRLCPGVWGFPPSCQPCQCNHADDCTVTEGCLSCODYTTGNHCERCLA	900
QY	901	GYGDPILIGSDGRCPCPCDPGDSGRQFARSCVQDPVTIQLACVCDPGYIGSRCDDCAS	960
DB	901	GYGDPILIGSDGRCPCPCDPGDSGRQFARSCVQDPVTIQLACVCDPGYIGSRCDDCAS	960
QY	961	GYGNPSEVGSGSCQPCQCHNIDTTPDPAKDETRCLKCLYHTEGHCQFCRFGYVYGA	1020
DB	961	GYGNPSEVGSGSCQPCQCHNIDTTPDPAKDETRCLKCLYHTEGHCQFCQYGYVYGA	1020
QY	1021	LRQCRKVCNYLGTVOEHCHNGSCQCDKATGQCLCLPNVIGQNCDCAPNTWOLASGTG	1080
DB	1021	LRQCRKVCNYLGTVKEHCHNGSDCHDKATGQCSCLPNVIGQNCDCAPNTWOLASGTG	1080

QY	1081	CDPCNCAAHSGFSPSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPDVCECRACDCDPRGIE	1140
DB	1081	CGPCNCAAHSGFSPSCNEFTGQCCMPGFGGRTCSCEQLFWGDDPDVCECRACDCDPRGIE	1140
QY	1141	TPQCDQSTGQCVCEGVGPRCKCTRGYSVGPDPCTPCHQCTALMDVIIAELTNRTHRF	1200
DB	1141	TPQCDQSTGQCVCEGVGPRCKCTRGYSVGPDPCTPCHQCFALMDAIIIGELTNRTHKF	1200
QY	1201	LEKAKALKISVITGPIRETVDVSVERKVSEIKDILAQSPAAAEPLKNIGNLPEEAEKLIKDV	1260
DB	1201	LEKAKALKISVITGPIRETVDVSVEKKVNEIKDILAQSPAAAEPLKNIGILPEEAEKLIKDV	1260
QY	1261	TEMMAQVEVKLSDDTTSQSNSTAKELDSLOTEASLDMNTVKELAEQLFIKNSDIRGALDS	1320
DB	1261	TEKVAQVEVKLTDTSQSNSTAGELGALQAEASLDTVKELAEQLFIKNSDIQGALDS	1320
QY	1321	ITKYFQMSLEAEERVNASTTPEPSTVSQALMRDRVEDVMERESQFKEQEEQARLLDE	1380
DB	1321	ITKYFQMSLEAEERVNASTTPEPSTVSQALTRVEDLMERESPFKEQEEQARLLDE	1380
QY	1381	LAGKLSLDLSAAAEAMTCGTPPGASCSETCGGPNCTDGERKCGGPGCGGLVTVAHNA	1440
DB	1381	LAGKLSLDLSAAAEAMTCGTPPGADCSSECGGPNCTDEGEKCGGPGCGGLVTVAHSA	1440
QY	1441	WQKAMDLDQDVLALAEVEQLSKVWSEAKURADEAKQSAEDILIKTNATKEKMDKSNEEL	1500
DB	1441	WQKAMDLDQDVLALAEVEQLSKVWSEAKURADEAKQSAEDILIKTNATKEKMDKSNEEL	1500
QY	1501	RNLKIQINFTQDSADLDSIEAVANEVLKXMEPSTPQQLQNLTEDIRERVESLSQVEVI	1560
DB	1501	RNLKIQINFTQDSADLDSIEAVANEVLKXGNASTPQQLQNLTEDIRERVESLSQVEVI	1560
QY	1561	LOHSAADITARAEMLEAEAKRASKSATDVKVTADVMKALEAEAEKAAVAAEKAIQADEDI	1620
DB	1561	LQSAADITARAEMLEAEAKRASKSATDVKVTADVMKALEAEAEKAAVAAEKAIQADEDI	1620
QY	1621	QGTQNLTSISEETAASETLFNASQRISELERVVEELKRAAQNQSGEAEYIEKVYITVK	1680
DB	1621	QGTQNLTSISEETAASETLFNASQRISELERVVEELKRAAQNQSGEAEYIEKVYITVK	1680
QY	1681	QSAEDVKITLDELDEKVKYKVENIATKTESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
DB	1681	QNAEDVKITLDELDEKVKYKVENIATKTESADARRKAEMLQNEAKTLLAQANSKLQLL	1740
QY	1741	KDLERKYEDNQYLEDKAEQELARLEGEVRSLLKDISOXVAVYSTCL	1786
DB	1741	EDLERKYEDNQYLEDKAEQELARLEGEVRSLLKDISEKAVYSTCL	1786

RESULT 7  
US-10-037-182-12  
; Sequence 12, Application US/10037182  
; Publication No. US2003004899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thybøll, Jøll  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1725  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-12



Query Match		91.0%; Score 8873; DB 14; Length 1725;
Best Local Similarity		92.9%; Pred. No. 0;
Matches 1602; Conservative		71; Mismatches 52; Indels 0; Gaps 0;
Qy	62	BPVCIVSHLQDKKFCICNSQDPVHETLNPDSHLIENVVTFPAPNRLKIWQSENGVENV 121
Db	1	EPYCVIVSHLQDKKFCICNSQDPVHETLNPDSHLIENVVTFPAPNRLKIWQSENGVENV 60
Qy	122	TIQLDLBAEFHFTLIMTKTFRPAAMLIRSDSFGKWTGVYRYPAYDCEASPPGISTGP 181
Db	61	TIQLDLBAEFHFTLIMTKTFRPAAMLIRSDSFGKWTGVYRYPAYDCEASPPGISTGP 120
Qy	182	MKKVDDIICDSRYSDIIPSTEGEVIIFRALDPAFKIEDPYSPRIONLLKINLRIKFKVLH 241
Db	121	MKKVDDIICDSRYSDIIPSTEGEVIIFRALDPAFKIEDPYSPRIONLLKINLRIKFKVLH 180
Qy	242	TLGNLLDSRMEIREKIYAYAYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGCMCR 301
Db	181	TLGNLLDSRMEIREKIYAYAYDMVVRGNCFCYGHASECAPVDGFNEVEGMVHGCMCR 240
Qy	302	HTNGLNCELMDPYHDLPRPAPGRNSNACKCNCNEHSISCHFDMAVYLATNGVSGV 361
Db	241	HTNGLNCELMDPYHDLPRPAPGRNSNACKCNCNEHSISCHFDMAVYLATNGVSGV 300
Qy	362	CDDQHNMTGRNCQCKPFYQHPEIRDIRPNCERCTCDPAGSQNEGICDSYTDFTSL 421
Db	301	CDDQHNMTGRNCQCKPFYQHPEIRDIRPNCERCTCDPAGSQNEGICDSYTDFTSL 360
Qy	422	IAGCRKLVNVEGHCDCVKEGFDLSEDPFGKSCACNPLGTIPGNPCDSETHCYC 481
Db	361	IAGCRKLVNVEGHCDCVKEGFDLSEDPFGKSCACNPLGTIPGNPCDSETHCYC 420
Qy	482	KRLVTGRCDCQCLPQHGLSNDLQCRPCDCLGGALNNSCFABSGQSCRPHMIGRCQN 541
Db	421	KRLVTGRCDCQCLPQHGLSNDLQCRPCDCLGGALNNSCFABSGQSCRPHMIGRCQN 480
Qy	542	EVEPGYYPATLDHYLYEABEANLPGVSVIYERQVQIDRIPSWTCAGFVRPEGAYLEFFI 601
Db	481	EVEPGYYPATLDHYLYEABEANLPGVSVIYERQVQIDRIPSWTCAGFVRPEGAYLEFFI 540
Qy	602	DNIPYSMEVDILIRYEPOLPHWEKAVITVQRPKIPTSRRCGNTPDDNQVVSLSPGS 661
Db	541	DNIPYSMEVDILIRYEPOLPHWEKAVITVQRPKIPTSRRCGNTPDDNQVVSLSPGS 600
Qy	662	RYVVLPRVCEKGNNTYVRLLEPQYTSDDSDVSPYTLIDSLVMPYCKSLDIFTVGS 721
Db	601	RYVVLPRVCEKGNNTYVRLLEPQYTSDDSDVSPYTLIDSLVMPYCKSLDIFTVGS 660
Qy	722	GDGVVTSNAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALIHOTGLACEDPOGSL 781
Db	661	GDGVVTSNAWETFORVRCLENSRSVVKTPMTDVCNIIIFSALIHOTGLACEDPOGSL 720
Qy	782	SSVCDPNGQCCQCRPNVVGRTCNRCAPGTFGFGPGKPCCHLQGSVNAFCNPVTGQCH 841
Db	721	SSVCDPNGQCCQCRPNVVGRTCNRCAPGTFGFGPGKPCCHLQGSVNAFCNPVTGQCH 780
Qy	842	CFQGVYARQCDRLGSHGFFSPQCQCQCHADDDCVTGTCLNCDYVMGNHCNRCCLAG 901
Db	781	CFQGVYARQCDRLGSHGFFSPQCQCQCHADDDCVTGTCLNCDYVMGNHCNRCCLAG 840
Qy	902	YVGDPIIGSDHRCPCPCPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 961
Db	841	YVGDPIIGSDHRCPCPCPDGSGRQFARSCYQDPVTLQACVCDPGYIGSRCDCCASG 900
Qy	962	YFNGPSEVSGSCQPCQCHNIDTTPDCAKDETHGCLKLIHTHGEHCQFCRFGYGDAL 1021
Db	901	YFNGPSEVSGSCQPCQCHNIDTTPDCAKDETHGCLKLIHTHGEHCQFCRFGYGDAL 960
Qy	1022	RQDCKVCNLYGTVOEHCHGNSDCCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGC 1081
Db	961	RQDCKVCNLYGTVOEHCHGNSDCCDKATGQCLCLPNVIGQNCDCRCAPTWQLASGTGC 1020

RESULT 8  
US-10-443-349-4  
; Sequence 4, Application US/10443349  
; Publication No. US20040023956A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagman, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; FILE REFERENCE: 10287/021003  
; CURRENT APPLICATION NUMBER: US/10/443,349  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/161,872  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 08/735,893  
; PRIOR FILING DATE: 1996-10-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(250)

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; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (251)...(437)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (438)...(807)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (808)...(840)
; OTHER INFORMATION: Human B1 chain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (841)...(1196)
; OTHER INFORMATION: Human B1 chain
; US-10-443-349-4

Query Match 62.0%; Score 6044.5; DB 16; Length 1196;
Best Local Similarity 67.6%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;

QY 22 QPPEFSGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 80
DB 1 QPPEFSGCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 60
QY 81 SQDPYHETLNPDHSHLIENVVTTFAPNRLKIWMQSENGVENVTIQDLBAEFHFTLIMTF 140
DB 61 SQDPYHETLNPDHSHLIENVVTTFAPNRLKIWMQSENGVENVTIQDLBAEFHFTLIMTF 120
QY 141 KTFRPAAMLIERSDFGKTVGYRFAFYDCEASFPGISTGPMKKYDDIICDSRYSDIEPS 200
DB 121 KTFRPAAMLIERSDFGKTVGYRFAFYDCEASFPGISTGPMKKYDDIICDSRYSDIEPS 180
QY 201 TEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYY 260
DB 181 TEGEVIFRALDPAFKIEDPSPRIQNLKLTNLRKFVKLHTLGNLLDSRMEIREKYY 240
QY 261 AVDMVVRGNCFCYGHASECAPVDGNEVEGWHGHCNCRNTYGLNCELAMDYHDLIP 320
DB 241 AVDMVVRGNCFCYGHASECAPVDGNEVEGWHGHCNCRNTYGLNCELAMDYHDLIP 300
QY 321 WRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCQCKPF 380
DB 301 WRPAEGRNSNACKKNCNHSISCHFDMAVYLATGNVSGVCDCCOHNMTGRNCQCKPF 360
QY 381 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRKLNVEGEHCDVC 440
DB 361 YYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDFSTGLIAGQCRKLNVEGEHCDVC 420
QY 441 KEGFYDLSSDDPGCKSCACNPLGTTPGGNPCDSETHGHCYCKELVTGQHCDOCLPEHWGL 500
DB 421 KEGFYDLSSDDPGCKS----- 437
QY 501 SNLDGRCPCDCLGGLANNSCFAPSQCSCRPHEMIGRQCNEVEPGYFATLDHYLYEAB 560
DB 438 ----- 437
QY 561 EANLPGVSVIERQYIQDRIPSWTGAGFVRPBGAYLEFFIDNI PYSMEYDILIRYEPOL 620
DB 438 ----- 437
QY 621 PDHWEKAVITVQPRGRIPTSSRCGNTIPDDDNQWVSLSPGSRVYVLPFVPCFEGKNTYTV 680
DB 438 ----- 437
QY 681 RLELPQVTSDDSDVESPYTLIDSLVLPYCKSLDIFTVGGSGDVVNSAWETFFQYRCL 740
DB 438 ----- 437
QY 741 ENSRSVVKTEPMDVCRNIIFPSIGALLHOTGLACECDPQGSLSVCDPNGGCQCQRENNAVY 800
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RESULT 9

US-09-938-275-8

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DB 438 ----- 437
QY 801 RTCNRCAPGTFGFPGSGCKPCECHLQGSVNAFCNPVTGQCHCFQGYARQCRCLBHWG 860
DB 438 ----- 437
QY 861 FPSQPCQCNHADDCCDPVTGCLNCQDVTMGHNCERCLAGYVGDPIIGSDGHCPCPCP 920
DB 438 ----- 437
QY 921 DGPDSGRQFARSCYQDPVTLQLACVCDPGYIGSRCDDCASGYGNPSPSEVSGSQPCQCHN 980
DB 438 ----- 437
QY 981 NIDTTPBACDKETGRCLKCLYHTEGEHCQFCRFGYYGDALRQDCRCKCYCNVLTVOEHC 1040
DB 438 ----- 437
QY 1041 NGSDDCCDKATGQCCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPSCNEFT 1100
DB 451 NGSDDCCDKATGQCCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCAHSPSCNEFT 510
QY 1101 GQCCMPFGGRTCSBQELFWGDDPVECRACDCDPRGIETPCQDQSTGQCVCVEGEP 1160
DB 511 GQCCMPFGGRTCSBQELFWGDDPVECRACDCDPRGIETPCQDQSTGQCVCVEGEP 570
QY 1161 RCDKCTGYSVPPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRET 1220
DB 571 RCDKCTGYSVPPDCTPCHQCFALMDVIIAELTNRTHRFLEKAKALKISGVIGPYRET 630
QY 1221 DSVKRVSEIKDILAQSPAAEPLKNIUNFEEAEKLIKOVTEMAQVEVKLSPTTQSNS 1280
DB 631 DSVKRVSEIKDILAQSPAAEPLKNIUNFEEAEKLIKOVTEMAQVEVKLSPTTQSNS 690
QY 1281 TAKELDSLOTEASLONTVKELAEQLEFIKNSDIRGALDSITKYFOMSLAEAEVNASIT 1340
DB 691 TAKELDSLOTEASLONTVKELAEQLEFIKNSDIRGALDSITKYFOMSLAEAEVNASIT 750
QY 1341 EPNSTVQSALMDRVEDVMMERESQFKEQEQBARLLDELACKLQSLDLSAAAEVTCGT 1400
DB 751 EPNSTVQSALMDRVEDVMMERESQFKEQEQBARLLDELACKLQSLDLSAAAEVTCGT 810
QY 1401 PPGASCSETCCGPNCHTDEGERKCGGGLVTVVAHNAWQKAMOLDODVLSALAEVEQ 1460
DB 811 PPGASCSETCCGPNCHTDEGERKCGGGLVTVVAHNAWQKAMOLDODVLSALAEVEQ 870
QY 1461 LSKMVSBAKLRADEBAKQSAEDILLKTNAKMKDKNEELRNLIKQIRNFLTQDSADLDS 1520
DB 871 LSKMVSBAKLRADEBAKQSAEDILLKTNAKMKDKNEELRNLIKQIRNFLTQDSADLDS 930
QY 1521 IEAVANEVLKMEPSTPQOLONTEDIRERVESLSQVEVILQHSADIARAEMLLEAKR 1580
DB 931 IEAVANEVLKMEPSTPQOLONTEDIRERVESLSQVEVILQHSADIARAEMLLEAKR 990
QY 1581 ASKATDVKVTADVMKEALFEAEKAAQVAEKAQKQADEDIQGTQNLTLTSETAASEET 1640
DB 991 ASKATDVKVTADVMKEALFEAEKAAQVAEKAQKQADEDIQGTQNLTLTSETAASEET 1050
QY 1641 LFNASQRISELERVNEELKRAAQNQSGEAEYIEKVYTVTKQSAEDVKTLDGELDEKYYK 1700
DB 1051 LFNASQRISELERVNEELKRAAQNQSGEAEYIEKVYTVTKQSAEDVKTLDGELDEKYYK 1110
QY 1701 VENLIAKTTESADARRKAEMLQNEAKTLQAQNSKLQLLKDLKRYEDNORYLEDKQAE 1760
DB 1111 VENLIAKTTESADARRKAEMLQNEAKTLQAQNSKLQLLKDLKRYEDNORYLEDKQAE 1170
QY 1761 LARLEGEVRSLLKDISQKVAVYSTCL 1786
DB 1171 LARLEGEVRSLLKDISQKVAVYSTCL 1196
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; Sequence 8, Application US/09938275
; Patent No. US20020111309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; FILE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US20020111309Alveigicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
; US-09-938-275-8

Query Match      52.2%; Score 5088.5; DB 9; Length 1801;
Best Local Similarity 51.2%; Pred. No. 5e-281;
Matches 916; Conservative 303; Mismatches 550; Indels 21; Gaps 9;

QY      7 LAFSFLALCEARVRAQPEFSY-GCAEGSCYPATGDLIGRAQKLSVTSTCGLHKPEPYC 65
DB      21 LRGLLSVLATLAQVPSLDPGSCSGCYPATGDLVGRADRLITASSTCGLHSPQPYC 80
QY      66 IVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFPAPNRLKIWQSENGENVNTIQL 125
DB      81 IVSHLQEDKKCFICLSRRPFSARDNPNSHRIQNVVTSFAPQRTAWQSENGVPMVTIQL 140
QY      126 DLEAEHFHFLHNTFKTTPPAWMLTSSDRGKTGWVYFAYCEASFSGISGPMKKV 185
DB      141 DLEAEHFHFLHNTFKTTPPAWMLVERSADFGRTWRVYFSDYCGADFPGIPLAPPRW 200
QY      186 DDIICDSRYSDIEPSTEGEVIIFRALDPAFKIEDPYSPRIQNLKITNLRKFVKLHTLGD 245
DB      201 DVVCSRSYSEIPESTEGEVIIVRLDPAIPDPYSSRIQNLKITNLRVNLTRLHTLGD 260
QY      246 NLLDSRMEIREKYVAVDMVRGNCFCYGHASECAPVDGNEEVGHWGHCNCRNTK 305
DB      261 NLLDPREIREKYVAVELVIRGNCFCYGHASQCAPAPGAPAHAGVHGHACIKRNT 320
QY      306 GLNCELMDPYHDLPMWRPAEGRNSNACKKCNKNEHSISCHFDMAVYLATNGVSGVDDC 365
DB      321 GLNCEQCFYODLPMWPAEDGHTHACKCEKNGSHSCHEDMAVYLASNVSGVCDGC 380
QY      366 QHNTWGRNCEQCKPFYXOHPERDIRDPNFCERCTCDPAGSONEGICDSTYDFSTGLTAG 425
DB      381 QHNTAGHCELCPFFYRPTKMDRDPACRCPDCCDPMGSDQGRCDSDHDDPVLGLVSGQ 440
QY      426 CRCKNVEGEHCDVCKGEFDYLSSEDDPFGCKSCACNPLGTIPGNPCDSETHCYCKRLV 485
DB      441 CRCKEHVTRCQCQCRDGFGLSASNPGRQCQCQNSRGTPVGGTTPCDSSTGTCFCRLV 500
QY      486 TQGHCDQCLPEHFWLSNLDGCRPCDCLGALANNSCPAESGQSCSRPHMIGRQCNREVP 545
DB      501 TGGGCDRCLPGHGLSHLLGCRPCDCLVGGALDPQCDDEATGQCPCHPHMIGRCEGVQP 560
QY      546 GYFFATLHYLAEANLGPQSVISVERQYQDRIPSWTGAQFVRVPEGAYLFFIDNIP 605
DB      561 GYFRPFLDLTWEABGAH-GQVLEVERLVNTRTPSWTGVFVRLREGQVEFLVTSLP 619
QY      606 YSMVEDILIRYPPQLPDHWEKAVITVQRPGRIPITSSRCGNTIPDDDNQVLSLSPGSRVYV 665
DB      620 RANDYDLLLRWEPQVPEQWAELELVQRPVPSAHSFCGHVLPDRDDIQGLMHPNTEVLV 679
QY      666 LRPVCFEKGNTYVRLLELPQVTTSSDSDVESPYT-----LDSLVMPYCKSLDIFTVGG 721
DB      680 FPRVCLFPLGSLYKLLKLTG-TGGRAPHPETPYSGSGILIDSLVLQPHVLMLEMF-----S 734

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QY      722 GDGVVTSNAWETFOBYRCLENSRVVTKPMTDVCNIIIFSISALLHOTGLACEDPOGSL 781
DB      735 GGDAAALERRITFERIRCHERGLMPSKTPJUSEACVPLIISASSLVYNGALPCQCDPOGSL 794
QY      782 SSVCDPNGGQCCQRENYYVGRTCNRCAPGTFGFGSGCKPCHECHLQSGSNFACNPNVTQCH 841
DB      795 SSECNPHGQCRCKPGVVGRRCDACATGYGFGPAGCAQCSQCSQGLSALCEGTSQCL 854
QY      842 CFQGVYASQCDRCLPGHGWFPSCQPCOCHGADCDPVTGECNLCODYTWGHCNRCCLAG 901
DB      855 CRTGAFGLRCDHCQKQSGWGFNCRPCVCNCRADSCDAHTGACLCRDYTGEGHCERCIAG 914
QY      902 YYGDPFIISGDHCRPCPCPDGPDGSRQFARSCYODPVTLQACVCDPGYIGSRCDCCASG 961
DB      915 FHGDPRLPYGGQCRPCPCPEGFGSORHFAFSGHRDGYSSQIVCHCRAGYTGRLCEACAPG 974
QY      962 YFNGSEVGGSCQPCOCHNNITDTPACOKETGRCLKCLYHTEGECQCRFGYVGDAL 1021
DB      975 HFGDFSKFGRQJCEGSGNIDPTDPCADPHQCLRHTEGHPGHCCKPGFQGA 1034
QY      1022 RQDCKKVCNYLGTVQEHNGSD-CQCDKATGQCLCLPNVIGONCDRCAPNTWOLASGTG 1080
DB      1035 ROSCHRCTCNLLGTDPQPCSTDLCHCDPSTGQCPCLPHVQGLSCDRCAFNFNFTSGRG 1094
QY      1081 CDPNCNAAHSPGSCNEFTGQCCOCMBFGGRTCECOELFWGDPDVECRACDCCDPGIE 1140
DB      1095 CQPCACHPSRARGTCTNEFTGQCHCHAGFGRTCECOELHWGDPGLQCRACDCCDPGID 1154
QY      1141 TPQCDQSTGQCVVEGVGEGPCDCTRGYSGVFPDCTPHQCFCALMDVIIABLTNRTHRF 1200
DB      1155 KPQCHRSTGHCSCRFVSGVRCDQCARFGSGVFPACHPCFACFGDMVQDVAARTRRL 1214
QY      1201 LKAKALAKISGVIPIRETVDSEVERKSEIKDILA--QSPAAPLKNIGNLFEAEKL-- 1256
DB      1215 EQWAGELQQTGVLGAFSSFLNLQKLGVMQAIVAARNTSAATAK----LVBATGLRH 1270
QY      1257 IKQVTEMAQVYKLDSTTSQSNSTAKELDSLOTEAESLDNTVKELAEQLEFIKNSDIR 1315
DB      1271 EIGKTERLTQLEAELTDVDENFNANHALSGLERDGLALNLRLQDLDHLILKHSNFI 1330
QY      1316 GALDSITKYFQMSLEAEERNVASTTEPNSTVQSALMRDVEDVMMERESQPEKEQEA 1375
DB      1331 GAYDSIRAHQSQTEARRANASTFAIPSPVNSADTRRAEVLMAQRENFNRHLAQ 1390
QY      1376 RLDELAKLQSLDLSAAEMTCGTPGASCSETECGPNCRDDBGERKCGGPGCGGLVT 1435
DB      1391 QALGRLSTHTLTSLTGVNELVCGAPDAPCATSPCGAGCRDEGQPCGGGLGCSGAAA 1450
QY      1436 VAHNAQKAMDLODVLALAEVEQLSKMYSEAKLRADAEAKQSAEDILLKTNATKEKMDK 1495
DB      1451 TADIALGRARHTQAELOALVEGGILSRVSETRRQREAEQQAALDKANASRGQVEQ 1510
QY      1496 SNEELNLIKQIRNFLTQDSADLDSIEAVANVELKMEMPSTPOOLQNLTEDIRREVESLS 1555
DB      1511 ANQELRELIONVKDFLSQEGADPDSIEMVATRLDISIPASPEQIQRLASEIAERVSLA 1570
QY      1556 QVEVTLQSAADIARAEMLEAEKASKSATDVKTATDMVKEALAEAEKAAQAAEKAIKQ 1615
DB      1571 DVDITLANTGCDVRAQLQDQARASRAEGRQKAEVQVQAALEAEQRAQGAQIRG 1630
QY      1616 ADEDIQTQNLITISSETAASBETLNFASQRISELERNVEELKRAKAAQNSGBAEVIEKV 1675
DB      1631 AVDTQKTEQTLQVQSRVAGTEQSLNSASERARQLHALLEALKLRAGNSLAATAET.1690
QY      1676 VTVKQSAEDVKYKTLDELDEKVKYVENIJAKTTESSADARRKAEMLQNEAKTLQAQNS 1735
DB      1691 AGSAQSRAREAKQLREQVGDQVTVRALAEKAEGLAAQAAQAEQLRDEARGLLQAQD 1750
QY      1736 KLQJLKDLERYENQRYLEDKQAEKLARLEGEVRSLLKDISQKAVYSIC 1785
DB      1751 KLQELQLEEGTYEENERELEVKAAQDGLGEARMRSVLQAINLQVQYNTC 1800

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RESULT 10			Db		
US-09-938-275-9			Qy		
; Sequence 9, Application US/09938275			Db		
; Patent No. US2002011309A1			Qy		
; GENERAL INFORMATION:			Db		
; APPLICANT: Gerardo Castillo			Qy		
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications			Db		
; FILE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments			Qy		
; CURRENT FILING DATE: 2001-08-16			Db		
; NUMBER OF SEQ ID NOS: 11			Qy		
; SOFTWARE: FastSeq for Windows Version 4.0			Db		
; SEQ ID NO 9			Qy		
; LENGTH: 1798			Db		
; TYPE: PRT			Qy		
; ORGANISM: Homo Sapiens			Db		
; PUBLICATION INFORMATION:			Qy		
; DATABASE ACCESSION NUMBER: Swissprot P55268			Db		
; DATABASE ENTRY DATE: 1996-10-01			Qy		
US-09-938-275-9			Db		
Query Match 51.8%; Score 5052.5; DB 9; Length 1798;			Qy		
Best Local Similarity 50.3%; Pred. No. 5.6e-279;			Db		
Matches 901; Conservative 315; Mismatches 556; Indels 19; Gaps 8;			Qy		
1 MGLQLLAFSLALCARARVAQPEFSYCAEGSCYPATGDLILIGRAOKLSVTSTCGLHK 60			Db		
20 LGLL----LSVLAATLAQAPDVP---GCSRSCYPATGDLILVGRADLTASSTCGLNG 72			Qy		
61 PEPYCVSHLOEDKKCFIQNSQDPYHETLNPDSHLINVTTFAPNRLKIWQSENGVEN 120			Db		
73 POPYCVIYSHLODEKKCFCLDSRPFPSARDNPHFRIQNVVTSFAPORRAAWQSENGIFA 132			Qy		
121 VTIQDLAEAFHFTHLIMTKTFRPAAMLTERSDFKTMGVYRYPAYDCEASFPGISTG 180			Db		
133 VTIQDLAEAFHFTHLIMTKTFRPAAMLVERADFGRIWHVYRYSYDCGADFPVPLA 192			Qy		
181 PMKVVDDIIICDSYSDIEPSTEGEIVPRALDPAFKEDIPYSPRIQNLKITNRIKFKVL 240			Db		
193 PPRHWDVVCESYSEIEPSTEGEIVYRVLDPALPIPDYSSRIQNLKITNLRVNLTRL 252			Qy		
241 HTLGNLLDSMETREKYVAVDMVVRGNCFCVGHASECAPVDGPNEEVGVHGHCHMC 300			Db		
253 HTLGNLLDPREIREKIYVYALVELVVRGNCFCVGHASECAPAPAPAHAGNVHGCACIC 312			Qy		
301 RHNTKGLNCELMDFYHDLPRFAEGRNSNACKKCNCHSISCHFDMAVYLATGNVSG 360			Db		
313 KHNTRGLNCEQCQDFYRDLPRPAEDGHSHACRCKECHGTHSCHFDMAVYLAGNVSG 372			Qy		
361 VCDQCQNTWGRNCEQCKPFYQHPEDIRDPNFCERCTCDPAGSQNEGICDSYTDFTSG 420			Db		
373 VCDQCQNTAGRHCELCRPFYRDPDKLDRDPAVCRSCDDPMGSDGGRCDSHDDPALG 432			Qy		
421 LIAGQCRCKLNVEGHCDCVCKEGFYDLSSDPFGCKSCACNPLGTIPGNGPCDSETGHY 480			Db		
433 LVSGQCCKEHVVTRCQCQCRDGFGLSISDLGCRRCQCNARGTVPGSTPCDPNSGSCY 492			Qy		
481 CKRLVTQGHQDOCLPEHNGLSNDLDGCRPCDCLGGANNSCFABESGQSCSRPHMLGROC 540			Db		
493 CKRLVTGRCDCRLPGHGLSHDLGCRPCDGDVGGALDQCDEGTGQCHRCRHHVGRRC 552			Qy		
541 NEVEFGYVYFATLDHYLVEAEANLPGVSVISVERQYIQDRIPSWTGAGVVRVPEGAYLEFF 600			Db		
553 EQVQPGYFRPLDLHIAEADTR-GQVLDVVERLVTPGETPSTWTSVSGFVRLQSGQLLEFL 611			Qy		
601 IDNTPYMEVDILIRYEPQLPDHWEKAVITVQRPRIPTSSRCNTIPDDNQVSVLSPG 660			Db		
612 VASVPKAMDYDLRLRLEFPQVQWAELELIVQRPVPAHSLCGLHVPKDDRIQGTLPQH 671			Qy		
661 SRYVLPRPVCFEKGNTYVRLLELPQYTSDDSVESPYT----LIDSLVLMPYCKSLDIF 716			Db		

672	ARYLIFFNPVCLPFGISYKHLHLKLV- TGSAQAPETPYSGFGLLIDSLVLLPRVLVLEMF	730
717	TVGSGDGVVINSAMETFORVRCLENSRSVVKTPMTDVCRNIIIFSISALLHQTGLACECD	776
731	----SGDAALERQATFERVQCHEEGLVPSKTSPEACAPLLISLISLTIYNGALPCQCN	786
777	PGSLSSVCDPNNGQCCQRPNVVRTCNRCAPGTGFGPSGCKPCCECHLQGSVNAFCNPV	836
787	PGSLSSSECNPHGQCLCKPGVWGRCDLCAPGYGFGPTGCQACQSHGEGALSSLCEKT	846
837	TGQCHCFGVYAROCDRCLPGHMGFPSCQPCQCNHADDQDPVTGECINQODYTMGHNCE	896
847	SGQCLCRTGAFGLRCDRCQRGWGFPSRPCVNCNHADECNTHTGACLCRDTGGEHCE	906
897	RCLAGYGDPIIGSGDHCRPCPCPDGDDSGRQPARSCVQDPVTIQLACVCDPGVIGSRCD	956
907	RTIAGFHRDPLPYGGQCRPCPCPEGFGSQHFATSCQDEYSQQIVCHCRAGVTGRUCE	966
957	DCASGYGNPSEVSGSCQPCQCHNNIDTDPDCAEDKETGRCLKCLVHTEGHCQCFRFGY	1016
967	ACAFGHGDPSPRGRCQCLCECSGNIDPMDPADCDPHTGQCLRLCHHTEGPHCAHCKPGF	1026
1017	YGDALRQDCRKCVCNLYGTVOEHGNCSD- COCDKATGCLCLPNVIGQNCDCRCAPTWQL	1075
1027	HQAARQSRCHRTCNLLGTNPQCPSPDQCHCDSPSQCPCLPNVQGFSCDRCAFPNWL	1086
1076	ASGTGCDPCNCAHSGFPCSNBETGQCQCMPPFGGRTCECOELPWGDDPDVECRACDCD	1135
1087	TSGHGQCPACHPARGFTCNFTGQCHCAGRGRTCECQELHMGDPQLGQCHACDCD	1146
1136	PRGTETPCDDOSTGQCVCEGVEGRCDKCTRGYSGVFPDCTPCQCFALMDVIIAELTN	1195
1147	SRGIDTPCHRTGHCSRCRPGVSGVRCDQACRGSGIFPACHPCACFGDMDRVVQDLAA	1206
1196	RTHRELEXAKALKISGVIPYRETIVDSVERKYSIKLIL-AQSPAAEPLKNIGNLFEAE	1254
1207	RTQLEQRAQLQQTGVLGAFESSFVHWQKLGIVQGVGARNTSAASTAOLVATBELR	1266
1255	KLIKDVTEMAQVEKLSDDTTSQSNSTAKELDSIQTBAESLDNTVKELAELEBIFKNSDI	1314
1267	REIGBATHLTQLEADLTDVDENFNANHALSGLERDELALNLTQLDQHLDLHKSNF	1326
1315	RGALDSITKYFQMSLEAEERNVASTFENSTVQSGALMRDVEDVMMERESQFKEKEEQ	1374
1327	LCAYDSIRHAHSQSAEAERRANTSALAVPSPVNSASARHRTALMDAQEDFNSKEMAN	1386
1375	ARLLDELAKGLQSLDLSAAEWTCGTPGASCSETGCGPNCRDTEBERKCGPGCGGLV	1434
1387	ORALGKLSAHTHTLSLTDINELVCGAPGDAPCATSPCGAGACRDEDDQPRCGGLSCNGAA	1446
1435	TVAHNAWQKAMDLDQDVLALAEVEQLSKMWSEAKLRADAEAKQSAEDILLTNATKERM	1494
1447	ATADLALGRARHTQAEQLALAEAGSILSRVAETRRQASEAQQAALDKANASRGQVE	1506
1495	KSNEELNLIQIRNFLTQDSADLDSIEAVANEVLKMEMESTPOOLQNLTEDIRERVSL	1554
1507	QANQSLQELIOSVDFLNQEGADFDSIEMVATRVLELSIPASAEQIOHLAIAIERVSL	1566
1555	SOVEVILQHSADIARAEMILLEAKRASKSATDVKVTADMVKEALEAEAKQAQAAEKA	1614
1567	ADVDAIARTVGDVRAEQQLQDARRARSNAEDEKQAKETVQAALAEQAQAGIAQGAIR	1626
1615	QADEIQGTQNLTSIESETAASSETLENASQRISELEERNVEELKRAQNSGSAEYIEK	1674
1627	GAVADTRDTQTLVQVQERNVAGARLSSAGARARQDLALLEALKRAGNSLAATAEE	1686
1675	VYTVYVQSAEDVKKTLDGELDEKVKVKNLAKTTESSADARRKAEMLQNEAKTILAOAN	1734
1687	TAGSAGRAQAEQLLRPLGDOYQTVKALAEKRAQGVLAQAQAEQLRDEARDLLQAAQ	1746
1735	SKLQLLKLDERKYEDNQYLEDKQAEALARLEGEVRSLLKOISQKVAVYSTC	1785
1747	DKLQRLQELGTEGTYEENRALESKAAQLDGLFARMRSVLQAINLQVQIYNTC	1797

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RESULT 11
US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunkan, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001 AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-845-583-6

Query Match      51.8%; Score 5051.5; DB 9; Length 1799;
Best Local Similarity 50.8%; Pred. No. 6.4e-279;
Matches 907; Conservative 304; Mismatches 560; Indels 15; Gaps 8;

QY 7 LAFSFLACRAVRQAQEPFSY-GCAEGSCYPATGDLIGRAQKLSVTSGLHKKPYPYC 65
DB 21 LRGLLSLVAATLAQAPSLDPVPGSRGSCYPATGDLVGRADRLTASSTGLHSPQPYC 80
QY 66 IVSHLOEDKKFCICNSQSDPYHTLNPDSHLTENVVTFAPNRLKIWQSENGENVVTIOL 125
DB 81 IVSHLOEDKKFLCDSRRPFSARDPNSHRIQNVVTSFAPQRTAWQSENGENVVTIOL 140
QY 126 DLEAEHFHLLMTFTFRPAAMLERSDQKTVGVVRYFAYOCEASFPGISTGPMKKY 185
DB 141 DLEAEHFHLLMTFTFRPAAMLERSDQKTVGVVRYFAYOCEASFPGISTGPMKKY 200
QY 186 DOIICDSRYSDIEPSTESEGEVIFRALDPAPKIEDPYSPIQNLKTIWLRKFKVCLHTLGD 245
DB 201 DDVVCESRYSEIEPSTESEGEVIVRVLDPALPIFDPVSSRIQNLKTIWLRKFKVCLHTLGD 260
QY 246 NLLDSRMEIREKYYAVDMVVRGNCFCYGHASBECAPVDGNEVEGVGVRGHCWCRNTK 305
DB 261 NLLDPREREIREKYYALVELVIRGNCFCYGHASOCAPAPGAPAHAEQWVHGACICKNTR 320
QY 306 GLNCELCDMFYHDLPRPAEGRNSNACKKCNENHSISCHFDMAVYLATGNVSGGVCDCC 365
DB 321 GLNCEQCDQFYQDLPMHFAEDGHTACRKECNGHSHCHFDMAVYLATGNVSGGVCDCC 380
QY 366 QHNTWGRNCEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSYDTFSTGLIAGQ 425
DB 381 QHNTAGRHCFCRPFYFDRPTKMDRDPVAVCRPCDPMGSDQGGRCDSHDDPVLGLVSGQ 440
QY 426 CRCKLVNVEGHCVDVCEGFYDLSSDDPGCKSCACNPLGITPGGNPCDSTGHCYCKRLV 485
DB 441 CRCKHVVGTRCQCRDGFGLSASDPGCRQCQCNRSRGTVPGSSPCDSSSGTCPCKRLV 500
QY 486 TQCHCDQCLPEHWGLSNLDGCRPCDCLGALNNSCFASGQCSCEPHMIGRCQNEVP 545
DB 501 TGHGCDRLCPGHWSHLGDLGCRPCDCLGALNNSCFASGQCSCEPHMIGRCQNEVP 560
QY 546 GYFFATLDHLYAEAEANLGPQSVISVERQYIQDIRIPSWTGAQFVRVPEGAYLEFFINDIP 605
DB 561 GYFRFPDLHLTWEAAQA-QGVLEWVELVTNRETPTSWTGTGFRVLRREGQVEFLVTSLP 619
QY 606 YSMVEDILIRYEPQLPDWEKAVITVQRPGRIPSTSSRCGNTIPDDNQVSVLSFGSRVYV 665
DB 620 RAMVDYDLLLRWEPQFEQWASLELMVQRPVPSAHSFCGHVLPKDDRIQGMHLPHNTRVLV 679

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QY 666 LRRPYCFEKGTYTVRLLELPQYTSDDSDVESPYT--LIDSLVLMPCYCKSLDIFTVGSGD 723
DB 680 FRFPVCLFPGISYKUKKCLIG-TGGRAPQETSISGLLIDSLVQPHVIVLEMF-----SGG 734
QY 724 GVTNSAMETFORVRCLENSRSVVKTMPTDYCRNIIFSIALLHOTGLACECDPQGLSS 783
DB 735 DAAALERRTTTFRVRCHEEGLMPSKAPLSETCAPLLISVSALINYALPCQCDPQGLSS 794
QY 784 VCDPNGGOCQCRBNVVGTCNRCAPGTFGRGPSCKECEHLOGSVNAFCNPVPTGQCHCF 843
DB 795 ECPHGGQCRCKPGVVGRRCDVCATGYIFGACQACQCSPDGALSALCEGTSGGQPCFR 854
QY 844 QGVYARQCDRLPLGHGWPSPQPCQCNHADDCCDPTVTECLNCQDYMTHNCERCAGYY 903
DB 855 PGAFGLRCDHCQCGQGWGFPNCRPCVNCGRADCECDTHTGACLCGRDYTGGEHCERCIAGPH 914
QY 904 GDPILGSDHCRPCPCPDGPDGPFARSCVQDPVTIQLACVCDPGVIGSRCDCCASGYF 963
DB 915 GDPRLPYGGQCRPCPCPEGPGSRHFATSCRDGYSQIIVCHCRAGTYGLRCEACAFPP 974
QY 964 GNPSEVGSCQPCQCHNNIDTTPDACDKETGRCLKLYHTEGEBHCFRCFYGYGDALRQ 1023
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DB 1155 QCHRSTGHCSCRPVSGVRCQACGSGVFPACHPCACFGDWDVQDLAARTLEQ 1214
QY 1203 KAKALKISGVTPRETVDSEVERKSEIKOILAQSPAEEPLKNIGNLFEAEKL---IKD 1259
DB 1215 WAQELQOTGLVGAPESSFLMWQKLGVMVQAINARNAS--AASTAKLVEATEGLRHEIGK 1272
QY 1260 VTEWMAQVEVKLSDTTQSNSSTAKELDSLOTEAESLDNTVKELABOLEFTKNSDREGALD 1319
DB 1273 TTERLTQLEAELTAVQDENFNANHALSGLERDGFALNLTQLDQHLKHSNFGAYD 1332
QY 1320 SITKYFQMSLEABERVNASITPENSTVEQSALMRDVEDVMBERESQFKEQEQAARLD 1379
DB 1333 SIRHAQSQTEAERRANASTFAVPSPVSNADTTRRTTEVLMAQAKENFNRLHANOQALG 1392
QY 1380 ELAGKLOSLDLSAAAMTCGTTPGASCSETECGPNCRDTEGERKCGGCGGLVTVAHN 1439
DB 1393 RLSAHAHTLSLTGINELVCGAPGDAPCATSPCGAGCDEGQPCGGLGCSAAAPADL 1452
QY 1440 AWQKAMLDQDVLASALEVEQLSKWYSEAKLRADEAKQSAEDILLKTNATKEKWDKSNSE 1499
DB 1453 ALGRARHSQABLQALVEGGIILSRVSETRQAEAAQQAALDKANASRGQVEQANOE 1512
QY 1500 LRNLKIRIFLTQDSADLDSIEAVANEVLKMPSTPQOLNLTEDIRREVESLSQVEV 1559
DB 1513 LRELIVNQWFLSGAGADPDSIEWVATRVLDISIPASPEIQIOLASEIAERVRSADVDT 1572
QY 1560 ILQHSADIAEAMLLAEAKSATSVDKVTADMYKEALEEAKAQAQAEKAIKQADE 1619
DB 1573 ILAHTMGDVRAEQLLODAHRARSRAEGRKQAEVQAALBEAQRAQGAQGAIRAVVD 1632
QY 1620 IQGTQNLITSTESATASEETLFNASQRISELERNEVEELKRAAQNSEAEYIEKVIVTV 1679
DB 1633 TONTEQTLQVQESMAGAELSINSAGERARQLDALLEALKLKRAGNSLAASAEETAGSA 1692
QY 1680 QKSAEDVKKTLDELBDKYYKVENLAKTTEESADARRAEMLQNEAKTLAQAKSLQ 1739
DB 1693 QSRAREAEKQUREGVQGYQYTVRALAEKAEQVLAQAQAEQURDEARLQQAQKQ 1752
QY 1740 LKDLERYEDNQRYLEDKAEQELARLEGEVRSLLKDISQKVAVYSTC 1785

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Db 1753 LQELCTYEENALEGKAQDGLGLEARMRSLVQAINLQVQIYNTC 1798

RESULT 12

US-09-845-583-8  
; Sequence 8, Application US/09845583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champliand, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-845-583-8

Query Match 50.5%; Score 4921.5; DB 9; Length 1798;  
Best Local Similarity 49.6%; Pred. No. 1.6e-271;  
Matches 885; Conservative 309; Mismatches 576; Indels 15; Gaps 7;

QY 7 LAFSLALCARVRAQEPESYCAEGSCYPATGDLIGRAOKLSVTSTCGLHKPEPYCI 66  
Db 22 LLSVLAAUQAAPADVP---CGRGSCYPATADLLVGRADRLTASSICGLNGRQPYCI 78  
QY 67 VSHLOEDKKCFIENSQDPYHETLNPDSHLIENVVTPAPNKLKIWQSENGVENTIQLD 126  
Db 79 VSHLOEDKKCFIENSQDPYHETLNPDSHLIENVVTPAPNKLKIWQSENGVENTIQLD 138  
QY 127 LEAEFHTLIMFKFPAAMLIERSDDFGKTVYRYFAYDCEASFPGISTGPMKKVD 186  
Db 139 LEAEFHTLIMFKFPAAMLIERSDDFGKTVYRYFAYDCEASFPGISTGPMKKVD 198  
QY 187 DIICDSYSIDPSTEGEVIIFRALDPAFKIEDYSPRIQNLKILNLRKFKVLKHTLGN 246  
Db 199 DVCESSYSIEPSTEGEVIYRDLPAIPDPYSSRIQNLKILNLRKFKVLKHTLGN 258  
QY 247 LLSRMEIRKYYAVYDMVVRGNCFCYGHASCAPVDGNEVEGVWGHGCMCRHNTKG 306  
Db 259 LLDPRREIRKYYAVYDMVVRGNCFCYGHASCAPVDGNEVEGVWGHGCMCRHNTKG 318  
QY 307 LNCELMDFYHDLFWRPAEGRNSNACKKCNENHSISCHFDMAVYLATGNVSGVCDQC 366  
Db 319 LNCEQCCDFYRDLFWRPAEDGSHSHACKKDRHGHTSHCHFDMAVYLATGNVSGVCDQC 378  
QY 367 HNTWGRNCEOCKPFYOHPERDITDNFCBCTCDPAGSNEGICDSYTFDFTGLIAGOC 426  
Db 379 HNTAWRHCELCRPFYFDRDTPKLDPAVCRSCDPMGSDGGRCDSDHDDPALGLVSGQC 438  
QY 427 RCLNVEGEHCDVCKEGFYDLSSBDFPGCKSCACNPLGITPGGNPCDSETGHYCKRLVT 486  
Db 439 RCKEHVVTGRCQQRCDGFFGLSISDPSCRCQCQCNARGITVPGSTPCDPSGSCYCKRLVT 498  
QY 487 GQHCQDCLPHEWGLSNDLDCRCPDCLGALNNSCFAESGQSCSRPHMIGRCQNEVPG 546  
Db 499 GRGCDRLPHEWGLSNDLDCRCPDCLGALNNSCFAESGQSCSRPHMIGRCQNEVPG 558  
QY 547 YFPATDLHYLYEAEANLPGVSVIYERQYQDRIPSWTGAQVVRVPEGAYLEFFIDNIPY 606  
Db 559 YFRPFDLHYLYEAEANLPGVSVIYERQYQDRIPSWTGAQVVRVPEGAYLEFFIDNIPY 617  
QY 607 SMEDYILIRYEPQLPDHWEKAVITVQRPGRIPYSSRCNGTIPDDNQVSLSPGSRVYL 666

Db 618 AMDYDLLLLLEPQVPEQWAELELIVQPGVPVPAHSLCGHLVPRDDRIQGTLOPHARYLIF 677  
QY 667 PRPVCFEKGNTYVRLJELPOYTSSDSDVESPYT----LDSLVLMPYCKSLDIFTVGGSG 722  
Db 678 PNPVCLBPGISYKHLKXLR-TGSAQPEYTPGPGLLIDSLVLLPRVLVLEMP-----SG 732  
QY 723 DGVVTSAMETFORRYCLNRSRVVKTPTMDVCRNIIIFSISALLHQTGLACECDPQGSLS 782  
Db 733 GDAALERQATFERYQCHEGLVPSKTPSEACAPALLISLTLIYNGALPCQCNPGQSL 792  
QY 783 SVCDPNGGQCCRPNNVGRTCNRCAPOTFGFGSGGKPCCECHLOGSVNAECNPVTGQCHC 842  
Db 793 SECNPHGQCLCKFGVVGRECDTCAPIYGFPGTGCQACQCSPRGALUSSICERTSGQCLC 852  
QY 843 FQGVYARQCDRLCPGHGWFPSQPCQCNHADDCTPVTGECNQCQDYMGNHCERCLAGY 902  
Db 853 RTGAFGLRCACQRGQWGFSCPCVNCNGADECNTHTGACLCGRDLTGSEHCERCIAGE 912  
QY 903 YGDPHIGSDHCRPCPCPDGPDGSRQFARSCYQDPVTLOLACVCDPPIYISRCDDCASGY 962  
Db 913 HGDPLPYGAQCRPCPCPEGPGSQRHEFATSCHQDEYSQQIVCHCRAGYTGLRCSACAPGQ 972  
QY 963 FGNPSEVGGSCOPCQCHNNTDTPDPAEDKRETCGLKLVHTEGHEGQCFRFGYVGDALR 1022  
Db 973 FGDPSRPGRCQCLCECSGNIDPMDPDACDPHPGQCLRLHHTTEGPHCAHSPGFHQAAR 1032  
QY 1023 QDCRKCVCNVLGTQVQEHNGSD-CQCDKATGQCLCLPNVIGQNCNDRCAPNTWQLASGTC 1081  
Db 1033 QSHRCTCNLLGTNPQCPSPDQCHDPSQCPCLENVQALAVDRCAPNFWNLTSHGHC 1092  
QY 1082 DPCNCAHSPGSCNFTGQCMFGGRTGTCSECELFWGDVDECRACDCCDPRGIE 1141  
Db 1093 QPCACLPSPBEGPTCNFTGQCHLCGFGRTGTCSECELFWGDVDECRACDCCDPRGIE 1152  
QY 1142 PQDQSTGQCVGVGVGPRCDKCTRGVGVFPDCTPCHOCFALWDVIIAELTNTRHFL 1201  
Db 1153 PQCHFTGHTCTCRPGVSVGRCDQCARFGSGIFPACHFCACFGDWRVQDLAARTQLE 1212  
QY 1202 EKAKALKITSGVIGYRVTVDSEVERKVEIKDIL-AQSPAAEPLKNIKNLPEEAKLIKDV 1260  
Db 1213 QRAQELQGTGVLGAFESFWMQKLGIVQIGVARNITSAATQALVEATEELREGEA 1272  
QY 1261 TEMMAQVEVLSDTTSOSNSTAKELDSLOTEAESLDNTVKELARQLEFKINSDIRGALDS 1320  
Db 1273 TEHUTQLEADTVDQDENFNANHALSGLERDELALNLTLRQDQDLKXSNFLGAVDS 1332  
QY 1321 ITKYFQMSLEAEERNVASTTEPNSTVQSALMRDVEDVMWERSQFKEQEBQARLLDE 1380  
Db 1333 IRHAHSQSAEAERRANTSAALAVSPVSNASARHTEALDAQKEDFNSKMANQCALGK 1392  
QY 1381 LAGKLOSLDLAAAEWTCGTPPGASCSETGCGPNCRTEDEGRCGPGCGGLVTVAHNA 1440  
Db 1393 LSAHTHTLUSLTDINELVCGAQLHHDRTSPCGAGACRDEDOQPCGGLSCNGAATADLA 1452  
QY 1441 WQKAMDLDQDVLASALAEVQLSKXVSEAKLRADBAKQSAEDILLKTNATKMKDKSNEEL 1500  
Db 1453 LGRARHTQAEQLRALAEGGSILSRVAETRRQASEAQRAAALDKANASRQVQEQANQEL 1512  
QY 1501 RNLIKQINFLITQSDADLDSIEAVANEVLKXEMPTPQOLNLTEDIRERVESLSQVEVI 1560  
Db 1513 QELISQVDFLNQEGADPDSIEMVATRVLELUSIPASAEQIOHLAGATAERVRSADVDUI 1572  
QY 1561 LQHSAAIDTARAEMLIEAKRASKSATDVKTADVMVKEALEBAEAKQAAEKAIAKQADEI 1620  
Db 1573 LARTVGDVRRAEQLLDARRARSWAEDKQAEITVQAALBEAQRAQAGIAQGAIRGAVDT 1632  
QY 1621 QOTQNLISISSETTAASETTAFNASQRISELERVVEELKRAQAQNSGEAEVIEKVVTVK 1680  
Db 1633 RDTQETLYQVQERWAGAEALSSAGERARQDLAELKLRAGNSLAASAEETAGBAQ 1692  
QY 1681 QSAEDVKTLDGELDEKVKYKVENLIATKTEESADARRKAEMLQNEAKTLLAQANSKLQL 1740  
Db 1693 GRAQEAQLLRPLGDIQYQTVKALAEKQAGVLAQAARAEQLPDEARDLLQAQDKQLRL 1752





1603 EXAQAEEAKIAQADEDIQGTQNLTSIESETAASEETLFNASQRISELERNEVELKKA 1662  
1628 DQAYNNVTSVLEIDTMOVQARELIDKARNSTEAVEGKAQAANTTLAELEGVMSVK--- 1684  
1663 AQNSEAEYIEKVYVTVKQSAEDVKTLDGEL-----DEKYKVE-----NLIAKKT 1709  
1695 -----VEYLQ-----ISAKNALTTVDAAALAAATNAEQKQKQIOTDLERATELLEKGM 1733  
1710 EBSADARRAKAEMQLONEAKTLAQAANSKLQLKDLERKYEDNQRYLEDKAQELARLEGEVR 1769  
1734 EGVAPQQAERAKLREAAKLLYQAQRHNDIDNLSK--DSTEMRLDDVETILADNLSRL 1791  
1770 SLLKOISQKVAVSYTC 1785  
1792 RVTRDIHEKTDPHATC 1807

RESULT 14  
US-10-287-971-18  
; Sequence 18, Application US/10287971  
; Publication No. US20040067862A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook, et al  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-480A  
; CURRENT APPLICATION NUMBER: US/10/287,971  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/997,425  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 10/035,568  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/338,626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/401,479  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: 60/333,072  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/348,283  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/393,262  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: CuroSeqList version 0.1  
; SEQ ID NO 18  
; LENGTH: 1101  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-18

Query Match 31.5%; Score 3076.5; DB 12; Length 1101;  
Best Local Similarity 48.0%; Pred. No. 1.2e-166;  
Matches 546; Conservative 169; Mismatches 338; Indels 85; Gaps 12;

30 CARGSCVPATGDLIIIGRAQKLVSTICGLKPPYIVSHLQEDKCKFCNSQDPYHETL 89  
23 CNRGACHPTTGDLLVGRNTQJMASSSTGSLRAQKCYLLSYLEGEKCSICDSRFPDYPD 82

90 NPDSHLENTVVTTFAPNRLKIMWQSENGVENVTIQLDLAEFFHFTLIMTKTFRPAAML 149  
83 QPNSHTIENTVTSFEEDREKKWQSENGLDHVIRLDLEALFRFSLHLLTKTFRPAAML 142  
150 IERSSDFGKTVGVYFAYCEASFPGISGTGPMKKYDDIICDSRYSDIEPSTGEVIFRA 209  
143 VERSTDYGHNVKVKYFAKDCATSFNITSGAQGVGDIVCDYSKYSIDIEPSTGEVVLKV 202  
210 LDPAFKLEDPYSPRIQNLKATNLRIKFKVHLTLGNLDLSRM-EIREKYYAVYDMVVR 268  
203 LDPSEFEIENYSPYIQDLVTLNRLNFTKHLIGDALLGRRQNDLSLKYYALYEMIVR 262  
269 GNCFCYGHASECAPVDGFNEV---EGMVHGHCMCRHNTKGLNCELCMPDYHDLNRPAB 325

263 GSCFCNGHASECRPMQKRGDVFSPPGMVHGVCVQOHNITDGNPCERCKDFFQADWPRAA 322  
326 GRNSNACKNCNEHSISCHFDMAVYLATNYSVGGVCDCCQHNITMGRNCEQCKPFYVQHP 385  
323 DLQDNACRSCSNHSHRCHFDMTTYLASGSLGSGVCEDCQHNITGCHDCRCLPYRDP 382  
386 ERIDRPNFCERCTCDPAGSQNEGICDSYTDSTGLIAGQCRKLNVEGEHCDVCKEGFI 445  
383 LKTIISPYACIPCECDPDGTISGGICVSHSDPALGSAVGQCLCKENVEGAKCQCKPNHY 442  
446 DLSEBDFGCKSCACNPLGTIPGNCNCDSETGHYCYKRLVTGQHCDOCLPEHGLNDLD 505  
443 GLSATDPLGQPCDCNPLGSLP-FLTCDVDTGQCLSLSYVTGAHCBECTVGYMGLGNHLH 501  
506 GCRPCDCLGALNNSCFASGQSCRPMHIGQCNVEBPGYFATLDHYLYEAEAN-- 563  
502 GCSFPCDDIGAYSNVCSPPKNGQCECRPHVTGSCSEPAFGYFFAFLNFLYEAEEATTL 561  
564 -----LG-----PGVSIVERQYIQDRIPSWTGAQFVRVPSGAYLEFFIDNTPYSMEYD 611  
562 QGLAPLGSETFGQSPAVHVVLPFGPNVPTWTGPGFARVLPAGLRFVAVNNIPFPVDFT 621  
612 ILIRYEPQLPDHWEKAVITVORCPRTSSRCGNTIPDDNQVVSLSPGSRVYVVLPRPVC 671  
622 IAIHYEQSADMTVQIV-VNPPG---GSEHCIPKTLQSKPQSFALPAATRIMLLPTPIC 677  
672 FEKGTNTYVRLLELPQYTTSSDSVESPYTLIDSLVMPYCKSLDIFTVGGSGDGVVNSAW 731  
678 LEPDVQYSIDVYFSQPLQGESHAHS-HVLVDSLGLIPQINSLENF-----CSKQDL 727  
732 ETPORYCLENSRSVVKTPMTDVCNITIPSIALLHQTGLACEDCGSGSLSSVCDPNGGQ 791  
728 DEYQLHNCVEIASAMGPQVILFGACERLIISMSAKLHDGAVACKCHPQGSVSSCSRLGGQ 787  
792 CQCRPNVVGRTRCNRCAPGTGFGPSPGCKPCECHLQGSVNAFCNPNVTGQCHCFQGVARQC 851  
788 CQCKPLVVGRCDCSTGSYDLGHHGCHPCHCHPQGSKDTVCQVITGQCPCHEVSGRR 847  
852 DRCLPHGHWGPPSCOPCOCNHADDCCDVTGECNLQCDYTMHNCERCLAGYVGDPIIGSG 911  
848 DRCLAGYFGPSPCHPCNRFACELCDPETSFCNCGGFTTGRNCERCIDYGNP---SSG 905  
912 DHCRCPCPCPDGDSGROFARSCYQDPVTQLQACVCDPGYIGSRCDCCASGYFGNPSVGG 971  
906 QPCRPLCPCDDPSSNQYFAHSCYQNLWSSDVICNCLQYGTGTQCGECSTGYGNPRISGA 965  
972 SCQPCQCHNIDTTDPEACDKETGRCLKLYHTEGEHCQCFRGYIGDALRQDCKKVCVN 1031  
966 PCQPCACNNIDVTDPESCSRVTGECRLCLHTQGANCOLCKPGHYGSALNQTCCRCSCH 1025  
1032 YLGTVQEHCH--NGSDCOCCKATGQCLCLPNVIGQNCRCAPNTWQLASGTGCDPCNCNA 1089  
1026 ASGVSPMECPGGGACLCDDPVTGACPLPNVTGLACDRCADGYNNLVPRG----- 1076  
1090 HSFQPSCNFTGQCCQCMFGGRTCSQCQLFWGDPDVEGRACDPRGTETPOCDQS 1147  
1077 -----CQSCDCDPRTSQSHCDQA 1095

RESULT 15  
US-09-925-298-703  
; Sequence 703, Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103  
; CURRENT APPLICATION NUMBER: US/09/925,298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:49:23 ; Search time 10.1546 Seconds  
(without alignments)

6313.134 Million cell updates/sec

Title: US-10-037-182-6

Perfect score: 9754

Sequence: 1 MGLQLLAFSLALCRARVR.....EVRSLKXDISQKVAIVSTCL 1786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 240604 seqs, 35894274 residues

Total number of hits satisfying chosen parameters: 240604

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_New.\*

1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pcp.\*  
7: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9750	100.0	1786	6	US-10-796-280-770
2	6044.5	62.0	1196	6	US-10-841-139-4
3	5060.5	51.9	1798	6	US-10-796-307-899
4	5060.5	51.9	1798	6	US-10-796-307-900
5	3625.5	37.2	1670	1	PCT-US02-39555A-917
6	1675	17.2	1573	6	US-10-796-280-1353
7	1675	17.2	1573	6	US-10-796-280-1354
8	1645.5	16.9	3712	6	US-10-108-605A-103
9	1581	16.2	885	1	PCT-US02-39555A-2483
10	1574.5	16.1	3690	7	US-10-796-280-1384
11	1574.5	16.1	3690	7	US-60-568-219-509
12	1568.5	16.1	3690	1	PCT-US02-22858A-347
13	1568.5	16.1	3717	6	US-10-821-234-1076
14	1566	16.1	2107	6	US-10-796-280-1108
15	1566	16.1	2107	6	US-10-796-307-671
16	1566	16.1	2107	6	US-60-568-219-409
17	1566	16.1	2480	6	US-10-796-280-1106
18	1566	16.1	2480	6	US-10-796-307-669
19	1566	16.1	2480	7	US-60-568-219-407
20	1566	16.1	3116	6	US-10-796-280-1107
21	1566	16.1	3116	6	US-10-796-307-670
22	1566	16.1	3116	7	US-60-568-219-408
23	1525.5	15.6	3714	6	US-10-796-280-1383
24	1525.5	15.6	3714	7	US-60-568-219-508
25	1489	15.3	3332	1	PCT-US02-39555A-1160
26	1463	15.0	1165	6	US-10-841-139-2

27 1451.5 14.9 1147 6 US-10-841-139-3 Sequence 3, Appli  
28 1342 13.8 249 6 US-10-841-139-6 Sequence 6, Appli  
29 1077 11.0 1486 1 PCT-US02-39555A-2658 Sequence 2658, Ap  
30 1003 10.3 250 6 US-10-841-139-7 Sequence 7, Appli  
31 1001 10.3 628 6 US-10-831-979-5 Sequence 5, Appli  
32 993 10.2 628 6 US-10-831-979-2 Sequence 2, Appli  
33 991 10.2 628 6 US-10-100-683-8634 Sequence 8634, Ap  
34 671.5 6.9 1547 6 US-10-453-372-886 Sequence 886, Ap  
35 671.5 6.9 1577 6 US-10-453-372-882 Sequence 882, App  
36 671.5 6.9 1577 6 US-10-453-372-884 Sequence 884, App  
37 671.5 6.9 1620 6 US-10-453-372-868 Sequence 868, App  
38 671.5 6.9 1853 6 US-10-453-372-866 Sequence 866, App  
39 667 6.8 1594 6 US-10-453-372-860 Sequence 860, App  
40 662 6.8 1418 6 US-10-453-372-874 Sequence 874, App  
41 657.5 6.7 1450 6 US-60-563-440-1664 Sequence 1664, Ap  
42 657 6.7 4346 7 US-60-548-091-384 Sequence 384, App  
43 657 6.7 4346 7 US-60-548-219-343 Sequence 343, App  
44 657 6.7 4346 7 US-60-548-091-383 Sequence 383, App  
45 657 6.7 4347 7 US-60-548-091-383 Sequence 383, App

#### ALIGNMENTS

##### RESULT 1

US-10-796-280-770  
; Sequence 770, Application US/10796280  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001510  
; CURRENT APPLICATION NUMBER: US/10/796,280  
; CURRENT FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 68533  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 770  
; LENGTH: 1786  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-796-280-770

Query Match 100.0%; Score 9750; DB 6; Length 1786;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLQLLAFSLALCRARVRAQEPFSYCAEGSCYPATGDLIGRAQKLSVTSTGLHK 60  
Db 1 MGLQLLAFSLALCRARVRAQEPFSYCAEGSCYPATGDLIGRAQKLSVTSTGLHK 60  
QY 61 PEPCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
Db 61 PEPCIVSHLQEDKKCFICNSQDPYHETLNPDSHLIENVVTFAPNRLKIWQSENGVEN 120  
QY 121 VTIOLEAEFFHFTLIMTKTPAPAMLIERSDDFGKTGWYRYFAYDCASFPGLSTG 180  
Db 121 VTIOLEAEFFHFTLIMTKTPAPAMLIERSDDFGKTGWYRYFAYDCASFPGLSTG 180  
QY 181 PMKXVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240  
Db 181 PMKXVDIIICDSRYSDIEPSTEGEVIFRALDPAFKIEDPYSPIQNLLKITNLRIFVKL 240  
QY 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGNEVEGVHGHCMC 300  
Db 241 HTLGDNLLDSRMEIREKYYAVYDMVVRGNCFCYGHASECAPVDGNEVEGVHGHCMC 300  
QY 301 RHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGVNVS 360  
Db 301 RHNTKGLNCELMDYFHDLPWRPAEGRNSNACKKCNNEHSISCHFDMAVYLATGVNVS 360  
QY 361 VCDDCOHNTMGRCNEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYTFSTG 420  
Db 361 VCDDCOHNTMGRCNEQCKPFYQHPERDIRDPNFCERCTCDPAGSQNEGICDSTYTFSTG 420

QY 421 LIAGQCRCKLVNVEGHCYKQFYDLSSDPGKSCACNPLGTPGGNCPDSETHCY 480  
Db 421 LIAGQCRCKLVNVEGHCYKQFYDLSSDPGKSCACNPLGTPGGNCPDSETHCY 480  
QY 481 CKRLVTHQHCDCQLPEHGWGLSNDLDCRCDLGGALNNSCFASGQSCSRPHMIGRC 540  
Db 481 CKRLVTHQHCDCQLPEHGWGLSNDLDCRCDLGGALNNSCFASGQSCSRPHMIGRC 540  
QY 541 NEVEPGYFATLHYLYEABANLGVSVIYERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600  
Db 541 NEVEPGYFATLHYLYEABANLGVSVIYERQYIQDRIPSWTGAQFVRVPEGAYLEFF 600  
QY 601 IDNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPSSRCGNTPDDNQVVSLSG 660  
Db 601 IDNIPYSMEVDILIRYEPQLPDHWEKAVITVQRPGRIPSSRCGNTPDDNQVVSLSG 660  
QY 661 SRYVVLPRPVCFEKGNVTVRLBELPQYTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGG 720  
Db 661 SRYVVLPRPVCFEKGNVTVRLBELPQYTSDDSVESPYTLIDSLVLMPCYCKSLDIFTVGG 720  
QY 721 SGDGWVNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFISALLHQTGLACECDPQGS 780  
Db 721 SGDGWVNSAWETFORVRCLENSRSVVKTPMTDVCNIIIFISALLHQTGLACECDPQGS 780  
QY 781 LSSVCDPENGQCCQCRPNVVGRTCNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGQC 840  
Db 781 LSSVCDPENGQCCQCRPNVVGRTCNRCAPGTGFGPSGCKPCBCHLQGSVNAFCNPVTGQC 840  
QY 841 HCFQGVYARQCDRLPGHWGFRSCOCQNGHADDCTPVTECLNCQDVTMGHNCERCLA 900  
Db 841 HCFQGVYARQCDRLPGHWGFRSCOCQNGHADDCTPVTECLNCQDVTMGHNCERCLA 900  
QY 901 GYGDPIIGSGDHRCPCCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
Db 901 GYGDPIIGSGDHRCPCCPDGSDGRQFARSCYQDPVTQLACVCDPGYIGSRCDCCAS 960  
QY 961 GYFNPSEVGSQCPQCHNNIDTTDPEACKTGTGRCCLKLYHTEGHCQFCRFGYIDA 1020  
Db 961 GYFNPSEVGSQCPQCHNNIDTTDPEACKTGTGRCCLKLYHTEGHCQFCRFGYIDA 1020  
QY 1021 LRQDCRCVNYLGTVEHNGSCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080  
Db 1021 LRQDCRCVNYLGTVEHNGSCQCDKATGQCLCLPNVIGQNCDCRCAPNTWQLASGTG 1080  
QY 1081 CDPNCNAHSGFSCNEFTGQCCQMPGFGRTCEQELFWGDPDVECBACDPRGIE 1140  
Db 1081 CDPNCNAHSGFSCNEFTGQCCQMPGFGRTCEQELFWGDPDVECBACDPRGIE 1140  
QY 1141 TPQCDQSTGQCVGVGEGPRCDKTRGYSVPRPDCTPCHQCFALMDVIIAELTNRTHRF 1200  
Db 1141 TPQCDQSTGQCVGVGEGPRCDKTRGYSVPRPDCTPCHQCFALMDVIIAELTNRTHRF 1200  
QY 1201 LEKALKISGVIQFYRETVDVSRVSEIKDILAQSPAEPKJNIGNLFEAEKLIKDV 1260  
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QY 1261 TEMMAQVEVKLSDTQSNSAKELDSIQTEAESLNTVKEAELEFIKNSDIRGALDS 1320  
Db 1261 TEMMAQVEVKLSDTQSNSAKELDSIQTEAESLNTVKEAELEFIKNSDIRGALDS 1320  
QY 1321 ITKYFQMSLEABERNVASTTPEPNSVQSALMDRVEDVMVERESQFKEQOEQARLLDE 1380  
Db 1321 ITKYFQMSLEABERNVASTTPEPNSVQSALMDRVEDVMVERESQFKEQOEQARLLDE 1380  
QY 1381 LAGKQSLDLSAAAEWTCGTPPGASCSTECGGNCRDTERGCKGPGGGLVVAHNA 1440  
Db 1381 LAGKQSLDLSAAAEWTCGTPPGASCSTECGGNCRDTERGCKGPGGGLVVAHNA 1440  
QY 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTATKEMKDSNEEL 1500  
Db 1441 WQKAMDLDQDVLALAEVEQLSKMVSEAKLRADEAKQSAEDILLKTATKEMKDSNEEL 1500

QY 1501 RNLIKQIRNFLODSADLDSIEAVANEVLKQWEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560  
Db 1501 RNLIKQIRNFLODSADLDSIEAVANEVLKQWEMPSTPQQLQNLTEDIRERVESLSQVEVI 1560  
QY 1561 LQHSAAADIAEAEMLEBAKASATDVKTADWKEALBEAQAQVAEAKAIQADEDI 1620  
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QY 1621 QGTQNLTLTSESETAASEETLFNASQRISSELRNVEELKRAAQNSEAEYIEKVVTVK 1680  
Db 1621 QGTQNLTLTSESETAASEETLFNASQRISSELRNVEELKRAAQNSEAEYIEKVVTVK 1680  
QY 1681 QSAEDVKTLDGELDEKYYKVENLIANKTESADARRKAEMLQNEAKTLLAQAANSKLQLL 1740  
Db 1681 QSAEDVKTLDGELDEKYYKVENLIANKTESADARRKAEMLQNEAKTLLAQAANSKLQLL 1740  
QY 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLLKDIISOKVAVYSTCL 1786  
Db 1741 KDLERKYEDNORYLEDKAQELARLEGEVRSLLKDIISOKVAVYSTCL 1786

RESULT 2  
US-10-841-139-4  
; Sequence 4, Application US/10841139  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert E.  
; APPLICANT: Wagon, David W.  
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE  
; FILE REFERENCE: 10287/021003  
; CURRENT APPLICATION NUMBER: US/10/841,139  
; CURRENT FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US/10/443,349  
; PRIOR FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US/09/161,872  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 08/735,893  
; PRIOR FILING DATE: 1996-10-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
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; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
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; FEATURE:  
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; LOCATION: (438)...(807)  
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; NAME/KEY: DOMAIN  
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; OTHER INFORMATION: Human B1 chain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (841)...(1196)  
; OTHER INFORMATION: Human B1 chain  
; US-10-841-139-4

Query Match 62.0%; Score 6044.5; DB 6; Length 1196;  
Best Local Similarity 67.6%; Pred. No. 1.3e-249;  
Matches 1194; Conservative 0; Mismatches 1; Indels 571; Gaps 2;

QY 22 QPPEFSYCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 80  
Db 1 QPPEFSYCAEGSCYPATGDLIGRAQKLSVTS-TCGLHKPEPYCIVSHLOEDKKCFICN 60

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:26:08 / Search time 20.6673 Seconds

(without alignments)  
9158.169 Million cell updates/sec

Title: US-10-037-182-4

Perfect score: 19876

Sequence: 1 DLYCKLVGGPVGAGDPNQTI.....QGKALQTHAKPSVSLPLWH 3635

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19876	100.0	3718	1 LMA5_MOUSE	Q61001 mus musculu
2	15847	79.7	3695	1 LMA5_HUMAN	Q15230 homo sapien
3	6403.5	32.2	3333	1 LMA3_MOUSE	Q61789 mus musculu
4	5018.5	25.2	3712	1 LMA_DROME	Q00174 drosophila
5	4831.5	24.3	3672	1 LML2_CAEEL	Q21313 caenorhabdi
6	3096	15.6	3106	1 LMA2_MOUSE	G60675 mus musculu
7	3005	15.1	3110	1 LMA2_HUMAN	P24043 homo sapien
8	2792	14.0	3084	1 LMA1_MOUSE	P15137 mus musculu
9	2729.5	13.7	3075	1 LMA1_HUMAN	P25391 homo sapien
10	2182.5	11.0	1816	1 LMA4_HUMAN	Q16363 homo sapien
11	2149.5	10.8	1713	1 LMA3_HUMAN	Q16787 homo sapien
12	2132.5	10.7	1816	1 LMA4_MOUSE	P97927 mus musculu
13	1675	8.4	1798	1 LMA2_HUMAN	P55268 homo sapien
14	1672.5	8.4	1801	1 LMB2_MOUSE	P15800 rattus norv
15	1668.5	8.4	1799	1 LMB1_MOUSE	Q61292 mus musculu
16	1605	8.1	1786	1 LMB1_HUMAN	P07942 homo sapien
17	1584	8.0	1786	1 LMB1_MOUSE	P02469 mus musculu
18	1552	7.8	1790	1 LMB3_HUMAN	P11046 drosophila
19	1462.5	7.4	1587	1 LMB3_MOUSE	Q9Y6N6 homo sapien
20	1367	6.9	1581	1 LMB3_MOUSE	Q9X0B6 mus musculu
21	1344.5	6.8	1607	1 LMB1_MOUSE	P02468 mus musculu
22	1323.5	6.7	1609	1 LMB1_HUMAN	P11047 homo sapien
23	1312	6.6	1639	1 LMB1_DROME	P15215 drosophila
24	1221	6.1	1535	1 LML1_CAEEL	Q18823 caenorhabdi
25	1204	6.1	3707	1 PGEM_MOUSE	Q05793 mus musculu
26	1104	5.6	4391	1 PGEM_HUMAN	P98160 homo sapien
27	947	4.8	1191	1 LMB2_MOUSE	Q61092 mus musculu
28	946	4.8	1192	1 LMB2_HUMAN	Q13753 homo sapien
29	839	4.2	1172	1 LMB3_HUMAN	Q13751 homo sapien
30	799.5	4.0	1168	1 LMB3_MOUSE	Q61087 mus musculu
31	799	4.0	3375	1 UN52_CAEEL	Q06561 caenorhabdi
32	754	3.8	2321	1 NTC3_HUMAN	Q9UM47 homo sapien
33	699	3.5	2319	1 NTC3_RAT	Q9*172 rattus norv

34	698.5	3.5	2437	1 NTC1_BRABE	P46530 brachydanio
35	694.5	3.5	2556	1 NTC1_HUMAN	P46531 homo sapien
36	689.5	3.5	2318	1 NTC3_MOUSE	Q61982 mus musculu
37	677	3.4	606	1 NET1_CHICK	Q09022 gallus gall
38	675.5	3.4	2471	1 NTC2_HUMAN	Q04721 homo sapien
39	675.5	3.4	2703	1 NOTC_DROME	P07207 drosophila
40	670	3.4	604	1 NET1_MOUSE	O09118 mus musculu
41	666	3.4	604	1 NET1_HUMAN	C95631 homo sapien
42	665	3.3	2471	1 NTC2_RAT	Q9GW30 rattus norv
43	654	3.3	612	1 UNC6_CAEEL	P34710 caenorhabdi
44	651	3.3	2524	1 NOTC_XENLA	P21783 xenopus lae
45	649.5	3.3	2470	1 NTC2_MOUSE	O35516 mus musculu

ALIGNMENTS

RESULT 1  
LMA5\_MOUSE  
ID LMA5\_MOUSE STANDARD; PRT; 3718 AA.  
AC Q61001; Q9JHQ6;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin alpha-5 chain precursor.  
GN LMA5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.  
RX MEDLINE=21818471; PubMed=11829758;  
RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;  
RT "Complete sequence, recombinant analysis and binding to laminins and  
sulphated ligands of the N-terminal domains of laminin alpha3B and  
alpha5 chains.";  
RT Biochem. J. 362:213-221(2002).  
RN [2]  
RP SEQUENCE OF 84-3718 FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;  
RX MEDLINE=96081906; PubMed=7499364;  
RA Miner J.H., Lewis R.M., Sanes J.R.;  
RT "Molecular cloning of a novel laminin chain, alpha 5, and widespread  
expression in adult mouse tissues.";  
RL J. Biol. Chem. 270:28523-28526(1995).  
RN [3]  
RP REVIEWS.  
RA Miner J.H., Lewis R.M., Sanes J.R.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: Binding to cells via a high affinity receptor, laminin  
is thought to mediate the attachment, migration and organization  
of cells into tissues during embryonic development by interacting  
with other extracellular matrix components.  
CC -|- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF  
ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.  
CC -|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
different polypeptide chains (alpha, beta, gamma), which are bound  
to each other by disulfide bonds into a cross-shaped molecule  
comprising one long and three short arms with globules at each  
end.  
CC -|- SUBCELLULAR LOCATION: Extracellular; found in the basement  
membranes (major component).  
CC -|- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and  
kidney; lower in brain, muscle and testis; very low in liver, gut  
and skin. Expressed in many tissues in embryonic day 11.  
CC -|- DOMAIN: The alpha-helical domains I and II are thought to interact  
with other laminin chains to form a coiled coil structure.  
CC -|- DOMAIN: Domains VI, IV and G are globular.  
CC -|- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -|- SIMILARITY: Contains 22 laminin EGF-like domains.  
CC -|- SIMILARITY: Contains 2 laminin IV domains.  
CC -|- SIMILARITY: Contains 5 laminin G-like domains.

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 CC -----  
 DR EMBL; AJ293593; CAB99255.1; --  
 DR GO; GO:0005604; C:basement membrane; IDA.  
 DR GO; GO:0005178; F:integrin binding; IDA.  
 DR GO; GO:0030324; P:lung development; IMP.  
 DR InterPro; IPR008985; ConA like lec\_gl.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR08212; Lam\_N2.  
 DR InterPro; IPR000034; Laminin\_B.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR008211; LamNT.  
 DR Pfam; PF00052; laminin\_B; 1.  
 DR Pfam; PF00053; laminin\_EGF; 17.  
 DR Pfam; PF00054; laminin\_G; 2.  
 DR Pfam; PF00055; laminin\_Nterm; 1.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR ProDom; PD002082; Lam\_N2; 1.  
 DR ProDom; PD003031; Laminin\_B; 1.  
 DR SMART; SM00180; EGF\_Lam; 20.  
 DR SMART; SM00281; LamB; 1.  
 DR SMART; SM00282; LamG; 5.  
 DR SMART; SM00136; LamNT; 1.  
 DR PROSITE; PS00022; EGF\_1; 19.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01248; LAMININ TYPE EGF; 19.  
 DR PROSITE; PS50025; Lam\_G DOMAIN; 5.  
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 40  
 FT CHAIN 41 3718 LAMININ ALPHA-5 CHAIN.  
 FT DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).  
 FT DOMAIN 305 363 LAMININ EGF-LIKE 1.  
 FT DOMAIN 364 433 LAMININ EGF-LIKE 2.  
 FT DOMAIN 434 479 LAMININ EGF-LIKE 3.  
 FT DOMAIN 500 546 LAMININ EGF-LIKE 4.  
 FT DOMAIN 547 592 LAMININ EGF-LIKE 5.  
 FT DOMAIN 593 637 LAMININ EGF-LIKE 6.  
 FT DOMAIN 638 682 LAMININ EGF-LIKE 7.  
 FT DOMAIN 683 728 LAMININ EGF-LIKE 8.  
 FT DOMAIN 729 781 LAMININ EGF-LIKE 9.  
 FT DOMAIN 782 833 LAMININ EGF-LIKE 10.  
 FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE).  
 FT DOMAIN 856 1442 LAMININ DOMAIN IV 1 (DOMAIN IV B).  
 FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12.  
 FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13.  
 FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14.  
 FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15.  
 FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL).  
 FT DOMAIN 1643 1831 LAMININ EGF-LIKE 17.  
 FT DOMAIN 1832 1864 LAMININ EGF-LIKE 18.  
 FT DOMAIN 1865 1914 LAMININ EGF-LIKE 19.  
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Query Match				DB 1; Length 3718;			
Best Local Similarity				100.0%; Score 19876;			
Matches 3635; Conservative				0; Mismatches			
				0; Indels		0; Gaps	
QY	1	DLYCKLVGGPVAGGPNQTIQOYCDICTAANSNKAHVPVNAIDGTERWQSPPLSRGLE	60				
DB	84	DLYCKLVGGPVAGGPNQTIQOYCDICTAANSNKAHVPVNAIDGTERWQSPPLSRGLE	143				
QY	61	YNEVNTLDLGOVHVAVYVILKFNAPSRLDLVLERSTDFGHTYQWQFPFASCKDCLER	120				
DB	144	YNEVNTLDLGOVHVAVYVILKFNAPSRLDLVLERSTDFGHTYQWQFPFASCKDCLER	203				
QY	121	FGPRLERITODDDVICTTEYSRIVPLENGEIVWSLVNRPALNFSYSPLLRDPFKATN	180				
DB	204	FGPRLERITODDDVICTTEYSRIVPLENGEIVWSLVNRPALNFSYSPLLRDPFKATN	263				
QY	181	IRLRLFRNTLLGHLMKALRDPVTTRYYYSIKDISIGRCVCHGHADVDCAKPLDPF	240				
DB	264	IRLRLFRNTLLGHLMKALRDPVTTRYYYSIKDISIGRCVCHGHADVDCAKPLDPF	323				
QY	241	RLOCAQHNTCGSCDRCCPGNQPKPATTDSDANEQSCNCHGHAIDCYDPEVDRRN	300				
DB	324	RLOCAQHNTCGSCDRCCPGNQPKPATTDSDANEQSCNCHGHAIDCYDPEVDRRN	383				
QY	301	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	360				
DB	384	ASQNDNVYQGGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG	443				
QY	361	TCEDLTGRCYCRPNFTGELCAACAGYTDFPHCYPLPFPFPHNDTREQVLPAQOIVNCDON	420				
DB	444	TCEDLTGRCYCRPNFTGELCAACAGYTDFPHCYPLPFPFPHNDTREQVLPAQOIVNCDON	503				
QY	421	AAGTQGNACRKDPRLGRCKVKNFRGAHCELCAFGHPGSPCHPCQSSPGVANSLCDPES	480				
DB	504	AAGTQGNACRKDPRLGRCKVKNFRGAHCELCAFGHPGSPCHPCQSSPGVANSLCDPES	563				
QY	481	GOCMRTFEGEDRCHCALGYHFFPLCQLCGSPAGTLPBGDEAGRCOCRPGDPHCD	540				
DB	564	GOCMRTFEGEDRCHCALGYHFFPLCQLCGSPAGTLPBGDEAGRCOCRPGDPHCD	623				
QY	541	RCLPGYHGYPDCHACADPRGALDQCGVGGVCHCRPGNTGATCQECSPFGFPSPCIPC	600				
DB	624	RCLPGYHGYPDCHACADPRGALDQCGVGGVCHCRPGNTGATCQECSPFGFPSPCIPC	683				
QY	601	HCSADGSLHTTCDPTTGGQCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	660				
DB	684	HCSADGSLHTTCDPTTGGQCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL	743				
QY	661	PETQAPCMRAHVEGSPCDRCRPGYWGLSASNEPGCTRCSDPRGTLGGVTECQNGQCF	720				
DB	744	PETQAPCMRAHVEGSPCDRCRPGYWGLSASNEPGCTRCSDPRGTLGGVTECQNGQCF	803				
QY	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRDVGALGQGCBEKPTGACRCRPNTOGPT	780				
DB	804	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRDVGALGQGCBEKPTGACRCRPNTOGPT	863				
QY	781	CSEPAKHVLPDLHNRLELEAATPEGHAVRFGNPLEFENFSWRGVAHMAIOPRIVA	840				
DB	864	CSEPAKHVLPDLHNRLELEAATPEGHAVRFGNPLEFENFSWRGVAHMAIOPRIVA	923				
QY	841	RLNVTSPDLFRLVFRVYNRGTSVNGQISVRBEGKLSCTNCTEQSQPVAFPSTEPAPFV	900				
DB	924	RLNVTSPDLFRLVFRVYNRGTSVNGQISVRBEGKLSCTNCTEQSQPVAFPSTEPAPFV	983				
QY	901	TPQORGEGFPVLNPGIOWALLVEAGVLLDYVLLPSTVYEALLOHRVTEACTYRBSAL	960				
DB	984	TPQORGEGFPVLNPGIOWALLVEAGVLLDYVLLPSTVYEALLOHRVTEACTYRPSAL	1043				
QY	961	HSTENCLVYAHLPDQGFPSAAGTEALCRDHSNLSRPRCTEQLSPSHPPLATCFGSDVDIQ	1020				
DB	1044	HSTENCLVYAHLPDQGFPSAAGTEALCRDHSNLSRPRCTEQLSPSHPPLATCFGSDVDIQ	1103				

QY	1021	LEMAVQPQGOYVLVVEYVGEDSQEMGVAVHTPQRAPOQGVNLNHPCTPYSSLCRSPARDT	1080
DB	1104	LEMAVQPQGOYVLVVEYVGEDSQEMGVAVHTPQRAPOQGVNLNHPCTPYSSLCRSPARDT	1163
QY	1081	QHHLAIFHLDSBASIRLTAEOAHFFLHSVTLVPVEEFSFEFVEPRVFCVSSHGCTNPSSA	1140
DB	1164	QHHLAIFHLDSBASIRLTAEOAHFFLHSVTLVPVEEFSFEFVEPRVFCVSSHGCTNPSSA	1223
QY	1141	ACLASFPPKPPQIILKDCQVLPPLDPLPTQSQELSPGAPPEGPQPRPPTAVDPNAEPT	1200
DB	1224	ACLASFPPKPPQIILKDCQVLPPLDPLPTQSQELSPGAPPEGPQPRPPTAVDPNAEPT	1283
QY	1201	LLRHPOGTVFTTQVPTLGRYAEFLHGYQVHPSPFVFEVLINGRIMQGHANASFCPHGY	1260
DB	1284	LLRHPOGTVFTTQVPTLGRYAEFLHGYQVHPSPFVFEVLINGRIMQGHANASFCPHGY	1343
QY	1261	GCRTLVLCGQWMLDVTNDELTVTVRVPGRWLWLDVLIIVPEDAYSSSYLOEPELDKSY	1320
DB	1344	GCRTLVLCGQWMLDVTNDELTVTVRVPGRWLWLDVLIIVPEDAYSSSYLOEPELDKSY	1403
QY	1321	DFISHCATQYHISPSSSSPFCRNAATSLFVYNNGALPGCCHVEGAVSPTCFPGQCP	1380
DB	1404	DFISHCATQYHISPSSSSPFCRNAATSLFVYNNGALPGCCHVEGAVSPTCFPGQCP	1463
QY	1381	CRGHVIGDCSRCATGYWGPNCRCDCGARLCCDELGTQCICPPRTVPPDCLVCQPSFG	1440
DB	1464	CRGHVIGDCSRCATGYWGPNCRCDCGARLCCDELGTQCICPPRTVPPDCLVCQPSFG	1523
QY	1441	CHPLVGCBEENCSPGVQVELTPTCDMDSGQCRPNVAGRRCDTCAPOFYGPSRCPD	1500
DB	1524	CHPLVGCBEENCSPGVQVELTPTCDMDSGQCRPNVAGRRCDTCAPOFYGPSRCPD	1583
QY	1501	CHEAGTVASVCDPLTGQCHCKENVQSRCDQCVGTFSLDAANPKGCTCFCGATERCG	1560
DB	1584	CHEAGTVASVCDPLTGQCHCKENVQSRCDQCVGTFSLDAANPKGCTCFCGATERCG	1643
QY	1561	NSNLARHEFVDMEGWLLSSDRQVWPHRPELLEHDLRSVADTFSELYWQAPPSYLG	1620
DB	1644	NSNLARHEFVDMEGWLLSSDRQVWPHRPELLEHDLRSVADTFSELYWQAPPSYLG	1703
QY	1621	DRVSSYGGTLYHELHSETQRGDIFIPIYESRDPVVLQGNQMSIAFLAYLPPPOVHRGQL	1680
DB	1704	DRVSSYGGTLYHELHSETQRGDIFIPIYESRDPVVLQGNQMSIAFLAYLPPPOVHRGQL	1763
QY	1681	QLVEGNFRHLETHNPSREELMMVLAGELOQIRALFQSOTSSSVSLRRVVLVASEAGRG	1740
DB	1764	QLVEGNFRHLETHNPSREELMMVLAGELOQIRALFQSOTSSSVSLRRVVLVASEAGRG	1823
QY	1741	PPASNVELCMCPANYRGDSQOECAPGYRTDKGLFLGRVPCQCHGSHDRCLPSGICVVG	1800
DB	1824	PPASNVELCMCPANYRGDSQOECAPGYRTDKGLFLGRVPCQCHGSHDRCLPSGICVVG	1883
QY	1801	COHNTGDCQECRCPGVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1860
DB	1884	COHNTGDCQECRCPGVSSDPSPNPASPCVSCPCPLAVPSNNFADGCVLRNGRTQCLCRP	1943
QY	1861	GYAGASCERCAPGFPNGPLVIGSSQPCDCSGNDGPNMIFSDCDPLTGACRGCLRHHTGP	1920
DB	1944	GYAGASCERCAPGFPNGPLVIGSSQPCDCSGNDGPNMIFSDCDPLTGACRGCLRHHTGP	2003
QY	1921	HCERCAPGFVGNALLPQNCITRCDSPGTCGTCDPQSGRCLCKAGVTGQRCDCLGVEFG	1980
DB	2004	HCERCAPGFVGNALLPQNCITRCDSPGTCGTCDPQSGRCLCKAGVTGQRCDCLGVEFG	2063
QY	1981	BQCGCPCACGPAAGKSECHPOSGOCHQCFGTGTPQCLECAPGYWGLPKGCRRCQCPR	2040
DB	2064	BQCGCPCACGPAAGKSECHPOSGOCHQCFGTGTPQCLECAPGYWGLPKGCRRCQCPR	2123
QY	2041	GHCDPHTGHTCTCPPLSGRCDTCSQOQVVPVPGKPGGHHIHCVECDHCVVLLDLDLERA	2100
DB	2124	GHCDPHTGHTCTCPPLSGRCDTCSQOQVVPVPGKPGGHHIHCVECDHCVVLLDLDLERA	2183
QY	2101	GALLPAIREQLOGINASSAAWALHRLNLSIADLQSLRRPPGPRVYQAAQQLQTLQOQSI	2160



Db 2184 GALLPAIREQLOGINASSAARLHRLNASIADLQSKLRPPGPRYQAAQLQILEQOSI 2243  
 QY 2161 SLOODTERIGSQATGCGAGQQLDITTESTIGRAOKLLESRAVGRALNELASRMGGOSP 2220  
 Db 2244 SLOODTERIGSQATGCGAGQQLDITTESTIGRAOKLLESRAVGRALNELASRMGGOSP 2303  
 QY 2221 GDALVPSGEOLRWALLAEVERLLWDMRTRDLGAQGAABAELAEALQMARVQEQITSFWE 2280  
 Db 2304 GDALVPSGEOLRWALLAEVERLLWDMRTRDLGAQGAABAELAEALQMARVQEQITSFWE 2363  
 QY 2281 ENOSLATHRDQLAQYESGLMDLRALNQAQVNTTREAELSRNQERKVEALQKQELSQ 2340  
 Db 2364 ENOSLATHRDQLAQYESGLMDLRALNQAQVNTTREAELSRNQERKVEALQKQELSQ 2423  
 QY 2341 DNATKATLQAASLILGHVSELLOGIDQAKEDLEHAAASLDGAMTPLLKRMQAFSPASSK 2400  
 Db 2424 DNATKATLQAASLILGHVSELLOGIDQAKEDLEHAAASLDGAMTPLLKRMQAFSPASSK 2483  
 QY 2401 VDLVEAEEHAKINQALNLSGIIILGINQDRFIQRAVEASNAVSSILQAVQAAEDAAQ 2460  
 Db 2484 VDLVEAEEHAKINQALNLSGIIILGINQDRFIQRAVEASNAVSSILQAVQAAEDAAQ 2543  
 QY 2461 ALRQASRTWEMVQVGLAAGARQLLANSSALEETILGHQRLGLAAGRLQAGIQLHNVM 2520  
 Db 2544 ALRQASRTWEMVQVGLAAGARQLLANSSALEETILGHQRLGLAAGRLQAGIQLHNVM 2603  
 QY 2521 ARKNQAAQIOEAQAMLANMDTSETSEKTAHAKAVAAEALSTATHVOSQLOQMKNVERWQ 2580  
 Db 2604 ARKNQAAQIOEAQAMLANMDTSETSEKTAHAKAVAAEALSTATHVOSQLOQMKNVERWQ 2663  
 QY 2581 SOLGGLQGGDLQOVERDASSVSTLEKTLPLQLAKLSRLNENRGVHNASLALSANIGVRK 2640  
 Db 2664 SOLGGLQGGDLQOVERDASSVSTLEKTLPLQLAKLSRLNENRGVHNASLALSANIGVRK 2723  
 QY 2641 LIAQASAAKVKVSKMKNRSGVRLRPPRLDADIAAATALKFHIQSPVPAPEPKNTGD 2700  
 Db 2724 LIAQASAAKVKVSKMKNRSGVRLRPPRLDADIAAATALKFHIQSPVPAPEPKNTGD 2783  
 QY 2701 HFVLYNGSRQATGDYNGVSLRNQKHWYVRLGKAGFTLSDENIGEOFAAVSIDRTLQF 2760  
 Db 2784 HFVLYNGSRQATGDYNGVSLRNQKHWYVRLGKAGFTLSDENIGEOFAAVSIDRTLQF 2843  
 QY 2761 GHMSVTVKQVHEIKGDTVAPSGSLNLRHPPDDFVYVGGYPSNFTPEPLRPPGLGC 2820  
 Db 2844 GHMSVTVKQVHEIKGDTVAPSGSLNLRHPPDDFVYVGGYPSNFTPEPLRPPGLGC 2903  
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 Db 2904 IEMETLNEEWSLYNFEQTFMLDTAVDKPCARSKATGDPMLTDGSLDGGSGFARISFEKQ 2963  
 QY 2881 FSNTRKFDQELRLVSYNGIIFPKQESQFLCLAVQSGTLVLFYDPSGLKKADPLQPPQA 2940  
 Db 2964 FSNTRKFDQELRLVSYNGIIFPKQESQFLCLAVQSGTLVLFYDPSGLKKADPLQPPQA 3023  
 QY 2941 LTAASKAIQVFLLAGNRKELVRVERATVFSVDQNMLEADAYVYLGVPPEQPLSLRQ 3000  
 Db 3024 LTAASKAIQVFLLAGNRKELVRVERATVFSVDQNMLEADAYVYLGVPPEQPLSLRQ 3083  
 QY 3001 LPFSGSVGCGCKIGKALGKYVDLKLNTTGISFGCTADLLVGRMTFHHGFLPLALPD 3060  
 Db 3084 LPFSGSVGCGCKIGKALGKYVDLKLNTTGISFGCTADLLVGRMTFHHGFLPLALPD 3143  
 QY 3061 VAPITEVYVSGFRGTQDNLLYRTSPDGPYQVSLREGHVTLRFNMNQEVETQVFPADG 3120  
 Db 3144 VAPITEVYVSGFRGTQDNLLYRTSPDGPYQVSLREGHVTLRFNMNQEVETQVFPADG 3203  
 QY 3121 APHYVAFSVNTGVMLYVDDQLOLVKSHERTTLMLOQPEPSRLILCGLPVSGTFNFS 3180  
 Db 3204 APHYVAFSVNTGVMLYVDDQLOLVKSHERTTLMLOQPEPSRLILCGLPVSGTFNFS 3263  
 QY 3181 GCISNVFVQRLRGPORFVLDLHQNMGSVNVSGCTPAQLIETSRATAQKVSRRSRQPSQDL 3240

Db 3264 GCISNVFVQRLRGPORFVLDLHQNMGSVNVSGCTPAQLIETSRATAQKVSRRSRQPSQDL 3323  
 QY 3241 ACTTTPWLPCTODAYOPGPIPSYLOFVGISPSHRNRIHLSMLVPRPAAAGCGLLSTAPM 3300  
 Db 3324 ACTTTPWLPCTODAYOPGPIPSYLOFVGISPSHRNRIHLSMLVPRPAAAGCGLLSTAPM 3383  
 QY 3301 SCRSPLSLFLNHGHFVAQTEGPGPRQLQVQSRQSRAGQWHRVSVRGMQOQIQLVVDGSG 3360  
 Db 3384 SCRSPLSLFLNHGHFVAQTEGPGPRQLQVQSRQSRAGQWHRVSVRGMQOQIQLVVDGSG 3443  
 QY 3361 TWSQALHHRVPRABRPPOPYTLISVGGIPASSYSKLPVSVGFSGLCKLQDKQPLRTPT 3420  
 Db 3444 TWSQALHHRVPRABRPPOPYTLISVGGIPASSYSKLPVSVGFSGLCKLQDKQPLRTPT 3503  
 QY 3421 QMVGVTPCVSGPLEDGLFPFGSEGVTLELPKAKMPVVSLEMRPLAAAGLIPLHGOAL 3480  
 Db 3504 QMVGVTPCVSGPLEDGLFPFGSEGVTLELPKAKMPVVSLEMRPLAAAGLIPLHGOAL 3563  
 QY 3481 ATPYNQKLVLEOVLLQANDGAGSEFTWVTYPKLDCGRHVRVAVMGRTILREVDQTSN 3540  
 Db 3564 ATPYNQKLVLEOVLLQANDGAGSEFTWVTYPKLDCGRHVRVAVMGRTILREVDQTSN 3623  
 QY 3541 HTTGLPESLAGSPALLHLGSLPKSSTARPELPAYRCGLAKLLINGAPVNVTVASVQIOGA 3600  
 Db 3624 HTTGLPESLAGSPALLHLGSLPKSSTARPELPAYRCGLAKLLINGAPVNVTVASVQIOGA 3683  
 QY 3601 VCMRCPCSGTLALSQKQKALTQTHAKPSVSPILLWH 3635  
 Db 3684 VCMRCPCSGTLALSQKQKALTQTHAKPSVSPILLWH 3718

## RESULT 2

LMA5 HUMAN STANDARD; PRT; 3695 AA.  
 ID LMA5 HUMAN STANDARD; Q9H1P1  
 AC 015320; Q9WZAT; Q9H1P1  
 DT 16-OCT-2001 (Rel. 40, created)  
 DT 28-FEB-2003 (Rel. 41, last sequence update)  
 DT 15-MAR-2004 (Rel. 43, last annotation update)  
 DE Laminin alpha-5 chain precursor.  
 GN LMA5 OR KIAA0533 OR KIAA1907.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dhami P.D., Dunn M.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharshah M.H., Leversha M.A., Lloyd C., Lloyd D.M., McMurray A.J.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., Mclay K., McMurray A.J.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Pzathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Roess M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20."

RL Nature 414:865-871(2001).  
RN [2]  
RP SEQUENCE OF 197-1934 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=21456161; PubMed=11572484;  
RA Nagase T., Kikuno R., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XXI.  
RT The complete sequences of 60 new cDNA clones from brain which code for  
RT large proteins.";  
RL DNA Res. 8:179-187(2001).  
RN [3]  
RP SEQUENCE OF 2051-3695 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 5:31-39(1998).  
RN [4]  
RP SEQUENCE OF 2743-3695 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=97415435; PubMed=9271224;  
RA Durkin M.E., Loechele F., Mattei M.-G., Gilpin B.J., Albrecht R.,  
RA Wewer U.M.;  
RT "Tissue-specific expression of the human laminin alpha5-chain, and  
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal  
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";  
RL FEBS Lett. 411:296-300(1997).  
RN [5]  
RP EXPRESSION IN RETINA.  
RX MEDLINE=20422761; PubMed=10964957;  
RA Libby R.T., Champlaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,  
RA Koch M., Burgesson R.E., Hunter D.D., Brunken W.J.;  
RT "Laminin expression in adult and developing retinae: evidence of two  
RT novel CNS laminins.";  
RL J. Neurosci. 20:16517-16528(2000).  
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -1- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three  
CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by  
CC disulfide bonds into a cross-shaped molecule comprising one long  
CC and three short arms with globules at each end.  
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement  
CC membranes (major component).  
CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal  
CC muscle, pancreas, retina and placenta. Little or no expression in  
CC brain and liver.  
CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding  
CC site located in the long arm of the laminin heterotrimer.  
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.  
CC -1- SIMILARITY: Contains 2 laminin IV domains.  
CC -1- SIMILARITY: Contains 5 laminin G-like domains.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; AL354836; CAC22309.1; ALT\_SEQ.  
CC EMBL; AL354836; CAC22310.1; -.  
CC EMBL; AB067494; BAB67800.1; -.  
CC EMBL; AB011105; BAA25459.1; -.  
CC EMBL; Z95636; CAB09137.1; -.  
CC HSSP; P02468; 1KLO.  
CC Genew; HGNC:6485; LAMA5.

DR MM; 601033; -.  
DR InterPro; IPR008985; ConA like\_lec\_gl.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR008212; Lam\_N2.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin\_B; 1.  
DR Pfam; PF00053; laminin\_EGF; 18.  
DR Pfam; PF00054; laminin\_G; 2.  
DR Pfam; PF00055; laminin\_Nterm; 1.  
DR PRINTS; PRO0011; EGF\_LAMININ.  
DR ProDom; PD002082; Lam\_N2; 1.  
DR ProDom; PD003031; Laminin\_B; 1.  
DR SMART; SM00180; EGF\_Lam; 20.  
DR SMART; SM00281; LamB; 1.  
DR SMART; SM00282; LamG; 5.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 19.  
DR PROSITE; PS01186; EGF\_2; 3.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 19.  
DR PROSITE; PS00025; LAM\_G\_DOMAIN; 5.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 35  
FT CHAIN 36 3695 LAMININ ALPHA-5 CHAIN.  
FT DOMAIN 36 299 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 300 358 LAMININ EGF-LIKE 1.  
FT DOMAIN 359 428 LAMININ EGF-LIKE 2.  
FT DOMAIN 429 474 LAMININ EGF-LIKE 3.  
FT DOMAIN 494 540 LAMININ EGF-LIKE 4.  
FT DOMAIN 541 586 LAMININ EGF-LIKE 5.  
FT DOMAIN 587 631 LAMININ EGF-LIKE 6.  
FT DOMAIN 632 676 LAMININ EGF-LIKE 7.  
FT DOMAIN 677 722 LAMININ EGF-LIKE 8.  
FT DOMAIN 723 775 LAMININ EGF-LIKE 9.  
FT DOMAIN 776 828 LAMININ EGF-LIKE 10.  
FT DOMAIN 829 850 LAMININ EGF-LIKE 11 (INCOMPLETE).  
FT DOMAIN 851 1437 LAMININ DOMAIN IV 1 (DOMAIN IV B).  
FT DOMAIN 1438 1483 LAMININ EGF-LIKE 12.  
FT DOMAIN 1484 1527 LAMININ EGF-LIKE 13.  
FT DOMAIN 1528 1576 LAMININ EGF-LIKE 14.  
FT DOMAIN 1577 1627 LAMININ EGF-LIKE 15.  
FT DOMAIN 1628 1637 LAMININ EGF-LIKE 16 (N-TERMINAL).  
FT DOMAIN 1638 1830 LAMININ DOMAIN IV 2 (DOMAIN IV A).  
FT DOMAIN 1831 1863 LAMININ EGF-LIKE 16 (C-TERMINAL).  
FT DOMAIN 1864 1912 LAMININ EGF-LIKE 17.  
FT DOMAIN 1913 1968 LAMININ EGF-LIKE 18.  
FT DOMAIN 1969 2022 LAMININ EGF-LIKE 19.  
FT DOMAIN 2023 2069 LAMININ EGF-LIKE 20.  
FT DOMAIN 2070 2116 LAMININ EGF-LIKE 21.  
FT DOMAIN 2117 2166 LAMININ EGF-LIKE 22.  
FT DOMAIN 2167 2329 LAMININ G-LIKE 1.  
FT DOMAIN 2330 2335 LAMININ G-LIKE 2.  
FT DOMAIN 2336 2392 LAMININ G-LIKE 3.  
FT DOMAIN 2393 3115 LAMININ G-LIKE 4.  
FT DOMAIN 3116 3124 LAMININ G-LIKE 5.  
FT DOMAIN 3125 3513 LAMININ G-LIKE 5.  
FT DOMAIN 3514 3520 LAMININ G-LIKE 5.  
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Query Match 79.7%; Score 15847; DB 1; Length 3695;  
 Best Local Similarity 79.4%; Pred. No. 0;  
 Matches 2876; Conservative 276; Mismatches 451; Indels 18; Gaps 8;

FT DISULFID 431 447 BY SIMILARITY.  
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QY 1 DLYCKLVGGPVAGGDPNQTIOQYCDICTAANSKHAHPVSNADICTERWQSPPLSRGLE 60  
 DB 79 DLYCKLVGGPVAGGDPNQTIOQYCDICTAANSKHAHPVSNADICTERWQSPPLSRGLE 138

QY 61 YNEVNVTLDDGVFHVAYVLIKFPANSPRDLWVLRSTDFGHTYQWQOFFPASSKEDCLER 120  
 DB 139 YNEVNVTLDDGVFHVAYVLIKFPANSPRDLWVLRSTDFGHTYQWQOFFPASSKEDCLER 198

QY 121 FGRTLERITQDDVICTTEYSRIPLVLENGEIVWSLVNVRPGALNFYSPLLRDFTKATN 180  
 DB 199 FGRTLERITQDDVICTTEYSRIPLVLENGEIVWSLVNVRPGALNFYSPLLRDFTKATN 258

QY 181 IRLRPLRTNLLGLMKGKALRDPVTRRYYSIKDISIGGRVCHGHADVCADKOPDPPF 240  
 DB 259 VRLRPLRTNLLGLMKGKALRDPVTRRYYSIKDISIGGRVCHGHADVCADKOPDPPF 318

QY 241 RLQACQHNCTCGSDRCRCPGPNQPKPATDTSANECQSCNCHGHAYDVCYDDPEVDNRN 300  
 DB 319 RLQCTCOHNTCGTCDRCRCPGPNQPKPATDTSANECQSCNCHGHAYDVCYDDPEVDNRN 378

QY 301 ASQNDNVYGGGVCLDCOHTTGNCERCLPGFPFRAPDQILDSPHVCRCDCSDFTDG 360  
 DB 379 ASQSLDGTYYGGGVCLDCOHTTGNCERCLPGFPFRAPDQILDSPHVCRCDCSDFTDG 438

QY 361 TCEDLTGRCYCRPNFTGELCAACAEYTDTPHCYPLPSFPNDRTEQVLPAGQVINCDCN 420  
 DB 439 TCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYFTPS--SSNDTREQVLPAGQVINCDCS 497

QY 421 AGTQGNACKDPRLEGRCVCKENPRGAHCELCAQFHPGSPCHPCQCSGPGVANSCLDPES 480  
 DB 498 AGTQGNACKDPRVGRCLCKPNFGTHCELCAQFHPGSPCHPCQCSGPGVANSCLDPES 557

QY 481 GQCMRTGPEGDRCDHLCALGYHFFPLCQLCGSPAGTLPEGCDEAGRCQCRPGPDGPHCD 540  
 DB 558 GQCMRTGPEGDRCDHLCALGYHFFPLCQLCGSPAGTLPEGCDEAGRCQCRPGPDGPHCD 617

QY 541 RCLPGVHYPCDHACACDPRGALDQCGVGLCHCRPGNTGATQECSPGFYGPSPCIPC 600  
 DB 618 RCLPGVHYPCDHACACDPRGALDQCGVGLCHCRPGNTGATQECSPGFYGPSPCIPC 677

QY 601 HCSADGSLHTTCDPTTGQCRCPRTVTLGLHCDMCPFGAYNFFPYCEAGSCHPAGLAPANPAL 660  
 DB 678 HCSADGSLHTTCDPTTGQCRCPRTVTLGLHCDMCPFGAYNFFPYCEAGSCHPAGLAPANPAL 737

QY 661 PETQAPCMCHRAHVEGSPCDRCBPGVWGLSASNPEGCTRCSDPRGTLGGVTECO--GNQC 719  
 DB 738 PETQAPCMCHRAHVEGSPCDRCBPGVWGLSASNPEGCTRCSDPRGTLGGVTECO--GNQC 797

QY 720 FCKAHVCGKTCACDKGDFGLDYADYFGCRSCRDVGGALQCGCEPKTGTACRCRPNQTGP 779  
 DB 798 FCKAHVCGKTCACDKGDFGLDYADYFGCRSCRDVGGALQCGCEPKTGTACRCRPNQTGP 857

QY 780 TCSEPAKHLYPLDLHMELELEEAATPEGHAVRFGFNPLEFENFWSWGYAHMAIOPRIV 839  
 DB 857 TCSEPAKHLYPLDLHMELELEEAATPEGHAVRFGFNPLEFENFWSWGYAHMAIOPRIV 916

DB 858 TCSEPAKHLYPLDLHMELELEEAATPEGHAMRFGFNPLEFENFWSWGYAHMAIOPRIV 917  
 QY 840 ARNLVTSPLDLFRLVRYNVRGTSVNGOISVREEGKLSCTNCTEQSOQVAFPPSTEDAF 899  
 DB 918 ARNLVTSPLDLFRLVRYNVRGTSVNGOISVREEGKLSCTNCTEQSOQVAFPPSTEDAF 977  
 QY 900 VIVPQGFGEFVPLNPGIWLVAEGVLLDVFVLLPSTYYEALLQHRVTEACTYRPSA 959  
 DB 978 ITVPQGFGEFVPLNPGIWLVAEGVLLDVFVLLPSTYYEALLQHRVTEACTYRPSA 1037  
 QY 960 LHSSTENCLVYAHPLDGFPSAAGTEALCRHDSNLRPCPTQOLSPSHPLATCFGSVDI 1019  
 DB 1038 QSGDNCCLYTHPLDGFPSAAGTEALCRHDSNLRPCPTQOLSPSHPLATCFGSVDI 1097

QY 1020 QLEMAVPOQGVVIVVEVGEDSHOEMGVAVHTPORAQOQGVILNHPCPYSGLCRSPARD 1079  
 DB 1098 QLEMAVPOQGVVIVVEVGEDSHOEMGVAVHTPORAQOQGVILNHPCPYSGLCRSPARD 1157

QY 1080 TORHLAIFHLDSIASIRLTAEQAHHFHLHSVTLVVEEFSTFEFVPRVFCVSSHGTFFNPSS 1139  
 DB 1158 TORHLAIFHLDSIASIRLTAEQAHHFHLHSVTLVVEEFSTFEFVPRVFCVSSHGTFFNPSS 1217

QY 1140 AACLASRPKPPPIILKDCOVLLPDPDLPTQSOQLSPGAPPEGPQPRPTAVDPNAEP 1199  
 DB 1218 AACLASRPKPPPIILKDCOVLLPDPDLPTQSOQLSPGAPPEGPQPRPTAVDPNAEP 1277

QY 1200 TLLRHPQGTVFTTQVPTLGRYAFLLHGYQVHPSPFVVEVLINGRIWQHGHANASFCPHG 1259  
 DB 1278 TLLRHPQGTVFTTQVPTLGRYAFLLHGYQVHPSPFVVEVLINGRIWQHGHANASFCPHG 1337

QY 1260 YGCRVLVCEGQTLMDVTDNELTVTVRVPBGWMLDYLVLPEDATSSSYLQSEPLDKS 1319  
 DB 1338 YGCRVLVCEGQTLMDVTDNELTVTVRVPBGWMLDYLVLPEDATSSSYLQSEPLDKS 1397

QY 1320 YDFISHCATQGHYHSPSSSSPFCRNAATSLFYNNGALPCGCHGVGAVSPTCSPFGQC 1379  
 DB 1398 YDFISHCATQGHYHSPSSSSPFCRNAATSLFYNNGALPCGCHGVGAVSPTCSPFGQC 1457

QY 1380 PCRGHVGSDCSRATGWPFGNCRPCDCCGRLCDELGTGQICPPRTVPDCLVCQDQSF 1439  
 DB 1458 PCRGHVGSDCSRATGWPFGNCRPCDCCGRLCDELGTGQICPPRTVPDCLVCQDQSF 1517

QY 1440 GCHPLVGCBECCSGPGVQELTDTCDMDSGQCRCPNVRAGRCDDTCAPGFYGPSPCRPC 1499  
 DB 1518 GCHPLVGCBECCSGPGVQELTDTCDMDSGQCRCPNVRAGRCDDTCAPGFYGPSPCRPC 1577

QY 1500 DCHAGTMAVSDPLTQCHCKENVQSCRDCQCRVGFSLDAANPKGCTCFGATERC 1559  
 DB 1578 DCHAGTMAVSDPLTQCHCKENVQSCRDCQCRVGFSLDAANPKGCTCFGATERC 1637

QY 1560 GNSNLARHEFVDMGWLSSDRQVWPHHRPELLEHDLR---SVADTFSELYWQAP 1615  
 DB 1638 GNSNLARHEFVDMGWLSSDRQVWPHHRPELLEHDLR---SVADTFSELYWQAP 1697

QY 1616 PSYLGDRVSSYGGTLHYELHSETORGDIPTPYSRPPVVLQGNMSTAFLELAYPPGQV 1675  
 DB 1698 PSYLGDRVSSYGGTLHYELHSETORGDIPTPYSRPPVVLQGNMSTAFLELAYPPGQV 1757

QY 1676 HRGQLQVLEGNFRLETHNPVSREELMMVLALQEQIRALFQISVSSVRLRVALEVAS 1735  
 DB 1758 HRGQLQVLEGNFRLETHNPVSREELMMVLALQEQIRALFQISVSSVRLRVALEVAS 1817

QY 1736 BAGRGPPASNVELCMCANVGRSCQECAPGYRDTKGLFLGRVCPQCHGSDRCLPGS 1795  
 DB 1818 BAGRGPPASNVELCMCANVGRSCQECAPGYRDTKGLFLGRVCPQCHGSDRCLPGS 1877

QY 1796 GICVGCQHNTEGDCRCRPFVSSPSNPASPCVCPPLAVPSNFAFGCVLRNRTQ 1855  
 DB 1878 GICVGCQHNTEGDCRCRPFVSSPSNPASPCVCPPLAVPSNFAFGCVLRNRTQ 1936

QY 1856 CLCPGVAGASCCRCAPFGNPLVILGSSCQPCDCCSGNDGNPMI FSDCPLTGACRGLR 1915  
 DB 1937 CLCPGVAGASCCRCAPFGNPLVILGSSCQPCDCCSGNDGNPMI FSDCPLTGACRGLR 1996

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: May 18, 2004, 14:26:08 ; Search time 21.0085 Seconds  
(without alignments)  
9158.169 Million cell updates/sec  
Title: US-10-037-182-2  
Perfect score: 20118  
Sequence: 1 MAKRLCAGSALCVRGPGPA.....AMTRSEVHGAVGAGGCPAA 3695  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match length	Description
1	20093	99.9	015230 homo sapien
2	16101.5	30.0	061001 mus musculus
3	6689.5	33.3	061789 mus musculus
4	5097	25.3	020174 drosophila
5	4974	24.7	021313 caenorhabdi
6	3141.5	31.06	060875 mus musculus
7	3103.5	15.4	P24043 homo sapien
8	2933	14.6	P19137 mus musculus
9	2854	14.2	P25391 homo sapien
10	2360.5	11.2	Q16787 homo sapien
11	2147.5	10.7	Q16363 homo sapien
12	2128.5	10.6	P97927 mus musculus
13	1613.5	8.0	P15800 rattus norv
14	1604	8.0	Q61292 mus musculus
15	1600.5	8.0	P55268 homo sapien
16	1573.5	7.8	P07942 homo sapien
17	1572.5	7.8	P02469 mus musculus
18	1525.5	7.6	P11046 drosophila
19	1460	7.3	Q9Y6N6 homo sapien
20	1403.5	7.0	Q9R0B6 mus musculus
21	1348.5	6.7	P02468 mus musculus
22	1338	6.7	P15215 drosophila
23	1313	6.5	P11047 homo sapien
24	1296	6.4	Q05793 mus musculus
25	1234	6.1	Q18823 caenorhabdi
26	1140	5.7	P98160 homo sapien
27	956.5	4.8	Q13753 homo sapien
28	923.5	4.6	Q61092 mus musculus
29	916.5	4.6	Q13751 homo sapien
30	870	4.3	Q61087 mus musculus
31	814	4.0	Q06561 caenorhabdi
32	799	4.0	Q9um47 homo sapien
33	781	3.9	Q61982 mus musculus

ALIGNMENTS			
RESULT 1			
ID	LMAS_HUMAN	STANDARD;	PRT; 3695 AA.
AC	015230; Q8WZ7; Q9H1P1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Laminin alpha-5 chain precursor.		
GN	LMAS5 OR KIAA0533 OR KIAA1907.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21638749; PubMed=11780052;		
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,		
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,		
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,		
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,		
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,		
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,		
RA	Clegg S., Cobley V.B., Collier R.E., Connor R.E., Corby N.R.,		
RA	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,		
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,		
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,		
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,		
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,		
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,		
RA	Lehvasaiaho V.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,		
RA	Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,		
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,		
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,		
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,		
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,		
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,		
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,		
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,		
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,		
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,		
RA	Rogers J.;		
RT	"The DNA sequence and comparative analysis of human chromosome 20.";		
RL	Nature 414:865-871(2001).		
RN	[2]		
RP	SEQUENCE OF 197-1934 FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=21456161; PubMed=11572484;		
RA	Nagase T., Kikuno R., Ohara O.;		
RT	"Prediction of the coding sequences of unidentified human genes. XXI.		
RT	The complete sequences of 60 new cDNA clones from brain which code for		
RT	large proteins.";		
RL	DNA Res. 8:179-187(2001).		
RN	[3]		
RP	SEQUENCE OF 2051-3695 FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=98290545; PubMed=9628581;		

Q9r172 rattus norv  
Q90322 gallus gall  
Q09118 mus musculu  
Q95631 homo sapien  
Q04721 homo sapien  
Q35516 mus musculu  
P34710 caenorhabdi  
Q99466 homo sapien  
P46531 homo sapien  
Q07008 rattus norv  
Q9q30 rattus norv  
P46530 brachydanio

RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 5:31-39(1998).  
RN [4]  
RP SEQUENCE OF 2743-3695 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=97415425; PubMed=9271224;  
RA Durkin M.E., Loecheil F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,  
RA Wewer U.M.;  
RT "Tissue-specific expression of the human laminin alpha5-chain, and  
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal  
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";  
RL FEBS Lett. 411:296-300(1997).  
RN [5]  
RP EXPRESSION IN RETINA.  
RX MEDLINE=20422761; PubMed=10964957;  
RA Libby R.T., Champlaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,  
RA Koch M., Burgess R.E., Hunter D.D., Brunken W.J.;  
RT "Laminin expression in adult and developing retinae: evidence of two  
RT novel CNS laminins.";  
RL J. Neurosci. 20:6517-6528(2000).  
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -!- SUBUNIT: Laminin-15 complex is a heterotrimer composed of three  
CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by  
CC disulfide bonds into a cross-shaped molecule comprising one long  
CC and three short arms with globules at each end.  
CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement  
CC membranes (major component).  
CC -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal  
CC muscle, pancreas, retina and placenta. Little or no expression in  
CC brain and liver.  
CC -!- DOMAIN: Domain G is globular and is part of the major cell-binding  
CC site located in the long arm of the laminin heterotrimer.  
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.  
CC -!- SIMILARITY: Contains 2 laminin IV domains.  
CC -!- SIMILARITY: Contains 5 laminin G-like domains.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; AL354836; CAC22309.1; ALT\_SEQ.  
CC EMBL; AL354836; CAC22310.1; -;  
CC EMBL; AB067494; BAB7800.1; -;  
CC EMBL; AB011105; BAA25459.1; -;  
CC EMBL; Z95636; CAB09137.1; -;  
CC HSP; P02468; IKLO.  
CC Genew; HGNC:6485; LAMAS.  
CC MIM; 601033; -;  
CC InterPro; IPR008985; ConA\_like\_lec\_gl.  
CC InterPro; IPR006209; EGF\_like.  
CC InterPro; IPR008212; Lam\_N2.  
CC InterPro; IPR000034; Laminin\_B.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR001791; Laminin\_G.  
CC InterPro; IPR008211; LamNT.  
CC Pfam; PF00052; laminin\_B; 1.  
CC Pfam; PF00053; laminin\_EGF; 18.  
CC Pfam; PF00054; laminin\_G; 2.  
CC Pfam; PF00055; laminin\_Nterm; 1.  
CC PRINTS; PR00011; EGF\_LAMININ.  
CC ProDom; PD002082; Lam\_N2; 1.

DR ProDom; PD003031; Laminin\_B; 1.  
DR SMART; SM00180; EGF\_Lam; 20.  
DR SMART; SM00281; LamE; 1.  
DR SMART; SM00282; LamG; 5.  
DR SMART; SM00136; LamNT; 1.  
DR PROSITE; PS00022; EGF\_1; 19.  
DR PROSITE; PS01186; EGF\_2; 3.  
DR PROSITE; PS01248; LAMININ TYPE EGF; 19.  
DR PROSITE; PS00025; LAM G DOMAIN; 5.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 35 POTENTIAL  
FT CHAIN 36 3695 LAMININ ALPHA-5 CHAIN.  
FT DOMAIN 36 299 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 300 358 LAMININ EGF-LIKE 1.  
FT DOMAIN 359 428 LAMININ EGF-LIKE 2.  
FT DOMAIN 429 474 LAMININ EGF-LIKE 3.  
FT DOMAIN 494 540 LAMININ EGF-LIKE 4.  
FT DOMAIN 541 586 LAMININ EGF-LIKE 5.  
FT DOMAIN 587 631 LAMININ EGF-LIKE 6.  
FT DOMAIN 632 676 LAMININ EGF-LIKE 7.  
FT DOMAIN 677 722 LAMININ EGF-LIKE 8.  
FT DOMAIN 723 775 LAMININ EGF-LIKE 9.  
FT DOMAIN 776 828 LAMININ EGF-LIKE 10.  
FT DOMAIN 829 850 LAMININ EGF-LIKE 11 (INCOMPLETE).  
FT DOMAIN 851 1437 LAMININ DOMAIN IV 1 (DOMAIN IV B).  
FT DOMAIN 1438 1484 LAMININ EGF-LIKE 12.  
FT DOMAIN 1484 1527 LAMININ EGF-LIKE 13.  
FT DOMAIN 1528 1576 LAMININ EGF-LIKE 14.  
FT DOMAIN 1577 1627 LAMININ EGF-LIKE 15.  
FT DOMAIN 1628 1637 LAMININ EGF-LIKE 16 (N-TERMINAL).  
FT DOMAIN 1638 1830 LAMININ DOMAIN IV 2 (DOMAIN IV A).  
FT DOMAIN 1831 1863 LAMININ EGF-LIKE 16 (C-TERMINAL).  
FT DOMAIN 1864 1912 LAMININ EGF-LIKE 17.  
FT DOMAIN 1913 1968 LAMININ EGF-LIKE 18.  
FT DOMAIN 1969 2022 LAMININ EGF-LIKE 19.  
FT DOMAIN 2023 2069 LAMININ EGF-LIKE 20.  
FT DOMAIN 2070 2116 LAMININ EGF-LIKE 21.  
FT DOMAIN 2117 2166 LAMININ EGF-LIKE 22.  
FT DOMAIN 2167 2735 DOMAIN II AND I.  
FT DOMAIN 2736 2929 LAMININ G-LIKE 1.  
FT DOMAIN 2941 3115 LAMININ G-LIKE 2.  
FT DOMAIN 3124 3292 LAMININ G-LIKE 3.  
FT DOMAIN 3340 3513 LAMININ G-LIKE 4.  
FT DOMAIN 3520 3692 LAMININ G-LIKE 5.  
FT DOMAIN 2203 2221 COILED COIL (POTENTIAL).  
FT DOMAIN 2335 2466 COILED COIL (POTENTIAL).  
FT DOMAIN 2510 2670 COILED COIL (POTENTIAL).  
FT SITE 1722 1724 CELL ATTACHMENT SITE (POTENTIAL).  
FT SITE 1838 1840 CELL ATTACHMENT SITE (POTENTIAL).  
FT SITE 300 309 BY SIMILARITY.  
FT DISULFID 302 322 BY SIMILARITY.  
FT DISULFID 324 333 BY SIMILARITY.  
FT DISULFID 336 356 BY SIMILARITY.  
FT DISULFID 359 368 BY SIMILARITY.  
FT DISULFID 361 393 BY SIMILARITY.  
FT DISULFID 396 405 BY SIMILARITY.  
FT DISULFID 408 426 BY SIMILARITY.  
FT DISULFID 429 440 BY SIMILARITY.  
FT DISULFID 431 447 BY SIMILARITY.  
FT DISULFID 449 458 BY SIMILARITY.  
FT DISULFID 461 471 BY SIMILARITY.  
FT DISULFID 496 515 BY SIMILARITY.  
FT DISULFID 517 526 BY SIMILARITY.  
FT DISULFID 529 538 BY SIMILARITY.  
FT DISULFID 541 553 BY SIMILARITY.  
FT DISULFID 543 560 BY SIMILARITY.  
FT DISULFID 562 571 BY SIMILARITY.  
FT DISULFID 574 584 BY SIMILARITY.  
FT DISULFID 587 599 BY SIMILARITY.  
FT DISULFID 589 605 BY SIMILARITY.  
FT DISULFID 607 616 BY SIMILARITY.

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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 33.4531 Seconds  
(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-4  
Perfect score: 19876  
Sequence: 1 DLYCKLVGGPVAGDPNQT.....QKALTQRHAKPSVSPLLWH 3635

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19876	100.0	3635	T10053	laminin alpha 5 ch
2	5018.5	25.2	3712	S18253	laminin alpha-1 ch
3	4831.5	24.3	3672	T23433	hypothetical prote
4	4820.5	24.3	3704	T37316	probable laminin a
5	3096	15.6	3106	S53868	laminin alpha-2 ch
6	2792	14.0	3084	1 MMSA	laminin alpha-1 ch
7	2729.5	13.7	3075	S14458	laminin alpha-1 ch
8	2530	12.7	3102	T43291	laminin alpha chai
9	2460	12.4	2823	T23064	hypothetical prote
10	2460	12.4	2823	F87908	protein T22A3.8 i
11	2182.5	11.0	1816	1 S68960	laminin alpha-4 ch
12	2149.5	10.8	1713	2 A55347	adhesive ligand ep
13	1675	8.4	1798	2 S53869	laminin beta-2 cha
14	1672.5	8.4	1801	1 MMRTS	laminin beta-2 cha
15	1605	8.1	1786	1 MMHUB1	laminin beta-1 cha
16	1584	8.0	1786	1 MMSB1	laminin beta-1 cha
17	1582.5	8.0	1797	2 A55677	laminin beta-2 cha
18	1549	7.8	1790	1 MMEFBI	laminin beta-1 cha
19	1486	7.5	1808	2 T15099	hypothetical prote
20	1344.5	6.8	1607	1 MMSB2	laminin gamma-1 ch
21	1323.5	6.7	1609	1 MMHUB2	laminin gamma-1 ch
22	1311	6.6	1639	1 MMFPB2	laminin gamma-1 ch
23	1221	6.1	1557	2 T28911	hypothetical prote
24	1212.5	6.1	1751	1 MMHUBH	laminin alpha-2 ch
25	1204	6.1	3707	2 S18252	heparan sulfate pr
26	1104	5.6	4391	2 A38096	perlecan precursor
27	1033	5.2	1574	2 T13954	MEGF6 protein - ra
28	949	4.8	1193	2 A44018	laminin B2t chain
29	908.5	4.6	1192	2 S69000	laminin gamma 2 ch

30	900	4.5	1620	2	T27283	hypothetical prote
31	844	4.2	1170	2	A53612	laminin Blk chain
32	799.5	4.0	1168	2	I56985	kallinin B1 - mouse
33	799	4.0	3375	2	T19821	hypothetical prote
34	785.5	4.0	2295	2	C88369	protein unc-52 [im
35	781	3.9	1160	2	F88369	protein unc-52 [im
36	754	3.8	2321	2	S78549	notch3 protein - h
37	698.5	3.5	2437	2	S42612	transmembrane prot
38	697	3.5	2555	2	A40043	notch protein homo
39	689.5	3.5	2318	2	S45306	notch 3 protein -
40	677	3.4	606	2	A54665	netrin-1 precursor
41	675.5	3.4	1111	2	T26972	hypothetical prote
42	674.5	3.4	2703	1	A24420	notch protein - fr
43	665	3.3	2471	2	A49128	cell-fate determin
44	654	3.3	612	2	JH0799	laminin-related pr
45	653	3.3	1964	2	T09059	notch4 - mouse

ALIGNMENTS

RESULT 1

T10053  
laminin alpha 5 chain - mouse (fragment)  
C:Species: Mus musculus (mouse mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2003  
C:Accession: T10053  
R:Miner, J.H., Lewis, R.M.; Sanes, J.R.  
submitted to the EMBL Data Library, November 1997  
A:Reference number: Z16923  
A:Accession: T10053  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3635 <MIN>  
A:Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232  
C:Genetics:  
A:Gene: Lama5  
C:Keywords: basement membrane; cell binding; extracellular matrix  
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>  
F:1942-1970/Domain: EGF homology <EGF>

Query Match	100.0%;	Score	19876;	DB	2;	Length	3635;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	3635;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	DLYCKLVGGPVAGDPNQT	IGQYCDICTAANSKHA	FPVSN	NAIDGTER	WQSPPLSRGLE	60
Db	1	DLYCKLVGGPVAGDPNQT	IGQYCDICTAANSKHA	FPVSN	NAIDGTER	WQSPPLSRGLE	60
Qy	61	YNEVNTLDLQGVHAYVLI	KFANS	PRDLW	LERSTD	FGHTYQWQFPASSKRC	120
Db	61	YNEVNTLDLQGVHAYVLI	KFANS	PRDLW	LERSTD	FGHTYQWQFPASSKRC	120
Qy	121	FGPRTLERITQDDVICT	TEYSRIVPLENGEIV	VS	LVN	GRFGALNFSYSPLLR	180
Db	121	FGPRTLERITQDDVICT	TEYSRIVPLENGEIV	VS	LVN	GRFGALNFSYSPLLR	180
Qy	181	IRLRLFTNTLLGLHMGK	ALRDP	PTVTR	RYYSIK	DISIGRCVCHGADVCDA	240
Db	181	IRLRLFTNTLLGLHMGK	ALRDP	PTVTR	RYYSIK	DISIGRCVCHGADVCDA	240
Qy	241	RLQACQHNCTGGSCDR	CCGFPNQ	PKPAT	TDSAN	CQSCNCHGHAYDCYD	300
Db	241	RLQACQHNCTGGSCDR	CCGFPNQ	PKPAT	TDSAN	CQSCNCHGHAYDCYD	300
Qy	301	ASQNDNVYQGGVCLD	QCHHTTG	INCER	CLP	OFFFRAPDQPLDS	360
Db	301	ASQNDNVYQGGVCLD	QCHHTTG	INCER	CLP	OFFFRAPDQPLDS	360
Qy	361	TCEDLTGRCYCRNFTG	ELCAACAG	EYTD	PHCYPL	SPFPHNDTREOVLPAG	420
Db	361	TCEDLTGRCYCRNFTG	ELCAACAG	EYTD	PHCYPL	SPFPHNDTREOVLPAG	420

QY 421 AAGTQGNACRKPRLGRVCVCKPNFRGAHCELCAPGPHGPPSCHPCQSSPGVANSLCDPES 480  
DB 421 AAGTQGNACRKPRLGRVCVCKPNFRGAHCELCAPGPHGPPSCHPCQSSPGVANSLCDPES 480  
QY 481 GQCMCRGFGPDGDCDHGALGYFHFPLCOLGCCPAGTLPBGCDGAGRCOCRCRPFDFPHCD 540  
DB 481 GQCMCRGFGPDGDCDHGALGYFHFPLCOLGCCPAGTLPBGCDGAGRCOCRCRPFDFPHCD 540  
QY 541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCQCSPGFYFPSCIPC 600  
DB 541 RCLPGYHGYPDCHACADPRGALDQCGVGLCHCRPGNTGATCQCSPGFYFPSCIPC 600  
QY 601 HCSADGSIHTTCDPTTQCCRCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660  
DB 601 HCSADGSIHTTCDPTTQCCRCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660  
QY 661 PETQAPCMCAHVEGSPCDCKCPGYWGLSASNBEGCTRCSCDPRGTLLGGVTECGNGQCF 720  
DB 661 PETQAPCMCAHVEGSPCDCKCPGYWGLSASNBEGCTRCSCDPRGTLLGGVTECGNGQCF 720  
QY 721 CKAHVCKTCAACXKDGFFGLDYADYFCRCRCRDVGGALQCGCEBPTGTACRCRPNQGP 780  
DB 721 CKAHVCKTCAACXKDGFFGLDYADYFCRCRCRDVGGALQCGCEBPTGTACRCRPNQGP 780  
QY 781 CSEPAKHLYLPLDHMELELEEAATPEGHAVRFGFNLEFENFSWRYAHMMAIQPRIVA 840  
DB 781 CSEPAKHLYLPLDHMELELEEAATPEGHAVRFGFNLEFENFSWRYAHMMAIQPRIVA 840  
QY 841 RLNVTSPLFLVRYVNRGTSVNGQISVREEKJSSCTNCTEQSQPVAFPPSTEPAFV 900  
DB 841 RLNVTSPLFLVRYVNRGTSVNGQISVREEKJSSCTNCTEQSQPVAFPPSTEPAFV 900  
QY 901 TVPORGEPVLPNGFWALLVEAGVLLDVVLLPSTYVEALLQHRVTEACTYPSAL 960  
DB 901 TVPORGEPVLPNGFWALLVEAGVLLDVVLLPSTYVEALLQHRVTEACTYPSAL 960  
QY 961 HSTENCLVYAHPLDGFPSAAGTEALCRHDSNLPFCPTQLSPSHPLATCFGSVDIQ 1020  
DB 961 HSTENCLVYAHPLDGFPSAAGTEALCRHDSNLPFCPTQLSPSHPLATCFGSVDIQ 1020  
QY 1021 LEMAVPQGVYLVVEYVGEDSHOEMGVAHTPQAPQOQVNLHPCPYSSICSPARD 1080  
DB 1021 LEMAVPQGVYLVVEYVGEDSHOEMGVAHTPQAPQOQVNLHPCPYSSICSPARD 1080  
QY 1081 QHLLAI FHLDEASIRLTAEOAHFLLHSVTLVPVEEESTFVPRVFCVSSHGTFPSSA 1140  
DB 1081 QHLLAI FHLDEASIRLTAEOAHFLLHSVTLVPVEEESTFVPRVFCVSSHGTFPSSA 1140  
QY 1141 ACLASRPKPPQPIILKDCQVLPPLPDLPTQSOELSPGAPPEGPQRPPTAVDPNAEPT 1200  
DB 1141 ACLASRPKPPQPIILKDCQVLPPLPDLPTQSOELSPGAPPEGPQRPPTAVDPNAEPT 1200  
QY 1201 LLRHPQGVVFTTQVPTLGRVAFLLHGYQVHPSPFPVVEVLINGRIWQHANASFCPHGY 1260  
DB 1201 LLRHPQGVVFTTQVPTLGRVAFLLHGYQVHPSPFPVVEVLINGRIWQHANASFCPHGY 1260  
QY 1261 GCRTLVLCEGQTMLDVTDNELTVTVRVPBGRLWLDVYLVIPEDAYSSSYLQBEPLDKSY 1320  
DB 1261 GCRTLVLCEGQTMLDVTDNELTVTVRVPBGRLWLDVYLVIPEDAYSSSYLQBEPLDKSY 1320  
QY 1321 DFISHCATQGYHISPSSSSPCRNAATSLIFYNNGALPCGCHVEGVASTCPFPFGQCP 1380  
DB 1321 DFISHCATQGYHISPSSSSPCRNAATSLIFYNNGALPCGCHVEGVASTCPFPFGQCP 1380  
QY 1381 CRGHVIGDRCRCATGYWGFNCRFCDCGALRCLDELGTQCICPPRTVPPDCLVCQPSFG 1440  
DB 1381 CRGHVIGDRCRCATGYWGFNCRFCDCGALRCLDELGTQCICPPRTVPPDCLVCQPSFG 1440  
QY 1441 CHPLVGCBECSGPGVQELDPTCDMDSGQCRPNVAGRCDCAPGVGVPSCRPCD 1500  
DB 1441 CHPLVGCBECSGPGVQELDPTCDMDSGQCRPNVAGRCDCAPGVGVPSCRPCD 1500  
QY 1501 CHEAGTMASVCDPLTGQCHCKENVGSRCDQCRVGTFTSLDAANPKGCTRCFCFGATERCG 1560

DB 1501 CHEAGTMASVCDPLTGQCHCKENVGSRCDQCRVGTFTSLDAANPKGCTRCFCFGATERCG 1560  
QY 1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRASVADTTFSELYWQAPPSYLG 1620  
DB 1561 NSNLARHEFVDMEGWVLLSSDRQVVPHEHRPEIELLHADLRASVADTTFSELYWQAPPSYLG 1620  
QY 1621 DRVSSYGGTLYHELHSETQRGDIIFIPYBSRPDVVLQGNQMSIAFLELAYPPGQVHRQOL 1680  
DB 1621 DRVSSYGGTLYHELHSETQRGDIIFIPYBSRPDVVLQGNQMSIAFLELAYPPGQVHRQOL 1680  
QY 1681 QLVENGFPHLTHNPVSREELMMVLAGLEQLQIRALFSQTSSTSSVSLRRVVLVEASEAGRG 1740  
DB 1681 QLVENGFPHLTHNPVSREELMMVLAGLEQLQIRALFSQTSSTSSVSLRRVVLVEASEAGRG 1740  
QY 1741 PPASNVELCMCPANVRGDSQCECAPGYRDTKGLFLGRVCPQCHGSHDRCLPGSGICVVG 1800  
DB 1741 PPASNVELCMCPANVRGDSQCECAPGYRDTKGLFLGRVCPQCHGSHDRCLPGSGICVVG 1800  
QY 1801 COHNTGEGQCRRCRCPGFVSSDPSPASPCVSPCLAVPSNNFADGCVLRNGRTQCLCRP 1860  
DB 1801 COHNTGEGQCRRCRCPGFVSSDPSPASPCVSPCLAVPSNNFADGCVLRNGRTQCLCRP 1860  
QY 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPPNMFSDCDPLTGACRGCLRHHTGP 1920  
DB 1861 GYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPPNMFSDCDPLTGACRGCLRHHTGP 1920  
QY 1921 HCERCAPGYGNALLPGNCTRCDCSPGCTETCDPSGCLCKAGVTGORDCLLEGYFGF 1980  
DB 1921 HCERCAPGYGNALLPGNCTRCDCSPGCTETCDPSGCLCKAGVTGORDCLLEGYFGF 1980  
QY 1981 EQCQCRPCACGPAKSGEHCHPQSQCHQCPGTTGPQCLECAPGYWGLPEKGCRCRCQCP 2040  
DB 1981 EQCQCRPCACGPAKSGEHCHPQSQCHQCPGTTGPQCLECAPGYWGLPEKGCRCRCQCP 2040  
QY 2041 GHCDPHTCHTCTPPGLSERCDDTCSQHQVVPKPGKHGTHCEWCDCVLLDLDLERA 2100  
DB 2041 GHCDPHTCHTCTPPGLSERCDDTCSQHQVVPKPGKHGTHCEWCDCVLLDLDLERA 2100  
QY 2101 GALLPAIRERLOGINASSAAWARLHRLNASIADLQSKLRPPGPRYQAAQLOTLEQOSI 2160  
DB 2101 GALLPAIRERLOGINASSAAWARLHRLNASIADLQSKLRPPGPRYQAAQLOTLEQOSI 2160  
QY 2161 SLQOQTERLGSQATVQOQAGQLDPTTSTLGRAQKLLSVRAVGRALNELASRGQSP 2220  
DB 2161 SLQOQTERLGSQATVQOQAGQLDPTTSTLGRAQKLLSVRAVGRALNELASRGQSP 2220  
QY 2221 GDALVPSGBQLRWALAEVERILLWMDTRDLGAQGAVAEAEALAEQRLMARVQEQLTFSWE 2280  
DB 2221 GDALVPSGBQLRWALAEVERILLWMDTRDLGAQGAVAEAEALAEQRLMARVQEQLTFSWE 2280  
QY 2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREABELNSRNOERKEALQWQELSQ 2340  
DB 2281 ENQSLATHIRDOLAQYESGLMDLREALNQAVNTTREABELNSRNOERKEALQWQELSQ 2340  
QY 2341 DNATLKATLQAASTLGHVSELLQIGIDQAKXEDLEHLAASLDGAWTPLLKRWQAFSPASSK 2400  
DB 2341 DNATLKATLQAASTLGHVSELLQIGIDQAKXEDLEHLAASLDGAWTPLLKRWQAFSPASSK 2400  
QY 2401 VDLVEAAEHAQKLNQALNSGIIILGINQDRFQRAVEASNAYSSTIIOVAQAEADAQ 2460  
DB 2401 VDLVEAAEHAQKLNQALNSGIIILGINQDRFQRAVEASNAYSSTIIOVAQAEADAQ 2460  
QY 2461 ALRQASRTWEMVVRGLAAGARQLLANSALLEETILGHQRLGLAQGLQAAQIQLHNW 2520  
DB 2461 ALRQASRTWEMVVRGLAAGARQLLANSALLEETILGHQRLGLAQGLQAAQIQLHNW 2520  
QY 2521 ARKNQALAQIOBAQAWLAMDTSSETSEKIAHAKAVAAEALSTATHVQSOLOGQKQKVRWQ 2580  
DB 2521 ARKNQALAQIOBAQAWLAMDTSSETSEKIAHAKAVAAEALSTATHVQSOLOGQKQKVRWQ 2580  
QY 2581 SOLGGLQGDLSQVERDASSUSTLEKTLPLLAKLSLENEGVAHNASILASINGRYRK 2640



2581	Db	SOJGGLQGQDLSQVERDASSVSTLEKTIPLQLLAKJSLRLENRGVHNASIALSANIGRVRK	2640
2641	Qy	LIAQARSAAKSVKVSMMKFNCRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPFPKNTG	2700
2641	Db	LIAQARSAAKSVKVSMMKFNCRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPFPKNTG	2700
2701	Qy	HFVLYNGSRCATGDYMGVSIRNQKXHVWYELGKAGPTTILSIDENIGEOPAAVSIIDRTLOF	2760
2701	Db	HFVLYNGSRCATGDYMGVSIRNQKXHVWYELGKAGPTTILSIDENIGEOPAAVSIIDRTLOF	2760
2761	Qy	GHMSVTVVEKQWHEIIGKDTVAPGSEGLNLIHPDDFVYVUGGYPSNFTPTPEPLFPYGLGC	2820
2761	Db	GHMSVTVVEKQWHEIIGKDTVAPGSEGLNLIHPDDFVYVUGGYPSNFTPTPEPLFPYGLGC	2820
2821	Qy	IENETLNEEVVSYLNPEQTFMLTAVDKPCARSKATCDPWLTDGSLVLDGSGFARIISPEKQ	2880
2821	Db	IENETLNEEVVSYLNPEQTFMLTAVDKPCARSKATCDPWLTDGSLVLDGSGFARIISPEKQ	2880
2881	Qy	FSNTKRFDQBLRVLVSYNGIIIFFLKQESQIFCLAVOEGTLLFYDFDPSGLKKAADLPQPPQA	2940
2881	Db	FSNTKRFDQBLRVLVSYNGIIIFFLKQESQIFCLAVOEGTLLFYDFDPSGLKKAADLPQPPQA	2940
2941	Qy	LTAASKAIQVFLIAGNKRVLVVERATVSVSDQDNMLEADAYILGGVPEQPLSLRQ	3000
2941	Db	LTAASKAIQVFLIAGNKRVLVVERATVSVSDQDNMLEADAYILGGVPEQPLSLRQ	3000
3001	Qy	LFPSGGSVRGCIKGIKALGKYVDLKRLLNTTGISFGCTADLLVGRTTFPHGHGLPLALPD	3060
3001	Db	LFPSGGSVRGCIKGIKALGKYVDLKRLLNTTGISFGCTADLLVGRTTFPHGHGLPLALPD	3060
3061	Qy	VAPITEVYVYSGFGRGCTODNNLIAYRTPSGDPQVSLREGHVTLRFMNQVEVQRVFDAG	3120
3061	Db	VAPITEVYVYSGFGRGCTODNNLIAYRTPSGDPQVSLREGHVTLRFMNQVEVQRVFDAG	3120
3121	Qy	APHYVAFYSNVTVGWLVDYDQLOLVKSHERTTLMQLQPEPESRLILGGLFVSGTTFHNF	3180
3121	Db	APHYVAFYSNVTVGWLVDYDQLOLVKSHERTTLMQLQPEPESRLILGGLFVSGTTFHNF	3180
3181	Qy	GCTSNVTVQBLRGPORVFDLHONMGSVNVSVCCTPAQLIETSRATQKVSRRSRQPSQDL	3240
3181	Db	GCTSNVTVQBLRGPORVFDLHONMGSVNVSVCCTPAQLIETSRATQKVSRRSRQPSQDL	3240
3241	Qy	ACTTPTMLPGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM	3300
3241	Db	ACTTPTMLPGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM	3300
3301	Qy	SGRSPSLVLFLNHCHFVAQTEGCPRLQVQSRQHSRAGQWHRVSVRWGMQOQIOLVVDGSG	3360
3301	Db	SGRSPSLVLFLNHCHFVAQTEGCPRLQVQSRQHSRAGQWHRVSVRWGMQOQIOLVVDGSG	3360
3361	Qy	TWSQKALHHRVPRAEERPQPYTLTVSGGLPASSYSKSLPVSVFSGCCLKQLDKQPLRTPT	3420
3361	Db	TWSQKALHHRVPRAEERPQPYTLTVSGGLPASSYSKSLPVSVFSGCCLKQLDKQPLRTPT	3420
3421	Qy	QMVGVTPCVSGPLEDGLFPFGSGGVVTLFLPKAMPVYSILEWRLPAAAGLIFHLQOAL	3480
3421	Db	QMVGVTPCVSGPLEDGLFPFGSGGVVTLFLPKAMPVYSILEWRLPAAAGLIFHLQOAL	3480
3481	Qy	ATPTMQLKVLTEQVLLQANDGAGBFSTWVTYPKLCDGRWHRVAVIMGRDTRLLEVDTQSN	3540
3481	Db	ATPTMQLKVLTEQVLLQANDGAGBFSTWVTYPKLCDGRWHRVAVIMGRDTRLLEVDTQSN	3540
3541	Qy	HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKKLINGAPVNVTVASVQIOGA	3600
3541	Db	HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKKLINGAPVNVTVASVQIOGA	3600
3601	Qy	VGNRGCPSGTIALUSKQKALTQORHAKPSVSPLLJWH	3635
3601	Db	VGNRGCPSGTIALUSKQKALTQORHAKPSVSPLLJWH	3635

RESULT 2  
S18253

laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 16-Sep-1992 #sequence\_revision 24-Jul-1997 #text\_change 10-Dec-1999  
C:Accession: S28399; S18253  
R:Kusache-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, J.H.  
EMBO J. 11, 4519-4527, 1992  
A:Title: Laminin A chain: expression during Drosophila development and genomic sequence.  
A:Reference number: S28399; MUID:93049203; PMID:1425586  
A:Accession: S28399  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-3712 <KUS>  
A:Cross-references: GB:M96388; NID:G157799; PIDN:AAA28662.1; PID:G157800  
R:Garrison, K.; MacKrell, A.J.; Fessler, J.H.  
J. Biol. Chem. 265, 22899-22904, 1991  
A:Title: Drosophila laminin A chain sequence, interspecies comparison, and domain structure  
A:Reference number: S18253; MUID:92078147; PMID:1744083  
A:Accession: S18253  
A:Molecule type: mRNA  
A:Residues: 1762-3712 <GAR>  
A:Cross-references: EMBL:M75882; NID:G157797; PIDN:AAA28661.1; PID:G157798  
C:Genetics:  
A:Gene: FlyBase: LANA  
A:Cross-references: FlyBase:FBgn0002526  
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h-h  
C:Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular  
F:273-330/Domain: laminin-type EGF-like homology <LEG>  
F:333-400/Domain: laminin-type EGF-like homology <LE02>  
F:541-584/Domain: laminin-type EGF-like homology <LE01>  
F:1776-2115/Domain: III <DOM3>  
F:1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>  
F:1809-1856/Domain: laminin-type EGF-like homology <LE2>  
F:1859-1914/Domain: laminin-type EGF-like homology <LE3>  
F:1917-1967/Domain: laminin-type EGF-like homology <LE4>  
F:1970-2014/Domain: laminin-type EGF-like homology <LE5>  
F:2017-2061/Domain: laminin-type EGF-like homology <LE6>  
F:2064-2109/Domain: laminin-type EGF-like homology <LE7>  
F:2116-2697/Domain: I/II, heptad repeats <DOM2>  
F:2698-3712/Domain: G <DOM3>  
F:2698-2863/Domain: repeat G1 <RG1>  
F:2864-3048/Domain: repeat G2 <RG2>  
F:3049-3223/Domain: repeat G3 <RG3>  
F:3079-3200/Domain: laminin G repeat homology <LG3>  
F:3334-3528/Domain: repeat G4 <RG4>  
F:3529-3712/Domain: repeat G5 <RG5>  
F:1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3130

Query Match 25.2%; Score 5018.5; DB 2; Length 3712;  
Best Local Similarity 31.3%; Pred No. 5, 7e-222;  
Matches 1227; Conservative 595; Mismatches 1527; Indels 569; Gaps 122;

Qy 1 DLYCKLVGGPVAGGDPN-QTIQGVYCDICTAANSKHAHPVSNALDTERWQSPPLSRGL 59  
51 ELYCKLVGANTHEPHIDYSVIQGVQVCDYCDPTVPERNHPPENALDTEAWQSPPLSRGM 110  
Qy 60 EYNEVNTLDLGQVPHVAYVLIKFANSRPDLWLVERSTDFGHTYQWPOFFASAKRDCLE 119  
111 KFEVNTLTINFEQPHVAYLIRMGNSPRGLWTLKSTDYKTIWTPWGHFSDTPADCET 170  
120 RFGPRTLEIRITQDDDVICTTYSRIYVPLENGEIVVSVLVNRPGLALNFYSPLLRDTFKAT 179  
171 YFGKDTYKPIRQDDDVICTTYSKIVPLENGEIPVLLNERPSSSTNYFNSTVLQEWTRAT 230  
Qy 180 NIRLRPLRTNTLLGHLMGKALRDPVTTRYRYYSIKDIStGGCVCHGHADVCDKADPLDP 239  
231 NVRIIRLLTNKLLGHLMGKALRDPVTTRYRYYSIKDIStGGCMCNHGHADTCVDKPKXP 290  
Qy 240 FR-LQCAQHNTCGSCDRCCPGFNQKQPKWATTDTSANECQSCNCHGHAYDCYDPEVDR 298  
291 VRILACRQHTTCGIQCNECCFGEQKWRQNTNARPNCPCNCHGHSHNECKYDEEVR 350  
Qy 299 RNASONQNVYGGGVCLDCCQHTTGINCERCLPGFFRAPDPLDSPHVCRPCDCSDFT 358

Db 351 KGLSLDTHGVGGVQCNQHTVGINCMCKPKYRPGKJHNETDVCSPCQCDYFES 410  
Qy 359 DGTCELTGRCYCRPNFTGBLCAACAGYTDFFPHCYPLPSFPHNDTREQVLPAGQIVNCD 418  
Db 411 TGHCEBTGCEKRAAFQPPSCDSCAYGYGYNCE-----RE-----CE 449  
Qy 419 ONAAGTOGNACRDXPLRGLRCVCKRPNFGAECALCAPGPHG-PSCHPCQSSPGVANSLCD 477  
Db 450 CNLNGTNGYCEAESG-QQCPCKINPAGAYKQCAEGYGFPECKACENKIGISINDCN 508  
Qy 478 PESQCMCRCTGFECDRCDHCHALGYFHPFLQOLGCGSPAGTLPBGCD-EAGRCOCRPGPDG 536  
Db 509 VTIGECKCLNFGGDNCRCKHGYFNYPTCSYCDNOGTESBICNKQSGQICREGPGG 568  
Qy 537 PHDRCLPGHYGYPDDCHACADPRGALDOQCGVGGIJCCHCPGNTGATCOECSGFGYFES 596  
Db 569 PRCDQCLPGFYNPDDCKPCNCSSTGSSAITCDNTGKCNLNNPAGKQCTLCTAGYYSYPD 628  
Qy 597 CIPCHCSADGSLHTCDPTTGQCRPRVTLGHDGCMVPGAYNPPYCEAGSCHPAGLAP- 655  
Db 629 CLPCHCDSHSGQVSON-SDGQCLCQNFDRGQDCSCKEYFNFPSCDCNCPAGVIDK 687  
Qy 656 -ANPALPETOAPCMRAHVGPSCDCKPGWGLSASNPBGCTRCSCDPRGTGGVTECQ 714  
Db 688 FAGCGSVFVGBELCKCKERVGTGRI CNECKPLYWNLNINTEGCEICDCWTDGTISALDTCT 747  
Qy 715 G-NGQCFCKAHVCGKTCACACKGFFGLDYADYFCRCRCRDVGALGQCGCEPXTGACRCR 773  
Db 748 SKSQGCPCKPHTQGRQOECBCEGDFDLDLSLFCKDCSDVGGWSQVCDKISGQCKCH 807  
Qy 774 PNTGQPTCEPAKHLYPLDLHMLLELEBAATPGHVAVRFGFNPLEFENFENSWGAYHAMMA 833  
Db 808 PRITGLACTQPLTHFFFTLHQFVEYEDGSLPSGTQVRYDYDEAAPPFGSSKGYVYFNA 867  
Qy 834 TOPRIVARLVNTSDPLRLVRYNRTGSTSNGOISVRESGKLSCTNCTEQOQVAFPP 893  
Db 868 IONDRNENNVFKSLVRIYVNPNAENTATISVTSNPLE-----VDQHVKVLQP 922  
Qy 894 STEPAFTV--PQRFGBPFVNLPGIWAALLVEA-EGVLLDYVLLPSTYYEAAALLQHRVT 950  
Db 923 TSEPOFTVAGPLGVKPSAIVLDGRYVFTTKANKWMLDYVLLPAAYEAGILTRHS 982  
Qy 951 EACTYRPSALHSTENCLVYALPLDGPSPAGTALCEHNSLPPCPCTQLSPH--- 1006  
Db 983 NPC-----ELGNMELCRHYKVASVEVSPAATPVI--GENSKFTNPTVETYPDEHLQIV 1035  
Qy 1007 -----PPLATCFGSDVDIQLEMAVPOGVVLVVEYVGE-----DSHQEMGVAHTPQRA 1056  
Db 1036 SHVGDIPLVS--GSONELHYIVDPRSGRYIVFVIDISDRNFPDSY--INLKLKDNP 1089  
Qy 1057 PQQGVNLNHPYSSLCRSPARDQHLIAIHLDS--ASRLTA---EQAHFPLHSVTL 1111  
Db 1090 DSETSVLLYPCLYSTICTSVNEDGMEKS-FYINKEDLPVILSADIEDGSRFPILSVTA 1148  
Qy 1112 VFVEBFSTFEVPRVFCVSSHGTNFPSSAACLASRFPKPPQPIILKDCQVLPPLPDLPLT 1171  
Db 1149 IPVDQWSIDYINPSVCVI-----HQQCATPKFRSVP-----DSKKIEFETD--- 1191  
Qy 1172 OSQELSPGAPPGPOPRPTAVDPNABETLL-RHQQGVVFTTQV----PTLGRYAEHLH 1226  
Db 1192 HEDRIATNKPYP-----ASLDERVKLVHLDSONEATIVESKVDAKPNL--FVILVK 1242  
Qy 1227 GYQVHPHFPPEVVLINGR-IWQHANASFCPHGYGCRTLVLCBQTMVDYDDELATVTV 1285  
Db 1243 YTPGHPKPYVYTTAGKNQVDFKFDIQHCPSSGCGRVTRPAGESFEI-DDEPKFTI 1301  
Qy 1286 RYVEGRWLWLDYVLVPEDAYSSSYLOBEPLDKSYDFISHCATQGYHISPSSSPPCRNA 1345  
Db 1302 TTDRSQSVWLDYLVVPLKQVNDLLVEETFDQKEFTQNCQCHDHFHIT-HNASDFCKKS 1360  
Qy 1346 ATSLSLFYNNGALPGCHEVGAVSTCBPFGQCPGRGHVIGRDCSRCATGYMFPNCRP 1405  
Db 1361 VFLSLADYNSGALPCNCPAGSTSPFCHPFGQCCCKENVIERTCGRCSRYYGFPDCKP 1420

Qy 1406 CDC-GARLDBELTQCCTCPRTVPDCLVCPQSPGCHPLVGCCECNCSGPGVQELTDP 1464  
Db 1421 CKCNPSACBPTTGECMCPNVIIGDLCEKAPNTYFQHVIGCECACNPMGIAN-GNSQ 1479  
Qy 1465 CDMDSGQCRCPNVAGRRCDTCAFGYGYPSRCPCDCHEAGTMAVSDPLTGQCHCKENV 1524  
Db 1480 CDLFNGTCECRONIEGRACDVCSNGYFNPHCEQCSCHKPGTELEVCDKIDGACFKKNV 1539  
Qy 1525 QGSRCDQCRVUTFSLDAAANPKGCTRCFCGATERCG-----NSNLARH-----BVD 1571  
Db 1540 VGRDCDQCVGTYNLQBSNPDGCTTCFCGKTSRCDLSAYLVNVVLLKHVSIITPFEHE 1599  
Qy 1572 MEGWLLSSDRQVVPHEHRPIEL-----LHAD--LRSVADTFSELYWQAPPSYLG----- 1620  
Db 1600 ES-----IKFDMWPVPAD--BILLNETTLKADFTLREVND-----ERPAYFGVLDYL 1644  
Qy 1621 ----DRVSYGGTLHYELHSETQGDIFIPYESRDPVVLQGNQMSIALELAYPPPGOVH 1676  
Db 1645 LNQNHHISAYGDLAYTLHFTSGFDGKYI---VAPDVLTFSEHNAALVHTSVEQSRNPPF 1701  
Qy 1677 RQOLQVSEGNFRHLETHNPFVSREELMMVLAGLEQIRALFSQTSSSVSLRVRVLEVAE 1736  
Db 1702 TNRVNIIVESQTTI-SGKPVSRADPMVLRDLKVFIRANYWEQTLVTHLSDVLTLADE 1760  
Qy 1737 AGRGPPASN---VELCMOPANYRGDSCOECAPGYRYDTKGLFLGRCPVCOCHGSDRCLP 1793  
Db 1761 DADGTGEYQFLAVERSCPPGYSGHSCDCAPGYRDPSPGYGYCIPCECNHSETCDC 1820  
Qy 1794 GSGICVGOHNTGEGDQCRCPGFVSSDPSPNAPSPVSCPCPLAVPSNPNFADGCVLRNGR 1853  
Db 1821 ATGICSKQHTGEGDHCRCVSGYGNATNGTPGDCMICACPLPDSNNFATCSBESSG 1880  
Qy 1854 TO--CLCRPGVAGASCERCAPGFONPLVLGSSQPCDCSNGNDNMIFSCDPLTGACR 1911  
Db 1881 DQIHCECKPGYTGPRCESCANGFYGEPSIGQVCKPCECSNINPEDQGS--CDTRTGEL 1939  
Qy 1912 GLRHHTTGPHERCAPGVGNALLPGNCTRCDCSPGTETCDPOSGRCLCKAGVTGQRCD 1971  
Db 1940 RCLNNTFGAACLNCPAGFYGDAIKUNQSCDCCDLGTQCDPFGVGTCHENVIGRCD 1999  
Qy 1972 RCLGYFFEQCGQCRCPACGPAKSECHPSQSGOCHQCPGTGTGOCLECAPGYWGLBEK 2031  
Db 2000 RCKPDHYGFESGVGRACDQGAASNSTQCDPHTGHACKSGVTGRCQDCAVDHMKYKD 2059  
Qy 2032 GCRQCPRGH-----CDPHTGHTCPCLSGERCDTCSQHQVVPVPGKPGHGHICRVC 2086  
Db 2060 GCTPCNCGYGRGFCGNPNTGKQCLPGVIGDRCDACPNRW---VLKDEG---QCEC 2112  
Qy 2087 DHCWLLDLDLBRAGALLPAIREQLQGINASSAAWARLHRLN-----ASLADLOSKLRP 2141  
Db 2113 NKCHALLDVTDMRYQIDSV---LEDFNSVTLAFTTQKLYYDQLADELEPKVKLLDP 2169  
Qy 2142 PGPVYQAAQLOTLBQOSISLOQDTERLGSQATVQGOAGOLLDTTESTLGRAQXLLBSV 2201  
Db 2170 -----NSVDLSFKKANSLESDAKQVQNTLANAFDIRERSSTLTGNITVAY--- 2220  
Qy 2202 RAVGRALNELSRMGQSGPDALVPSGEQLRWALAEVERLLWDMRTRDLGAQGAVAEAL 2261  
Db 2221 -----DEAVKSADQAKAIAASVEALSKNLE-----AAASTKIDAL 2256  
Qy 2262 AEAQRLMARVQ-----EQLTSFWENOSLATHIRDO---LAQYESSGLMDLRE 2305  
Db 2257 EQAHLIGQINGTSTIELTPNEQVLEKARKLYSEVNTLVPKAKQKSNLALNDIGFSD 2316  
Qy 2306 ALNQAQVNTTREAELNSRNOERVKALQWKQSLSQDNATLKATLOA-----A 2352  
Db 2317 HLEDLFNWS-EASQASADVERNVANQKAFNSKFDTVSEQLQAKENIKDAGNPLING 2375  
Qy 2353 SLTGHVSBELLOGIQAKEDLHLSAASLDGAWTPLLKRMQAFSPASSKVDLYEAAFAHQ 2412  
Db 2376 DLTINQINQKLNLRDALNELNSFNKNVD---EELFVREDQHKHEADALTDOAE-----Q 2426

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:58 ; Search time 34.0053 Seconds  
(without alignments)  
10452.141 Million cell updates/sec

Title: US-10-037-182-2  
Perfect score: 20118  
Sequence: 1 MAKRLCAGSALCVGRGPA.....AMTRSVFHVGVAGSGCPAA 3695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15839	78.7	3635	2 T10053	laminin alpha 5 ch
2	5097	25.3	3712	2 T18953	laminin alpha-1 ch
3	4974	24.7	3672	2 T23433	hypothetical prote
4	4964	24.7	3704	2 T37316	probable laminin a
5	3141.5	15.6	3106	1 S53868	laminin alpha-2 ch
6	2933	14.6	3084	1 MMMSA	laminin alpha-1 ch
7	2854	14.2	3075	2 S14458	laminin alpha-1 ch
8	2601	12.9	3102	2 T43291	laminin alpha ch
9	2514	12.5	2823	2 T23084	hypothetical prote
10	2514	12.5	2823	2 F87908	protein T2A3.8 [i
11	2260.5	11.2	1713	2 A55347	adhesive 1.9 and ep
12	2147.5	10.7	1816	1 S68950	laminin alpha-4 ch
13	1613.5	8.0	1801	1 MMRTS	laminin beta-2 cha
14	1602.5	8.0	1798	2 S53869	laminin beta-2 cha
15	1573.5	7.8	1786	1 MMHUB1	laminin beta-1 cha
16	1572.5	7.8	1786	1 MMHUB1	laminin beta-1 cha
17	1532.5	7.6	1790	1 MMFF51	laminin beta-1 cha
18	1509.5	7.5	1797	2 A55677	laminin beta-2 cha
19	1498	7.4	1808	2 T15099	hypothetical prote
20	1348.5	6.7	1607	1 MMMS2	laminin gamma-1 ch
21	1337	6.6	1639	1 MMHUB2	laminin gamma-1 ch
22	1313	6.5	1609	1 MMHUB2	laminin gamma-1 ch
23	1296	6.4	1707	2 T18252	heparan sulfate pr
24	1234	6.1	1557	2 T28811	hypothetical prote
25	1224.5	6.1	1751	1 MMHUB6	laminin alpha-2 ch
26	1146	5.7	4391	2 A38096	perlecan precursor
27	1004.5	5.0	1574	2 T13954	MEGF6 protein - ra
28	957.5	4.8	1193	2 A44018	laminin B2t chain
29	921	4.6	1620	2 T27283	hypothetical prote

30	917.5	4.6	1170	2 A53612	laminin B1k chain
31	887	4.4	1192	2 S69000	laminin gamma 2 ch
32	870	4.3	1168	2 I56985	kallinin B1 - mouse
33	814	4.0	3375	2 T19821	hypothetical prote
34	799	4.0	2295	2 C88369	protein unc-52 [im
35	799	4.0	2321	2 S78549	notch3 protein - h
36	794.5	3.9	1160	2 F88369	protein unc-52 [im
37	781	3.9	2318	2 S45306	notch 3 protein -
38	739.5	3.7	606	2 A54665	netrin-1 precursor
39	707	3.5	612	2 JH0799	laminin-related pr
40	695	3.5	2555	2 A40043	notch protein homo
41	692.5	3.4	2471	2 A49128	cell-fate determin
42	691.5	3.4	2437	2 S42612	transmembrane prot
43	690	3.4	2531	2 S18188	notch protein homo
44	684	3.4	581	2 B54665	netrin-2 precursor
45	676.5	3.4	2703	1 A24420	notch protein - fr

ALIGNMENTS

RESULT 1

T10053  
laminin alpha 5 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2003  
C:Accession: T10053  
R:Miner, J.H.; Lewis, R.M.; Sames, J.R.  
submitted to the EMBL Data Library, November 1997  
A:Reference number: Z16923  
A:Accession: T10053  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3635 <MIN>  
A:Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232  
C:Genetics:  
A:Gene: Lamas  
C:Keywords: basement membrane; cell binding; extracellular matrix  
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>  
F:1942-1970/Domain: EGF homology <EGF>

Query Match	78.7%	Score	15839;	DB 2;	Length	3635;			
Best Local Similarity	79.4%	Pred. No.	0;						
Matches	2874;	Conservative	277;	Mismatches	452;	Indels	18;	Gaps	8;
QY	79	DIYCKLVGGPVAGDPNQITRGVYCDICTAANSKHAHPASNAIDGTERWQSPPLSRGLE	138						
Db	1	DIYCKLVGGPVAGDPNQITRGVYCDICTAANSKHAHPVSNALDGTERRWQSPPLSRGLE	60						
QY	139	YNEVNVNTLDLQGVFFVAVYVLIKFAVNSPRDLWVLEERSMDFGRTYQWPQFPAKSKEDCLER	198						
Db	61	YNEVNVNTLDLQGVFFVAVYVLIKFAVNSPRDLWVLEERSMDFGRTYQWPQFPAKSKEDCLER	120						
QY	199	FGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFYSPLLRFTKATN	258						
Db	121	FGPRLERITQDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRFTKATN	180						
QY	259	VLRFLRNTLTLGHLMGKALRDPVTTRYYYSIKDISIGRCVCHGHADACADKPTDPF	318						
Db	181	IRLRLRNTLTLGHLMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADKPLDPF	240						
QY	319	RLOCTCOHNTCGTCDRCPCGPNQPKPATANSANECQSCNVCYGHATDYDPEVDRRR	378						
Db	241	RLOCAQHNTCGGSCDRCPCGPNQPKPATDTSANECQSCNCHGHAYDYCYDPEVDREN	300						
QY	379	ASQSLDGTYYGGGVGICDQHHTAGVNCERCLPGFVRSNNHPLDPSHVCRNCESDFTDG	438						
Db	301	ASQNQDNVYGGGVGICDQHHTTGINCERCLPGFFRAPQPLDSHVCRPCDCESDFTDG	360						
QY	439	TCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCTPTPS--SSNDRQVILPAQIVNCCGS	497						
Db	361	TCEDLTGRCYCRPNFTGBLCAACAEYTDFFHCVPPLSPSPHNDTRQVILPAQIVNCCDN	420						

QY 498 AAGTQGNACRDKPRVGRCLCKPNFQGTCHLCAFGYFGCOPCQCSSPGVADDRCDPT 557  
DB 421 AAGTQGNACRDKPRLGRCYCKPNFRGAHCELCAFGHFGSCHPCQCSSPGVANSLCDPES 480  
QY 558 GQCRVRFGGATCDRCAPGYFHPIQLCGCGSPAGTLPBGCDGAGRCCLCQPEPAGPHCD 617  
DB 481 GQCMCRTFEGEDRCDHAGLYFHPIQLCGCGSPAGTLPBGCDGAGRCCLCQPEPAGPHCD 540  
QY 618 RCRPGYHGFNCOACTCDPRGALDQLCGAGGLCRCPGYTGACQCSFGHFGFSCVPC 677  
DB 541 RCLPGYHGYDDCHACACDPRGALDQCGVGGLCHCPGNTGATCQCSFGHFGFSCVPC 600  
QY 678 HCSAEGSLHAACDPRSGQCSRRPRVTGLRCDTVPGAYNFPYCEAGSCHPAGLAPVDPAL 737  
DB 601 HCSADGSLHTTCDPTTQCRCPRTVGLHCDMCPVGYNFPYCEAGSCHPAGLAPANPAL 660  
QY 738 PEAOVPCMCRAHVEGSDCKEFGWGLSPNPEGTRCSDLRGLTGVAECOPGTGOC 797  
DB 661 PETQAPCMCRAHVEGSDCKEFGWGLSNASNEGTRCSDLRGLTGVTBEO-GNGQC 719  
QY 798 FCKPHVGOQACSKDGFGLDQADYFGCHRSRCDIGGALGQSCBPRGTGVCRCRNTQGP 857  
DB 720 FCKAHVCGTKCAAKDGFGLDQADYFGCHRSRCDVGGALGQCEPKTGACRCRNTQGP 779  
QY 858 TCSEPADHVLDPHLHLRLLEBAATPEGHAVZFGFNPLEFENFNRGYAQAAPQPRIV 917  
DB 780 TCSEPAKHVLPDLHHLRLLEBAATPEGHAVZFGFNPLEFENFNRGYAHMAIQPRIV 839  
QY 918 ARNLNTPDLFWLVRVYNGAMSVGRSVREGRSAACANCTAQSQVAPFPSTEPAP 977  
DB 840 ARNLNTPSDFLVRVYNGAMSVGRSVREGRSAACANCTAQSQVAPFPSTEPAP 899  
QY 978 ITVPQRGFGFPVLPNTWALRVEAGVLLDYVLLPSAYEAAALLQLRVTEACTYRPSA 1037  
DB 900 VTPVQRGFGFPVLPNGIMALLVEAGVLLDYVLLPSAYEAAALLQHRVTEACTYRPSA 959  
QY 1038 QQSDNCLLTHLPDGFPSAAGLEALCRODNLPRPCPTQOLSPSHPLITCTGSDVDV 1097  
DB 960 LHSTENCLVTAHLPDGFPSAAGTEALCRDNLPRPCPTQOLSPSHPLATCFGSDVDI 1019  
QY 1098 QLOVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGATRD 1157  
DB 1020 QLEMAVFPQGYLVVEYVEDSHQEMGVAVHTPQAPQOGLVNLHPCPYSSLCRSPARD 1079  
QY 1158 TODHLAVHLDSEASVLTAEQARFFLHGVTLPIEBFSEFVEPRVSCISSHAGFGPNS 1217  
DB 1080 TQHLAIFHLDEASIRLTAEQAHFFLHGVTLPIEBFSEFVEPRVFCVSSHGTNPSS 1139  
QY 1218 AACLPSPRPKPPQPIILRDQVILPPLPGLPLTHAQDLTPATSPAGPRPRPPTTAVDPDABP 1277  
DB 1140 AACLASRFPKPPQPIILKDCQVLPPLDPLTQSQELSPGAPPEGPQPRPPTTAVDPNAEP 1199  
QY 1278 TLLREPOATVFTTHVTILGRYAEFLHGYQPAHTTPEVEVLINAGRVMOGHANASFCPHG 1337  
DB 1200 TLLSHPOGTVFTTQVTLGRYAEFLHGYQVPHSPFVEVLINGRIWQGHANASFCPHG 1259  
QY 1338 YGCTTLVVEGOALLDVTHSELTVTVRVPGRMLVDYLVWPNVYVFGYLRREPLDKS 1397  
DB 1260 YGCTTLVCEQTMWDVTDNELTVTVRVPGRMLVDYLVWPNVYVFGYLRREPLDKS 1319  
QY 1398 YDFTSHCAAQYHISPSSSSLFCRNAASLSLFYNNGARPCGCHVEGATQPTCEPGGQC 1457  
DB 1320 YDFISHCATQYHISPSSSSPFCRNAATSLSFYNNGALPCGCHVEGAVSPTCEPGGQC 1379  
QY 1458 PCHAHVIGRDCSRCATGYWGPNCPCDCGARLDELDTGOCICPPRTIPDCLLCOPTF 1517  
DB 1380 PCRHVIGRDCSRCATGYWGPNCPCDCGARLDELDTGOCICPPRTVPPDCLVCQPSF 1439  
QY 1518 GCHPLVGECECNSGPGIQLTDTPTCDTDSQCKRCRNVTGRRCDTSPGHGPRCRPC 1577  
DB 1440 GCHPLVGECECNSGPGVQLTDTPTCDTDSQCKRCRNVTGRRCDTSPGHGPRCRPC 1499  
QY 1578 DCHAGTAPGVCDPLTGTGCYCKENVQKPCQCSLGTGTSLSLDAANPKGCTRCFCFGATERC 1637

DB 1500 DCHAGTAPGVCDPLTGTGCYCKENVQKPCQCSLGTGTSLSLDAANPKGCTRCFCFGATERC 1559  
QY 1638 RSSSVTQEFVDMEGWLLSTDROVWPHEROPGTGEMLRADLRHVPEAVPFAFPELYWQAP 1697  
DB 1560 GNSLAAHFEFVDMEGWLLSDROVWPHERPELLELHADLR---SVADTFSELYWQAP 1615  
QY 1698 PSYLGDRVSSYGGTLRYELHSETORGVDVFPVMSRPRDVTLOGNQMSITFLPAYPTGHV 1757  
DB 1616 PSYLGDRVSSYGGTLRYELHSETORGVDIFIPYESRPRDVTLOGNQMSITFLPAYPTGHV 1675  
QY 1758 HRGOLQVVEGNFRPRTETNTVSRREELMMVLASLEOLOIRALFISOISAVSLRRVALEVAS 1817  
DB 1676 HRGOLQVVEGNFRLEHTNVPVSRREELMMVLASLEOLOIRALFISOISAVSLRRVALEVAS 1735  
QY 1818 PAGOGALASNVVELCLCPASVYRGDSQCAPGPFYRDNVXGLFLGRVCPQCCHGSHDRCLPGS 1877  
DB 1736 EAGRGPPASNVVELCWPANVYRGDSQCAPGPFYRDNVXGLFLGRVCPQCCHGSHDRCLPGS 1795  
QY 1878 GVCYDCQHNTEGACERCOAGFMSS-RDDPSAPCVSCPCPLSVPSNNFAEGCVLRGGRTQ 1936  
DB 1796 GICVGCQHNTEGDCERCRPGFVSSDPSNFPASPCVPCPLAVPSNNFADGCVLRNGRTQ 1855  
QY 1937 CLCKPVGAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNLLFSDCDPLTGACRCGLR 1996  
DB 1856 CLCKPVGAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNMFSDCDPLTGACRCGLR 1915  
QY 1997 HTTGPRCBI CAPGYGNALLPGNCTRCDCCTPCGTGTEADPHSGHCLCKAGVTGRCDCRCE 2056  
DB 1916 HTTGPHERCAPGYGNALLPGNCTRCDCSPCTGTCDCSGRCLCKAGVTGRCDCRCE 1975  
QY 2057 GHFGNCGGCRPCACAPAAEGSECHPQSGOCHCRPGTMGPQCRCAAPGYWLPFEOGCR 2116  
DB 1976 GYFGEQCGCEPCACGPAKAGSECHPQSGOCHCRPGTMGPQCRCAAPGYWLPFEOGCR 2035  
QY 2117 CQCPGRCRDPHTGRCNCPPLGSGRCDCSCQOHOVPPGPGVGHSHICEVCDHCVLLLD 2176  
DB 2036 CQCPRGHCDPHTGCTCPCPLGSGRCDCSCQOHOVPPGPGVGHSHICEVCDHCVLLLD 2095  
QY 2177 DLERAGALLPAIHQLRGINASSMAWRLHRLNLSIADLOSQSLPLGRPHETAQOQLVL 2236  
DB 2096 DLERAGALLPAIRQLQGINASSMAWRLHRLNLSIADLOSQSLPLGRPHETAQOQLVL 2155  
QY 2237 EQQSTSLQDARRLGQAVGTRDQASQLLAGTETLGHAKTLLAAIRAVDRTLSBELMSQT 2296  
DB 2156 EQQSTSLQDTERLGSAQVGGQAGQLDTESTLGRQAQKLDESVRVAGSALMELASRM 2215  
QY 2297 GHLGLANASAPSGEQLLTAEVERILLWEMRARDLGAQPAQAAAEALAAQRLARVQEQ 2356  
DB 2216 GQSGPDALVPSGEQLRWALAEVERILLWDMTRDLGQAGVAEALAEARLMARVQEQ 2275  
QY 2357 SSLWEENQALATQTRDLRQAHEAGLMDLREALNRAVDATRAQELNSNRQRLBEALQK 2416  
DB 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNQAQVNTTREAELNSNRQRLBEALQK 2335  
QY 2417 QELSDNATLQATLHAARDTLASVFLRHSIDQAKEELERLAASIDGARTLLORMQWTF 2476  
DB 2336 QELSDNATLQATLQASLIIGHVSELQGDQAKEDLEHLAASLDGANTLLEKMQWTF 2395  
QY 2477 PAGESKRLVEAAHAHQQLGOLALNLSIILDVNQDLRTORAI EASNAYSILQAVQAAE 2536  
DB 2396 PASSKVDLVEAAHAHQKLNQALNLSIILGINQDRFIQRAVEASNAYSILQAVQAAE 2455  
QY 2537 DAAGALQOAHDTWATVROGLVDEAQOQLANSTALEEAMLOEQORLGLVMAALQARTQ 2596  
DB 2456 DAAGALQOAHDTWATVROGLVDEAQOQLANSTALEEAMLOEQORLGLVMAALQARTQ 2515  
QY 2597 LRDVRAKDKDQEAHTQAAQAQMLAMDTDETSTKIAHAKAVAAEAQDTATRVSOLOAMQEN 2656  
DB 2516 LHWVARKNQLAAQLOEAQAQMLAMDTDETSTSEKIAHAKAVAAEAQDTATRVSOLOAMQEN 2575  
QY 2657 VERWGOQVEGURGDQOGLQAVLDAGHSVSTLEKTLIPOLLAKUSILENRCVHNASALSASI 2716

2576 VERWOSQGLGLOGQDLQVERDASSVSTLEKTLQDILLAKLRLNRCVHNASLALSANI 2635  
2717 GRVRELIQAAGAAKVKVPMKFNCRSGVOLRTPRDLADLAAYTALKPYLQ--PEPEPG 2774  
2636 GRVRKLIQAAGAAKVKVPMKFNCRSGVOLRTPRDLADLAAYTALKPHIQSPVAPPEPG 2695  
2775 QGTEDRFVWYMGSRQATGDYMGVSLRDKKVHWVVLGEGAGPAVLSIDEDIGEQFAAASLD 2834  
2696 KNTGDFHFLVYMGSRQATGDYMGVSLRNQKRVHVVYKLGAGPTTUSIDENIGEQFAAASLD 2755  
2835 RTLQFGHMSVTVVERQMIQETKGDTPVAPGAEGLLNLRPDFFVYVGGYSTPTTPPLRFP 2894  
2756 RTLQFGHMSVTVVEKQWHEIKGDTVAPGSEGLNLRPDFFVYVGGYSTPTTPPLRFP 2815  
2895 GVRGCIEMDTLNEEVVSLINFBRTTOLDTAVDRPCARSKSTGDPWLTGSLDGTGPARI 2954  
2816 GYLGCIEMETLNEEVVSLYNEFTQEMLDTAVDKPCARSKATGDPWLTGSLDGTGSGFARI 2875  
2955 SFDQSIQSTTKRQEQLRVSVSGVLFLLKQSQFCLAVQSGSLVLLYDFGAGLKKAVPL 3014  
2876 SPEKQFSNTKRPDQELRLVSYNGIIFLLKQSQFCLAVQSGTLVLYDFGAGLKKADPL 2935  
3015 QPPPLTSASKAIQVFLGGSRKRVLRVERATVSVQDNLDLEADAYYLGVPDPOLP 3074  
2936 QPPQALTAASKAIQVFLLAGNRKRVLRVERATVSVQDNLDLEADAYYLGVPDPOLP 2995  
3075 PSLRLPFTGGSVRCVKGKALGVVLDKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLR 3134  
2996 LSLRLPFTGGSVRCVKGKALGVVLDKRLNTTGVSAAGCTADLLVGRAMTFHGHGFLP 3055  
3135 LALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVLSQOGRVSLQLRLTEVTQA 3194  
3056 LALPDVAPITEVYVSGFGFRGTQDNLLLYRTSPDGPYQVSLREHVTLRPMQNEVETQR 3115  
3195 GPADGAPHVAVYSNATGVWLVDDQLQOMKPHRGPPELOPEGPRLILGLGSPESGT 3254  
3116 VFADGAPHVAVYSNATGVWLVDDQLQOMKPHRGPPELOPEGPRLILGLGSPESGT 3175  
3255 IYNFSGCISNVFVRLQGPQVDFDQNLGSLVNVSTGCAPALQATPGLGPRGQATARK 3314  
3176 FNFSGCISNVFVRLQGPQVDFDQNLGSLVNVSTGCAPALQATPGLGPRGQATARK 3228  
3315 ASRRSQARHPACMLPHLRTRDSYQFGGSLSHLSEFVGLARHNRWPSLSMHVLP 3373  
3229 VSRRSQPSQDLACTPMLPGTIQDAYQFGGLPSYLOFVGLSPSHRNLHSLMVRPHA 3288  
3374 SSRGLLFTARLPQSPSLALFLSNHGFVAQMEGLGTRLRQAQRGRPRGRHVKSVRWE 3433  
3289 ASQGLLSTAPMSGRSPSLVFLNHHGFVAQTEGPGPLQVQSRQHSRAGQHWVSRWG 3348  
3434 KNRILLVTDGARAMQEGPHRQHAEPHQHTLFPVGLPASHSKSLPVTVGSGCVKR 3493  
3439 MQQIQLVVDGSGQTSQKALHHRVPRAPRPQPYTLISVGLPASYSKSLPVSQVSGCLKK 3408  
3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFPFGSGVITLDPGATLPDVGLELEVRPLA 3553  
3409 LQLDQPLRTPQWVGVTCPVSGPLEDGLFPFGSEGVVTELPKAKMPYVSELEMRPLA 3468  
3554 VTGLIFHLGQARTPYLOQVTEKOVLLRADDGAGEFSTVTRPSVLCDGQHRHLAYMKS 3613  
3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTVTPK-LCDGRHVRVAVIMG 3527  
3614 GNVLEVDASNNHVTGPLAALAAAGAPVLYGLPEPMAVQPPPCYACGQWRBLAVNRS 3673  
3528 RDTLEVDTSNHTTGLRPSLAGSPALLHLGSLFKSSTARPELPAYRGCILRKLINGA 3597  
3674 PYAMTRSVRHHGAVGASGCPA 3694  
3598 PNVVTASVQIQGAVMRCGPS 3608

RESULT 2  
S18253

laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 16-Sep-1992 #sequence\_revision 24-Jul-1997 #text\_change 10-Dec-1999  
C:Accession: S28399; S18253  
R:Kusche-Gullberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, J.H.  
EMBO J. 11, 4519-4527, 1992  
A>Title: Laminin A chain: expression during Drosophila development and genomic sequence.  
A:Reference number: S28399; MUID:93049203; PMID:1425586  
A:Accession: S28399  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-3712 <KUS>  
A:Cross-references: GB:M96388; NID:G157799; PIDN:AAA28662.1; PID:G157800  
R:Garrison, K.; Mackrell, A.J.; Fessler, J.H.  
J. Biol. Chem. 266, 22899-22904, 1991  
A>Title: Drosophila laminin A chain sequence, interspecies comparison, and domain structure.  
A:Reference number: S18253; MUID:92078147; PMID:1744083  
A:Accession: S18253  
A:Molecule type: mRNA  
A:Residues: 1762-3712 <GAR>  
A:Cross-references: EMBL:M75882; NID:G157797; PIDN:AAA28661.1; PID:G157798  
C:Genetics:  
A:Gene: FlyBase: Lana  
A:Cross-references: FlyBase: FBgn0002526  
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h  
C:Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular  
F:273-330/Domain: laminin-type EGF-like homology <LEG>  
F:333-400/Domain: laminin-type EGF-like homology <LE02>  
F:541-584/Domain: laminin-type EGF-like homology <LE01>  
F:1776-2115/Domain: III <DOM3>  
F:1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>  
F:1809-1856/Domain: laminin-type EGF-like homology <LE2>  
F:1859-1914/Domain: laminin-type EGF-like homology <LE3>  
F:1917-1967/Domain: laminin-type EGF-like homology <LE4>  
F:1970-2014/Domain: laminin-type EGF-like homology <LE5>  
F:2017-2061/Domain: laminin-type EGF-like homology <LE6>  
F:2064-2109/Domain: laminin-type EGF-like homology <LE7>  
F:2116-2697/Domain: I/II, heptad repeats <DOM2>  
F:2698-3712/Domain: G <DOMG>  
F:2698-2863/Domain: repeat G1 <RG1>  
F:2864-3048/Domain: repeat G2 <RG2>  
F:3049-3223/Domain: repeat G3 <RG3>  
F:3079-3200/Domain: laminin G repeat homology <LG3>  
F:3329-3712/Domain: repeat G4 <RG4>  
F:3529-3712/Domain: repeat G5 <RG5>  
F:1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

Query Match 25.3%; Score 5097; DB 2; Length 3712;  
Best Local Similarity 31.7%; Pred. No. 3.3e-217;  
Matches 1248; Conservative 609; Mismatches 1541; Indels 540; Gaps 122;  
QY 45 LHPPYTNLAEGARIAASATCGEEAPARGSPRPTELYCKLVGPGVAGGDPN-OTIRGQYVC 103  
Db 24 LTPPYTNLATGRKIYATATCG---PDTDGP---ELYCKLVGANTHEDHIDYSVIGQVVC 76  
QY 104 DICTAANSNKAMPASNAIDGTERWQSPPLSGLENEVNVTLDLGQVHFVAVLKIFAN 163  
Db 77 DYCDTPVRNHPPEINAIDGTERWQSPPLSGLENEVNVTLINFEQEHFVAFLIRMG 136  
QY 164 SPFPDLVWLSRMDFORTYQPMQFFASSKRCDCLEFPQTLERITRDDAAICTTEYSRIV 223  
Db 137 SPFGLWLEKSTDYKKTWTNQHFSDDPADCTETFGKDYKPTTRDDDDVICTTEYSKIV 196  
QY 224 PLENGIIVSVLNGRPGAMNFSYSPLLREFTKATNVRFLRFLNTLLGHLMKALRDPV 283  
Db 197 PLENGEIPVLLNERPSSNYSFNSTVQLQEWTKATNVRILLRATKXLLGHLMVARQDPV 256  
QY 284 TRRYYSIKDISIGRCVCHGHADACADKADPDTPFR-LOCTQHNTCGTCDCRCCPGNQ 342  
Db 257 TRRYFSIKDISIGRCMCNCHADTCDVKDPKSPVILLACRQHHCTCG:QCNECCGPFQ 316  
QY 343 QPWKPAANSANECQSCNCGHATDCYDPEVDRRRASQSLDGTGQGGVCIQCHHTAG 402

Db 317 KWRQNTNARPNCEPCNCHGSHNECKYDEBNRKGSLDLHGHYDGGVQCNQCHNTVG 376  
Qy 403 VNCERCLPGFYRSPNHPDLSPHYCRRNCNCEBDFDTGTCEDLTGRCYCRPNFSGERCDVCA 462  
Db 377 INCNCKPKYRPGKHWNEDTVCSPCQCDYFSTGHCSEETGNCCEAAFPQPPSCJSCA 436  
Qy 463 EGTGPPSCYPTPSSSNDTREQVLPAQOIVCNCDSAGTQGNACRDXPRVGRCLCKPNFO 522  
Db 437 YGYGVPC-----RE-----CECNLNGTNGYHCEAESG-QQCPCKINFA 475  
Qy 523 GTHCELCAPIFYG-PGQPCQCSPPGVADDCDDPDGQCRVCPGFGATCDRCAPGYFHP 581  
Db 476 GAYCKQCAEGYGFPECKACEKNKIGSITNDCNVTGEBCKLTFNGDNCERCKHGYFNY 535  
Qy 582 PLQLOCCSPAGLTPGCD-EAGRCLOPEFAGPHDCRCPGVHGFPPNCOACTCDPRGAL 640  
Db 536 PTCYCDNDQGTSEITCNKQSQICREGFGGPRCDQLPGFYNYDPCKPNCSTGSS 595  
Qy 641 DQLCGAGLCRCRPGVTGTACQSPGFHGFPCVPCCHGSAEGSLHAAADPRSGQSCRP 700  
Db 596 AITCDNTGKCNLNNFAGKQCTICTAGYYSYDCLPCHCDSHGSGVSCN-SDGQCLCOP 654  
Qy 701 RVTGLRCDTCVPGAYNFPYCEASCHPAGLAPVDPALPEAQP-----CMCRAHVGPSCD 756  
Db 655 NFDGRQDCSKEGFYNFPSCDCNCDPAGV--IDKFAGCGSVPGVGBLCKCKERVTCRICN 712  
Qy 757 RCKEGFWGLSPNPEGCTRCSDLRTGLGVARQPGTQCFCKPHVCGQACASCKDGF 816  
Db 713 ECKPLYNWLNMISTEGEICDCWTDGTISALDTCTSKSGQCPCKPHTQRRCOECRDGTF 772  
Qy 817 GLPOADYFGCRCDTGGALGOSCEPTRCVGCRCRNTQPTCESEPARDHYLPDLHLRL 876  
Db 773 DLDSASLFGKDCSCDVGGSQSWQCKISQCKCHPRITGLACTQPLTHFFPTLHQFY 832  
Qy 877 ELEBAATPEGHARFGNPLPEEFNFWRGVQAQAPQPRIVARLNLTSPLFLVRYN 936  
Db 833 EYEDGSLPGTQRYDIDEAAPFGFSKGVVFNALQNDVRNENVFKSLRIVLRYN 892  
Qy 937 RGAMSVGRSVREBEGSAAACNCTAQSPVAPPSTEPAFITV--PORGFGEPFVLPNG 994  
Db 893 PNAENVATISVTSNDELE----VDGHVVLQPTSEPOFVTVAGFLGKPSAIVLDPG 947  
Qy 995 TWALRVEA-RGVLLDYVLPASYEALQLQVTEACTYRPSAQSGDNCULLYTHPLD 1053  
Db 948 RYVFTTKANKXNMLDYVLLPAAYYEAGILTRHISNPCEL-----GNMELCRHYKIASVE 1002  
Qy 1054 GTPSAAGLEALCRDNLPRCPTEQLSPSHPLIT-----CTGSDVDVQLQVAVPQ 1106  
Db 1003 VFSFAA--TFPVIGENSKPINVETITDPEHLQIVSHVGDIPVLSGSQNELHYIVDVPS 1060  
Qy 1107 GRVALVVEY-ANEDARQGVAVHTPORAPQOGLLSLHPCLYSTLCRGRTARDQDHLAVF 1165  
Db 1061 GRVIFVDYISDRNFPDYSYINLKNPDSETSVLLYPCLYSTICR-TSVNEDGMEKSF 1119  
Qy 1166 HLDSSE-ASVELTA--EQARFFLGHVTLVPIEEFGFVEPRVSTISSHGAPGPNAAAC 1220  
Db 1120 YINKEDLOPVIISADIEDGRFIIISVTAIPVQWSIDYINFPVCVI-----HDQOC 1172  
Qy 1221 LPSRFPKPPQPIILRDCQVIELPPGLPLTHAQLDLPATSPAGRPPTAVDPDAEPTLL 1280  
Db 1173 ATPFRSVP-----DSKKIEFE-----TDHEDRIATNKP-----PYASLDERVKLVHL 1215  
Qy 1281 -REPOATVUTTHV-----PTLGRVAFLLHGYQPAHPTFPVEVLINAGR-VMOGHANASFC 1334  
Db 1216 DSQNEATVIESKVDATKPNL--FVILVKYIQSHPKYQVYITLTKQYQDKFQIQC 1273  
Qy 1335 PHYGCRITLVYCEQALLDTHSELTVTVRVPGRMLWLDVILVVPENYVSFGYLBEPFL 1394  
Db 1274 PSSSGCRGVIRPAGESFEI-DDEKFTITTDSSQSVMLDYLVVPLKQNDLLVEETF 1332  
Qy 1395 DKSVDFTSHCAAQYHISPSSSSLFCRNAASLSLFYNNCARPGCHEVATOPTCEPG 1454  
Db 1333 DOTKEFIQNCGHDFHITHNASD-FCKKSVFSTADYNSGALPCNCDYAGSTSEFCPPFG 1391

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 98.6077 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-4  
Perfect score: 19876  
Sequence: 1 DLYCKLVGPVAGDPNQTI.....QKALTQKHAKPSVPLMH 3635

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19876	100.0	3635	5	AB81589 Mouse lam
2	19876	100.0	3635	5	AA50357 Mouse lam
3	15839	79.7	3695	5	AB81588 Human lam
4	15830.5	79.6	3696	5	AA17310 Human lam
5	15815	79.6	3705	5	AA17309 Human lam
6	14771	74.3	3600	5	AB09501 Human lam
7	14706.5	74.0	3597	5	AB09503 Human lam
8	12354.5	62.2	2743	5	AB81598 Human lam
9	6643.5	33.4	3332	7	AD80894 Novel pro
10	6092	30.7	1640	5	AB09504 Human lam
11	5871.5	29.5	1601	4	AA39009 Human pol
12	5012.5	25.2	3712	4	AB64954 Drosophil
13	3968.5	20.0	1486	7	AD609114 Novel pro
14	3488.5	17.6	953	5	AA50358 Human lam
15	3325	16.7	908	5	AB09502 Human lam
16	3096	15.6	3084	3	AA19796 Mouse lam
17	3096	15.6	3106	3	AA19795 Mouse lam
18	3096	15.6	3106	3	AD61792 Rat Prote
19	3022	15.2	3122	7	AD61794 Human Pro
20	3010.5	15.1	3089	3	AA19792 Human lam
21	3010.5	15.1	3110	3	AA19791 Human lam
22	3005	15.1	3088	3	AA19794 Human lam
23	3005	15.1	3110	2	AA19793 Merosin m
24	3005	15.1	3110	2	AA15460 Human lam
25	3005	15.1	3110	3	AA19793 Human lam

ALIGNMENTS

RESULT 1

AB81589  
ID AB81589 standard; protein; 3635 AA.

- AC AB81589;
- DT 19-SEP-2002 (first entry)
- DE Mouse laminin alpha 5 amino acid sequence SEQ ID NO:4.
- KW Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation; tissue repair development; laminin; healing; vascular tissue; re-endothelialisation; vascular injury; cell attachment; cell stasis; proliferation; migration.
- OS Mus musculus.
- FN WO200250111-A2.
- PD 27-JUN-2002.
- PF 21-DEC-2001; 2001WO-US051035.
- PR 21-DEC-2000; 2000US-0257449P.
- PR 28-MAR-2001; 2001US-0279282P.
- PR 13-NOV-2001; 2001US-00279282.
- PA (BIOS-) BIOSTRATUM INC.
- PI Tryggvason K, Doi M, Thyboll J;
- DR WPI; 2002-557650/59.
- DR N-PSDB; ABQ72907.
- PT New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.
- PS Claim 9; Page 94-105; 231pp; English.
- CC The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has vulnery activity. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing injuries of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialisation at the site of vascular injuries, and promote cell attachment and subsequent cell stasis.



CC	proliferation, differentiation, and/or migration. The present sequence									
CC	represents mouse laminin alpha 5 which is used in the exemplification of									
CC	the present invention									
XX										
SQ	Sequence 3635 AA;									
	Query Match	100.0%;	Score 19876;	DB 5;	Length 3635;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 3635;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
Qy	1	DLYCKLVGGPVAGDPPNQTIGQYCDICTAANSKHAHPVSNADIGTERWQSPPLSGGLE	60							
Db	1	DLYCKLVGGPVAGDPPNQTIGQYCDICTAANSKHAHPVSNADIGTERWQSPPLSGGLE	60							
Qy	61	YNEVNTLIDGQVPHVAVLIKANSRPPDLWLSTDFGHTYQWQFPASSKRCCLER	120							
Db	61	YNEVNTLIDGQVPHVAVLIKANSRPPDLWLSTDFGHTYQWQFPASSKRCCLER	120							
Qy	121	FGPRTLERITQDDVDICTEYSRIVPLENGEIVVSLVNGRPGALNPSYSLPLDFTKATN	180							
Db	121	FGPRTLERITQDDVDICTEYSRIVPLENGEIVVSLVNGRPGALNPSYSLPLDFTKATN	180							
Qy	181	IRLRFLENTLLGHMGKALRDPVTRRYYSIKDISIGRCVCHGADVCDKADPLDPF	240							
Db	181	IRLRFLENTLLGHMGKALRDPVTRRYYSIKDISIGRCVCHGADVCDKADPLDPF	240							
Qy	241	RLQACAHNTCGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRN	300							
Db	241	RLQACAHNTCGSCDRCCPGFNQPKPATTDSANECQSCNCHGHAYDCYDPEVDRN	300							
Qy	301	ASQNDVNYGGGVCLDCQHHITGINCERCLPGFFRAPDQLDSPHVCRPCDCESFTDG	360							
Db	301	ASQNDVNYGGGVCLDCQHHITGINCERCLPGFFRAPDQLDSPHVCRPCDCESFTDG	360							
Qy	361	TCEDLTGRCYCRNFTGELCAACAEYTDPHCYPLPSFPFNDTREQVLPAQIVNCDN	420							
Db	361	TCEDLTGRCYCRNFTGELCAACAEYTDPHCYPLPSFPFNDTREQVLPAQIVNCDN	420							
Qy	421	AAGTQGNACRDXDPRIGRCVKNPRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	480							
Db	421	AAGTQGNACRDXDPRIGRCVKNPRGAHCELCAPGFHGPSCHPCQCSSPGVANSLCDPES	480							
Qy	481	GOCMRTGFEGRDCHCALGYFHPPLCQCCSPAGTLPCEGCBAGRCQCRPGFDGPHCD	540							
Db	481	GOCMRTGFEGRDCHCALGYFHPPLCQCCSPAGTLPCEGCBAGRCQCRPGFDGPHCD	540							
Qy	541	RCLPGYHGYPDCHACADPRGALDQCCGVGLCHCRPGNTGATCEBSPGFYFPSPICP	600							
Db	541	RCLPGYHGYPDCHACADPRGALDQCCGVGLCHCRPGNTGATCEBSPGFYFPSPICP	600							
Qy	601	HCSADGSLHTTCDPTTGQCRCPBVTGLHCDMCPGAINPYCEAGSCHPAGLAPANPAL	660							
Db	601	HCSADGSLHTTCDPTTGQCRCPBVTGLHCDMCPGAINPYCEAGSCHPAGLAPANPAL	660							
Qy	661	PETQAPCMCRARHVEGPSCDRCCKPGYGLSASNPEGCTRCSCDPRGTLGGVTECQNGQCF	720							
Db	661	PETQAPCMCRARHVEGPSCDRCCKPGYGLSASNPEGCTRCSCDPRGTLGGVTECQNGQCF	720							
Qy	721	KAHVCGTKTCAACKDGFGLDYADYFGCRSCRDVGGALGOCBPKTGACRCRNTQGT	780							
Db	721	KAHVCGTKTCAACKDGFGLDYADYFGCRSCRDVGGALGOCBPKTGACRCRNTQGT	780							
Qy	781	CSEPAKHVLPDLHMRLEBEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	840							
Db	781	CSEPAKHVLPDLHMRLEBEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIVA	840							
Qy	841	RLNVTSPDLFRLVFRVNRGTSVNGQISVREBGLKSSCTNCTEQSQVAPPPSTEPAFV	900							
Db	841	RLNVTSPDLFRLVFRVNRGTSVNGQISVREBGLKSSCTNCTEQSQVAPPPSTEPAFV	900							
Qy	901	TVPORGFGEPFVLNFGIINALLVEAGSVLLDYVLLPSTIYEEAALLQHRVTEACTYRPSAL	960							
Db	901	TVPORGFGEPFVLNFGIINALLVEAGSVLLDYVLLPSTIYEEAALLQHRVTEACTYRPSAL	960							

Qy	961	HSTENCLVYAHLPDGGPSSAGTALCRHDSNLRPPCPTEQLSPSHPLATCFGSDVDIQ	1020
Db	961	HSTENCLVYAHLPDGGPSSAGTALCRHDSNLRPPCPTEQLSPSHPLATCFGSDVDIQ	1020
Qy	1021	LEMAVPQGGQVLYVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPQYSSSLCRSPARDT	1080
Db	1021	LEMAVPQGGQVLYVVEYVGEDSHQEMGVAVHTPQAPQQGVNLNHPQYSSSLCRSPARDT	1080
Qy	1081	QHHLAIFHLDSSEASIRLTAEQAHFLLHSVTLVPVEEFTSEFVEPRVFCVSSHGTFFNPSA	1140
Db	1081	QHHLAIFHLDSSEASIRLTAEQAHFLLHSVTLVPVEEFTSEFVEPRVFCVSSHGTFFNPSA	1140
Qy	1141	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSOELSPGAPPEGPQPRPPPTAVDPNABPT	1200
Db	1141	ACLASRFPKPPQPIILKDCQVLPPLPDLPLTQSOELSPGAPPEGPQPRPPPTAVDPNABPT	1200
Qy	1201	LLRHPOGVTVVTTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIWGHANAFPCPHGY	1260
Db	1201	LLRHPOGVTVVTTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIWGHANAFPCPHGY	1260
Qy	1261	GCRTLVLCCEGQTMLDVTDNLTVTVRVPEGRWLMDVYLVIPEDAYSSSYLQEEPLDKSY	1320
Db	1261	GCRTLVLCCEGQTMLDVTDNLTVTVRVPEGRWLMDVYLVIPEDAYSSSYLQEEPLDKSY	1320
Qy	1321	DFISHCATQGYHISPSSSSPFCRNAATSLSYFNNGALPCGCHEVGAUSPTCEPFGGQCP	1380
Db	1321	DFISHCATQGYHISPSSSSPFCRNAATSLSYFNNGALPCGCHEVGAUSPTCEPFGGQCP	1380
Qy	1381	CRGHVIGDCSRCACTGYMGFPNCRPCDCGARLCLDELTGQCICPPRTVPPDCLVQPOQSFQ	1440
Db	1381	CRGHVIGDCSRCACTGYMGFPNCRPCDCGARLCLDELTGQCICPPRTVPPDCLVQPOQSFQ	1440
Qy	1441	CHPLVGCBECCSGGVQELTDPCTCDMSGGCRCPNVAGRCDCPCAPGFYGVSCRPDC	1500
Db	1441	CHPLVGCBECCSGGVQELTDPCTCDMSGGCRCPNVAGRCDCPCAPGFYGVSCRPDC	1500
Qy	1501	CHEAGTMAVSDCLTGTQCHCKENQVSGRCDQCRVGTFTSLDAANPKGCTRCFCGATERCG	1560
Db	1501	CHEAGTMAVSDCLTGTQCHCKENQVSGRCDQCRVGTFTSLDAANPKGCTRCFCGATERCG	1560
Qy	1561	NSNLARHFVDMEGWVLLSSDRQVVPHEHREPIELHLDLSVADTFSELVQWAPPSVYG	1620
Db	1561	NSNLARHFVDMEGWVLLSSDRQVVPHEHREPIELHLDLSVADTFSELVQWAPPSVYG	1620
Qy	1621	DRVSSVGGTFLHYELHSETQRGDIPIPYESRDPVVLQGNQMSIAFLELAYPPPGQVHRQL	1680
Db	1621	DRVSSVGGTFLHYELHSETQRGDIPIPYESRDPVVLQGNQMSIAFLELAYPPPGQVHRQL	1680
Qy	1681	QLVEGNFRHLETHNPVSRREELMMVLQGLQIRALFSGTSSSVSLRVRVLEVAEAGRG	1740
Db	1681	QLVEGNFRHLETHNPVSRREELMMVLQGLQIRALFSGTSSSVSLRVRVLEVAEAGRG	1740
Qy	1741	PPASNVELCMCPANYRGSDCQECAPGYRDTKGLFLGRCPVQCHGHSRCLPQSGSICVQ	1800
Db	1741	PPASNVELCMCPANYRGSDCQECAPGYRDTKGLFLGRCPVQCHGHSRCLPQSGSICVQ	1800
Qy	1801	CQHNTEGDCQCRCPGFVSSDPSPNPAFCVSCPCPLAVPSNNFADGCVLNRGTQCLCRP	1860
Db	1801	CQHNTEGDCQCRCPGFVSSDPSPNPAFCVSCPCPLAVPSNNFADGCVLNRGTQCLCRP	1860
Qy	1861	GVAGASCERCAPGFNGNPLVIGSSCQPCDCSNGSDPNMIFSDCDPLTGACRCLRHTTGP	1920
Db	1861	GVAGASCERCAPGFNGNPLVIGSSCQPCDCSNGSDPNMIFSDCDPLTGACRCLRHTTGP	1920
Qy	1921	HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGRCRCLSGYFGF	1980
Db	1921	HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGRCRCLSGYFGF	1980
Qy	1981	EQCQGRCPACAPPAKGSCHPQSQCHQCPQTTGPOCLECAPGYWGLPEKGCRCQCPQR	2040
Db	1981	EQCQGRCPACAPPAKGSCHPQSQCHQCPQTTGPOCLECAPGYWGLPEKGCRCQCPQR	2040

2041 GHCDPHTGHTCPCPLSGERCDTCSQOHQVVPKPGQGHGHCVECDHCVVLLDLDLERA 2100  
 DB GHCDPHTGHTCPCPLSGERCDTCSQOHQVVPKPGQGHGHCVECDHCVVLLDLDLERA 2100  
 2101 GALLPAIREQLOGINASSAARHLRLNASTADIOSKLRPPGPRYQAAQOLOTLEQOSI 2160  
 DB GALLPAIREQLOGINASSAARHLRLNASTADIOSKLRPPGPRYQAAQOLOTLEQOSI 2160  
 2161 SIQOQTERLGSQATGQOAGQQLDITESTIGRAOKLLESVRAGRALNELASRMGQOSP 2220  
 DB SIQOQTERLGSQATGQOAGQQLDITESTIGRAOKLLESVRAGRALNELASRMGQOSP 2220  
 2221 GDALVPSGEQLRWALAEVERLLWMDTRDLGAQAGAVABAEALAEORLMARVOEQLTSWE 2280  
 DB GDALVPSGEQLRWALAEVERLLWMDTRDLGAQAGAVABAEALAEORLMARVOEQLTSWE 2280  
 2281 ENQSLATHIRDOLAQYESGLMDLRALNAQVNTTREAELNSRNOERKEALQWKQELSQ 2340  
 DB ENQSLATHIRDOLAQYESGLMDLRALNAQVNTTREAELNSRNOERKEALQWKQELSQ 2340  
 2341 DNATLKATIQAAASLLIGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAESPASSK 2400  
 DB DNATLKATIQAAASLLIGHVSELLOGIDQAKEDLEHLAASLDGAWTPLLKRMQAESPASSK 2400  
 2401 VDLVEAAEHAQKQLNALNLSGILGINQDRFIQRAVEASNAYSIIQAVQAEDAAGQ 2460  
 DB VDLVEAAEHAQKQLNALNLSGILGINQDRFIQRAVEASNAYSIIQAVQAEDAAGQ 2460  
 2461 ALRQASRTWEMVVRGLAAGAROLLANSALBETILGHQRLGAQRLQAAGIQLHNVM 2520  
 DB ALRQASRTWEMVVRGLAAGAROLLANSALBETILGHQRLGAQRLQAAGIQLHNVM 2520  
 2521 ARKQNLAAQIQBAQAWLAMDTSSEKIAHAKAVAAEALSTATHVQSOLQGMKQVVERWQ 2580  
 DB ARKQNLAAQIQBAQAWLAMDTSSEKIAHAKAVAAEALSTATHVQSOLQGMKQVVERWQ 2580  
 2581 SOLGGIQQODLSQVERDASSYSTLEKTLPLQAKLSRLNENGVNNAISLANSANTRYRK 2640  
 DB SOLGGIQQODLSQVERDASSYSTLEKTLPLQAKLSRLNENGVNNAISLANSANTRYRK 2640  
 2641 LIAQARSAASKVKVSMKFNRSGLNHPDDFVYVGGYPSNFTPEPLRPFPGYLGC 2700  
 DB LIAQARSAASKVKVSMKFNRSGLNHPDDFVYVGGYPSNFTPEPLRPFPGYLGC 2700  
 2701 HFVLYNGSQAOTGDYNGVSLRNQKHWVYRLKAGPTTISIDENIGEOFAAVIDRTLIQF 2760  
 DB HFVLYNGSQAOTGDYNGVSLRNQKHWVYRLKAGPTTISIDENIGEOFAAVIDRTLIQF 2760  
 2761 GHMSVTVEKQWVHEIKGDTVAPEGSEGLNHPDDFVYVGGYPSNFTPEPLRPFPGYLGC 2820  
 DB GHMSVTVEKQWVHEIKGDTVAPEGSEGLNHPDDFVYVGGYPSNFTPEPLRPFPGYLGC 2820  
 2821 IEMETLNEEVVSLYNEFQTFMLDTAVDKPCARSKATGDPMLTDGSLDGSFARISFEKQ 2880  
 DB IEMETLNEEVVSLYNEFQTFMLDTAVDKPCARSKATGDPMLTDGSLDGSFARISFEKQ 2880  
 2881 FSNTRKFDQELRLVSYNGIIFFLKQBSQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 2940  
 DB FSNTRKFDQELRLVSYNGIIFFLKQBSQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 2940  
 2941 LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQNMLEADAYILGGVPPQLPLSLRQ 3000  
 DB LTAASKAIQVFLLAGNRKRVLRVERATVFSVDQNMLEADAYILGGVPPQLPLSLRQ 3000  
 3001 LPPSGGSVRCIKGIALKGYVDLKLNTTGISFGCTADLLVGRMTWTHGHGFLPLALPD 3060  
 DB LPPSGGSVRCIKGIALKGYVDLKLNTTGISFGCTADLLVGRMTWTHGHGFLPLALPD 3060  
 3061 VAPITEVYVSGFGRGTQDNLLYRTSPDQPVQVSLREGHVTILRFMQQEVETQVRFADG 3120  
 DB VAPITEVYVSGFGRGTQDNLLYRTSPDQPVQVSLREGHVTILRFMQQEVETQVRFADG 3120  
 3121 APHYVAFYFNVTGWLIVDDQLQVKSHERITPMLQLOPEEPSRLLGLPVGSGTFHNF 3180

DB APHYVAFYFNVTGWLIVDDQLQVKSHERITPMLQLOPEEPSRLLGLPVGSGTFHNF 3180  
 QY GCISNVFVQRLRQORVFDLHONMGSVNVSVGCTPAQLIETGRATAQKVSRRSRQPSQDL 3240  
 DB GCISNVFVQRLRQORVFDLHONMGSVNVSVGCTPAQLIETGRATAQKVSRRSRQPSQDL 3240  
 3241 ACTTPMLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM 3300  
 DB ACTTPMLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM 3300  
 3301 SGRSPSILVFLNHHGFVAQTEGPGRLQVQSRHOSRAGOWHRVSVRWGMQOIQLVVDGSG 3360  
 DB SGRSPSILVFLNHHGFVAQTEGPGRLQVQSRHOSRAGOWHRVSVRWGMQOIQLVVDGSG 3360  
 3361 TWSQKALHHRVPRAPRPQPYTLLSVGGLPASSYSKLPVSVGFGSCCLKQLQDKQPLRTPT 3420  
 DB TWSQKALHHRVPRAPRPQPYTLLSVGGLPASSYSKLPVSVGFGSCCLKQLQDKQPLRTPT 3420  
 3421 QMGVTPCVSGPDLGDLFFPGSEGVVTLPLPKAKMPYVSLLEMRPLAAAGLIFFHLGOAL 3480  
 DB QMGVTPCVSGPDLGDLFFPGSEGVVTLPLPKAKMPYVSLLEMRPLAAAGLIFFHLGOAL 3480  
 3481 ATPMQLKVLTEOVLLQANDGAGEFSTWVTYPKLCDGRHVRVAVIMGRDTRLLEVDTQSN 3540  
 DB ATPMQLKVLTEOVLLQANDGAGEFSTWVTYPKLCDGRHVRVAVIMGRDTRLLEVDTQSN 3540  
 3541 HTTGRLPESLAGSPALLHIGSLPKSSTARPELPAYRGCLKLLINGAPVNVTSASVOIOGA 3600  
 DB HTTGRLPESLAGSPALLHIGSLPKSSTARPELPAYRGCLKLLINGAPVNVTSASVOIOGA 3600  
 3601 VGMGCPGSGTLALSQKQKALTQORHAKPSVSPILLWH 3635  
 DB VGMGCPGSGTLALSQKQKALTQORHAKPSVSPILLWH 3635

# RESULT 2

AAM50357  
 ID AAM50357 standard; protein; 3635 AA.  
 AC AAM50357;  
 DT 18-FEB-2002 (first entry)  
 DE Mouse laminin-15 alpha 5 chain.  
 KW Laminin-15; mouse; retina; eye; therapy; ophthalmological;  
 KW antiinflammatory; rod dyscrophy; rod-cone dystrophy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment.  
 OS Mus musculus.  
 PN WO200183516-A1.  
 PD 08-NOV-2001.  
 PF 01-MAY-2001; 2001WO-US013943.  
 PR 01-MAY-2000; 2000US-0200863P.  
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 PI Burgeson RE, Brunken W, Champlaud M, Hunter D;  
 DR WPI; 2002-041478/05.  
 DR N-PSDB; AAI70816.  
 PT Novel substantially pure preparation comprising laminin having laminin  
 PT chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders  
 PS such as retinitis pigmentosa, macular degeneration, retinal detachment.  
 PS Disclosure; Fig 1A-B; 58pp; English.  
 XX

CC The present sequence is that of the alpha 5 chain of mouse laminin-15, a  
 CC novel member of the laminin family that is produced in the retina. The  
 CC retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2,  
 CC gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed  
 CC within the inter-photoreceptor matrix and in the outer plexiform layer,  
 CC and may serve to stabilise retinal synapses. The invention provides  
 CC laminin-15 preparations and cells comprising a nucleic acid encoding the  
 CC laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of  
 CC producing laminin-15. The laminin-15 preparation is used in claimed  
 CC methods of: increasing retina immunophoreceptor matrix stability;  
 CC increasing the stability of retina photoreceptor compounds, especially an  
 CC outer segment, inner segment or synapse; increasing retina adhesion;  
 CC treating a disorder associated with retina degeneration, especially rod  
 CC dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration  
 CC and retinal detachment; increasing the stability of synapses of the  
 CC central nervous system or peripheral nervous system; stimulating an  
 CC neuroregeneration, axon outgrowth or synapse formation; preparing an  
 CC implant, e.g. a catheter, artificial joint, retinal implant, timed  
 CC releasing device, neural cell growth guide or artificial tissue, by  
 CC coating with the laminin-15 preparation; and increasing photosensitivity  
 CC by implanting a tip coated with the laminin-15 preparation into an eye.  
 CC The laminin may be recombinant, and the 3 chains co-expressed in the same  
 CC cell or expressed in different cells  
 XX Sequence 3635 AA;

Query Match 100.0%; Score 19876; DB 5; Length 3635;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYCKLVGGPVAGDPNQTIGQVCDICTAANSKAHPVSNADIGTRRWQSPPLSGLE 60  
 DB 1 DLYCKLVGGPVAGDPNQTIGQVCDICTAANSKAHPVSNADIGTRRWQSPPLSGLE 60

QY 61 YNEVNVTLDLGGVHVAYVLKFNANPRDLWLRLSTDFGHTYQPMQPFASSKRDCLER 120  
 DB 61 YNEVNVTLDLGGVHVAYVLKFNANPRDLWLRLSTDFGHTYQPMQPFASSKRDCLER 120

QY 121 FGPRLRLITQDDDVICTEYSRIVPLENGEIVLVNVRGALNFYSPLLRDFTKATN 180  
 DB 121 FGPRLRLITQDDDVICTEYSRIVPLENGEIVLVNVRGALNFYSPLLRDFTKATN 180

QY 181 IRLRLRLNTLGLHLMGKALRDPVTTRYYSIKDISIGRCVCHGADVCDAKDPLDPF 240  
 DB 181 IRLRLRLNTLGLHLMGKALRDPVTTRYYSIKDISIGRCVCHGADVCDAKDPLDPF 240

QY 241 RLQCAQHNTCGSDRCPCGPNQOPWKPATDTSANEQSCNCRGHAYDCYDDEVDRN 300  
 DB 241 RLQCAQHNTCGSDRCPCGPNQOPWKPATDTSANEQSCNCRGHAYDCYDDEVDRN 300

QY 301 ASQNDNVYQGGGVCLDCQHTTGNCERCLPGFPFRAPDQPLDSPHVCRPCDCSDFTDG 360  
 DB 301 ASQNDNVYQGGGVCLDCQHTTGNCERCLPGFPFRAPDQPLDSPHVCRPCDCSDFTDG 360

QY 361 TCEDLTGRCYCRPNFTGBELCAACABGYTDFPHCYPLPSFPNDRTEQVLPAGQIVNCDN 420  
 DB 361 TCEDLTGRCYCRPNFTGBELCAACABGYTDFPHCYPLPSFPNDRTEQVLPAGQIVNCDN 420

QY 421 AAGTGNACRKPRLGRVCKPNFRGACELCAPGFHGPSCHPCQCSFPGVANSLCDPES 480  
 DB 421 AAGTGNACRKPRLGRVCKPNFRGACELCAPGFHGPSCHPCQCSFPGVANSLCDPES 480

QY 481 GQCMCRTGPEGRCDHCAFGYHFFPLCQLCGCSPAGTLPEGCDBRAGCQCQPGFDGPHCD 540  
 DB 481 GQCMCRTGPEGRCDHCAFGYHFFPLCQLCGCSPAGTLPEGCDBRAGCQCQPGFDGPHCD 540

QY 541 RCLPGYHGVPDCHACADPRGALDQCCGVGGLCHCRPGNTGATQCECSPGFGPSCIPC 600  
 DB 541 RCLPGYHGVPDCHACADPRGALDQCCGVGGLCHCRPGNTGATQCECSPGFGPSCIPC 600

QY 601 HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVFGAYNFFPYCEAGSCHPAGLAPANPAL 660  
 DB 601 HCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPVFGAYNFFPYCEAGSCHPAGLAPANPAL 660

QY 661 PETQAPCMCRHVEGSPCDCKCKPGWGLSASNPCECTRCSCDPRGTGLGVTECQGNQCF 720  
 DB 661 PETQAPCMCRHVEGSPCDCKCKPGWGLSASNPCECTRCSCDPRGTGLGVTECQGNQCF 720

QY 721 CKAHVCGKTCACAKDGFGLDLYADYFGCRSCRCVGGALGQGCCEPKTGACRCRPNQOPT 780  
 DB 721 CKAHVCGKTCACAKDGFGLDLYADYFGCRSCRCVGGALGQGCCEPKTGACRCRPNQOPT 780

QY 781 CSEPAKHVLPDLHMRLELEBAATPEGHAVRFGNPLEFENFNSWRGVAHMAIOPRIVA 840  
 DB 781 CSEPAKHVLPDLHMRLELEBAATPEGHAVRFGNPLEFENFNSWRGVAHMAIOPRIVA 840

QY 841 RLNVTSPLDLRLVFRVYVNRGTSVNGQISVRBEGKLSCTNCTEQSQPVAFPPSTEPAFV 900  
 DB 841 RLNVTSPLDLRLVFRVYVNRGTSVNGQISVRBEGKLSCTNCTEQSQPVAFPPSTEPAFV 900

QY 901 TVPQRGFGPPVNLPGIINALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTVPSAL 960  
 DB 901 TVPQRGFGPPVNLPGIINALLVEAGVLLDYVLLPSTYYEALLQHRVTEACTVPSAL 960

QY 961 HSTENCLVYAHLPDLGFPSSAAGTEALCRHDSNLPRCPTEQLSPSHPLPLATCFGSDVDIQ 1020  
 DB 961 HSTENCLVYAHLPDLGFPSSAAGTEALCRHDSNLPRCPTEQLSPSHPLPLATCFGSDVDIQ 1020

QY 1021 LEMAVPQGOYVLVVEYGEDSHQEMGVAVHTPQAPQOQVNLNHPCPYSSLCRSPARDT 1080  
 DB 1021 LEMAVPQGOYVLVVEYGEDSHQEMGVAVHTPQAPQOQVNLNHPCPYSSLCRSPARDT 1080

QY 1081 QHHLAIFHLDSBASIRLTAEQAHHFLHSVTLVFEVEEFSTEFVEPRVFCVSSHGTFNPSSA 1140  
 DB 1081 QHHLAIFHLDSBASIRLTAEQAHHFLHSVTLVFEVEEFSTEFVEPRVFCVSSHGTFNPSSA 1140

QY 1141 ACLASRFPKPPPOPIILKDCQVLPPLPDLPLTOSQELSPGAPPEGPQPPPTAVDNPAPT 1200  
 DB 1141 ACLASRFPKPPPOPIILKDCQVLPPLPDLPLTOSQELSPGAPPEGPQPPPTAVDNPAPT 1200

QY 1201 LLRHPCGTVVFTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIGWGHANASCPHGY 1260  
 DB 1201 LLRHPCGTVVFTQVPTLGRYAFLLHGYPVHPSPFVEVLINGRIGWGHANASCPHGY 1260

QY 1261 GRTLVLCBGQTMLDVTNDELTVTVRPEGRWLWDVYLIVPEDAYSSYLQEEPLDKSY 1320  
 DB 1261 GRTLVLCBGQTMLDVTNDELTVTVRPEGRWLWDVYLIVPEDAYSSYLQEEPLDKSY 1320

QY 1321 DFISSHATCGYHISPSSSSPFCRNAATSLSFYNNGALPCGCHVEGAVSPTCEPFGQCP 1380  
 DB 1321 DFISSHATCGYHISPSSSSPFCRNAATSLSFYNNGALPCGCHVEGAVSPTCEPFGQCP 1380

QY 1381 CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCEBLTGQCI CPPRTVPDCLVCQPSFG 1440  
 DB 1381 CRGHVIGRDCSRCATGYWGFNCRPCDCGARLCEBLTGQCI CPPRTVPDCLVCQPSFG 1440

QY 1441 CHEPLVCEBNCNCGPGVQELTDPCTCDMSGQCRPNVAGRCDTCAPGFYGVPSCRPCD 1500  
 DB 1441 CHEPLVCEBNCNCGPGVQELTDPCTCDMSGQCRPNVAGRCDTCAPGFYGVPSCRPCD 1500

QY 1501 CHEAGTMASVCDPLTQCHCKENVOGSRCDQCRVGTFFSLDAANPKGCTCFCFGATERCG 1560  
 DB 1501 CHEAGTMASVCDPLTQCHCKENVOGSRCDQCRVGTFFSLDAANPKGCTCFCFGATERCG 1560

QY 1561 NSHLARHEFVDMEGWVLLSSDRQVVPHEHPEIILLHADLRVADTFESLYWQAPPSYLG 1620  
 DB 1561 NSHLARHEFVDMEGWVLLSSDRQVVPHEHPEIILLHADLRVADTFESLYWQAPPSYLG 1620

QY 1621 DRVSSYGGTLHYELHSETORGDI FIPYESRPPDVVLQGNQMSIAFLAYLPPGQVHRGQL 1680  
 DB 1621 DRVSSYGGTLHYELHSETORGDI FIPYESRPPDVVLQGNQMSIAFLAYLPPGQVHRGQL 1680

QY 1681 OLVEGNFRHLETHNPVSRBELMMVLQGLQIRALFQSTSSSVSLRRVVLVASEAGRG 1740  
 DB 1681 OLVEGNFRHLETHNPVSRBELMMVLQGLQIRALFQSTSSSVSLRRVVLVASEAGRG 1740





1578 DCHAGTAVGCDPLTGQCYCKENYQVKDCQCSLGTFSLDANPKGCTRCFCFATERC 1637  
1560 GNSNLARHFVDMEGWLLSSRDQVVPVHEHRPEIELLHADLR-----SVADTFSELYWOAP 1615  
1638 RSSSYTRQBFVDMEGWLLSTDRQVVPVHERQGTETMLRADLRHVPEAPEPELYWOAP 1697  
1616 PSYLGDRVSSYGTTHYELHSTQRTDIEIPYSEPDVVLQGNQMSIAFLELAYPPPGQV 1675  
1698 PSYLGDRVSSYGTTHYELHSTQRTDIEIPYSEPDVVLQGNQMSIAFLELAYPPPGQV 1757  
1676 HRGQQLVFNENPRHLETHNPVREBELMVLAGELOLQIRALFSQTSVSSVSLRRVLEVAS 1735  
1758 HRGQQLVFNENPRHLETHNPVREBELMVLAGELOLQIRALFSQTSVSSVSLRRVLEVAS 1817  
1736 EAGRGPPASNVLZCMCPANYRGDSQCECAPGVYRTDGLFLGRVPCOCHGSHSDCLPGS 1795  
1818 PAGQALASNVLCPCPASYRGDSQCECAPGVYRTDGLFLGRVPCOCHGSHSDCLPGS 1877  
1796 GICVGCQHNTEGQCBRCRPGFVSSDPNAPSPCVSCPCPLAVPNPNFADGCVLRNGRTQ 1855  
1878 GVCVDCQHNTEGAHCERCQAGFWS--RDDPSAPCVSCPCPLSVPNFANFAGCVLRNGRTQ 1936  
1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPMNIFSDCDPLTGACRGCLR 1915  
1937 CLCKPGYAGASCERCAPGFFGNPLVLGSSCQPCDCSNGDPMNIFSDCDPLTGACRGCLR 1996  
1916 HTTGPCHERCAPGYGNALLPGNTRCPCSGTETCDPQSGRCCKAGVTGQRCDCRLE 1975  
1997 HTTGPCHERCAPGYGNALLPGNTRCPCSGTETCDPQSGRCCKAGVTGQRCDCRLE 2056  
1976 GYFPGFCOCGRPCACGPAKSECHPOSGQCHCQPGTTPCCLBCAPCYWGLPEKGCRR 2035  
2057 GHFGFNGCGGRPCACGPAKSECHPOSGQCHCQPGTTPCCLBCAPCYWGLPEKGCRR 2116  
2036 CQCPRGHCPHTGHTCTCPPLGSGERCDCSCQHQVFPVPGKPGGHIHCEVDCCHCVLLLD 2095  
2117 CQCPRGHCPHTGHTCTCPPLGSGERCDCSCQHQVFPVPGKPGGHIHCEVDCCHCVLLLD 2176  
2096 DLERAGALLPATREQLQGINASAAWARLRLNLSADIQSLKRLPPGPRYQAAQLOTL 2155  
2177 DLERAGALLPATREQLQGINASAAWARLRLNLSADIQSLKRLPPGPRYQAAQLOTL 2236  
2156 EQQSILQDTERLGSQATGVQOAGQDLDTESTLGRAOKLLESVRAVGRALNELASRM 2215  
2237 EQQSTSLQDARLGGQAVTRDQASQALLAGTEATLGHAKTLLAARAVDRFTLSLMSQT 2296  
2216 GQSGPGDALVPSGEQURWALAEVERLLWDMTRDILGAQAVABEILAEARLMAVQBL 2275  
2297 GHGLANASAPSGEQLLRTLAVERLLWEMRARDLGAPOAAAEELAAARLLARVQBL 2356  
2276 TSFWEENQSLATHIRPOLAQYSGMLDLREALNOAVNTTREAELNSRNOERVKALQWK 2335  
2357 SSLWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAOELNSRNOERLEALQK 2416  
2336 QELSODNATLKATLOASLILGHVSELQGIQDAKEDLEHLAASLDGAWTPLKMQAFS 2395  
2417 QELSODNATLOATLHAARDTLASVFLRLSHSLDQAKEELERLAASLDGARTPLLRMQAFS 2476  
2396 PASSKVDLVEABAHAOKNOLAINLSIILGINODRFTORAVEASNYSSLILOVQAAE 2455  
2477 PAGSKURLVEABAHAQQLQJALNLSIILVDNQDRLTORAIEASNAYSRILQVQAAE 2536  
2456 DAAGQALQADHTWATVVRQGLVDRAQALLANSTALEEAMLEQEQRLGLVWAALQARTQ 2515  
2537 DAAGQALQADHTWATVVRQGLVDRAQALLANSTALEEAMLEQEQRLGLVWAALQARTQ 2596  
2516 LHNWAKKQALQAEQAEQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSLQGMQK 2575  
2597 LRDVRAKQDLQAEHIOQAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSLQGMQK 2656  
2576 VERWQSLQGLQGLQDLSQVERDASSVSTLEKTLPOLAKLSRLNENRGVHNASLANSI 2635

2657 VERWQSLQGLQGLQDLSQAVLDAGHSVSTLEKTLPOLAKLSRLNENRGVHNASLANSI 2716  
2636 GRVREKLTAQARSASAKVUSMKNRSGVRLRPRDLADLAAYTALKFHIQSPVPAPEPG 2695  
2717 GRVREKLTAQARSASAKVUSMKNRSGVRLRPRDLADLAAYTALKFHIQSPVPAPEPG 2774  
2696 KNTGDHFLVYMGSRQATGDYMGVSLRNQKWHVYRIGKAGPTTILSIDENTGEQFAAVSID 2755  
2775 QGTEDRFVYMGSRQATGDYMGVSLRNQKWHVYRIGKAGPTTILSIDENTGEQFAAVSID 2834  
2756 RTLOFGHMSVTVKQWHEIKGDTVAPGSEGLNLNLPDDDFVYVGGVPSNFTPEPLRPP 2815  
2835 RTLOFGHMSVTVKQWHEIKGDTVAPGSEGLNLNLPDDDFVYVGGVPSNFTPEPLRPP 2894  
2816 GYLGCIEMETINBEVWSLYNFETFMLDATAVDKPCARSKATGDPMTLDGSLYDGSQGFARI 2875  
2895 GYRGCIEBMDTLNBEVWSLYNFETFMLDATAVDKPCARSKATGDPMTLDGSLYDGSQGFARI 2954  
2876 SFEKQFNTKRFQOELRLVSNGIIFELKQESOFCLAVQEGTLVLFYDFGSGGLKADPL 2935  
2955 SFDQISITTKRFQOELRLVSNGIIFELKQESOFCLAVQEGTLVLFYDFGSGGLKADPL 3014  
2936 QPPOALTAASKATQVFLLAGNRKRLVRVERATVFSVDQDNMLEMADAYVYLGVPPEQLP 2995  
3015 QPPEPLTASAKATQVFLLAGNRKRLVRVERATVFSVDQDNMLEMADAYVYLGVPPEQLP 3074  
2996 LSLRQLPSPSGSVRGCIKIGIKALGVYDLKRLNTTGISPCGTADLLVGRWTMTHGFLP 3055  
3075 PSLRWLEPFTGSGVRGCVKIGIKALGVYDLKRLNTTGISPCGTADLLVGRWTMTHGFLP 3134  
3056 LALPDVAPIETEVVYSGPFRGTQDNLLYYRTSPDGPYOVLSREGHVTLRFMNOEVETQR 3115  
3135 LALSNAVPLTGNVYSGPFRGTQDNLLYYRTSPDGPYOVLSREGHVTLRFMNOEVETQR 3194  
3116 VFADGAPHYVAFVSNVTGVMVLYDDQLQVKSHERTTMPLQLOPEPSRLLGLPVSQT 3175  
3195 GFADGAPHYVAFVSNVTGVMVLYDDQLQVKSHERTTMPLQLOPEPSRLLGLPVSQT 3254  
3176 FHNESGCIINVFQRLGPGORVFDLHQNMGSVNVSVGCTPAQLIETS-----RATAOK 3228  
3255 IYFNSGCIINVFQRLGPGORVFDLHQNMGSVNVSVGCTPAQLIETS-----RATAOK 3314  
3229 VSRRSQPSQDLACTTTPMLPFTTQDAYQFGGLPSPYLFQVIGISPSHRNLHLMLVRPHA 3288  
3315 ASRRSRQPSRHPACMLPPHLRTTRDSYQFGGLSSHLEFVIGILARHNPWLSLMSHVLPR- 3373  
3289 ASQGLLSTAPMSGRSPSLVFLNNGHFVAQTGPGPRLQVQSGRQSRAGWHVSRWG 3348  
3374 SSRGLLFTARLRFSPSLALFUSNGHFVAQMEGLGTRUQAQRQSRQSRQSRQSRQSR 3433  
3349 MQQTLVVDGSGQTSQKALHHRVPRAPRPOPYTLVSGGLPSPASSYSSKLPVSVGFSGCLKK 3408  
3434 KNRILLVTDGARANSQSGPHRQHQGAHPQPHTLFVGGLPASSHSSKLPVTVGFSGCVKR 3493  
3409 LQDKQPLRTPQWGVTPCVSGPLEDGLFPFSGSEGVWTLLEPKAKMPYVUSLEMRPLA 3468  
3494 LRLHGRPLGAPTRMAGVTPCILGLEAGLFPFSGSGVITLDFGATLDFVGLGLEVRPLA 3553  
3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGBFTWVTPK-LCDGRHVRVAVMG 3527  
3554 VTGLIFHLGQARTPYLQLOVTEKQVLLRADDGAGBFTSTVTRPSVLCDGQWHLAWKS 3613  
3528 RDLRLLEVDQSNHTTQRLPESLAGSPALLHLGSLPKSSTARPELPAIRYOCRLKLLINGA 3587  
3614 GNVLRLLEVDQSNHTTQRLPESLAGSPALLHLGSLPKSSTARPELPAIRYOCRLKLLINGA 3673  
3588 PVNVYASVQIOGAVGMEGCPFS 3608  
3674 PVAMTRSVFVHGAAGSACCPA 3694

RESULT 4  
AAE17310

ID	AAEL17310 standard; protein; 3696 AA.	CC	spondyria, cystinuria, skeletal muscle disorders including hypoglycaemia
AC	AAEL17310;	CC	and tendinitis, gastrointestinal diseases including intestinal
XX		CC	obstruction and tropical sprue, spleen disorders including hypersplenism,
XX		CC	Hodgkin's disease and malignant lymphoma, testicular cancer, male
DT	18-APR-2002 (first entry)	CC	reproductive diseases including low testosterone and male infertility.
XX		CC	The present sequence is human laminin alpha protein
DE	Human laminin alpha protein, sbg417005LAMININ_ALPHA #2.	XX	
XX		SQ	Sequence 3696 AA;
KW	Human; therapy; wound healing disorder; vaccine; cancer; infection;		Query Match
KW	autoimmune disorder; haematopoietic disorder; inflammation; arthritis;		Best Local Similarity 79.6%; Score 15830.5; DB 5; Length 3696;
KW	Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;		Matches 2874; Conservative 279; Mismatches 450; Indels 19; Gaps 9;
KW	multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;		
KW	ischemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;		
KW	depression; cardiovascular disease; myocardial infarction; renal failure;		
KW	respiratory disease; liver disorder; myocardial infarction; spleen disorder;		
KW	type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;	QY	1 DLYCKLVGSPVAGGDPNQTIOGQCDICTAANSNAKHPVNAIDGTERWQSPPLSRGLE 60
KW	hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;	Db	79 DLYCKLVGSPVAGGDPNQTIRGQCDICTAANSNAKHPASNAIDGTERWQSPPLSRGLE 138
KW	nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;	QY	61 YNEVNVNTLDLGOVHVAVLKFANSRPPDLVWLERSTDGHTYQHPQFPASSKRDCLER 120
KW	haemostatic; vulvar; anticonvulsant; antirheumatic; neuroprotective;	Db	139 YNEVNVNTLDLGOVHVAVLKFANSRPPDLVWLERSTDGHTYQHPQFPASSKRDCLER 198
KW	nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;	QY	121 FGPRTLERITQDDVDICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDTKATN 180
XX	allergy; laminin alpha protein.	Db	199 FGPQTLERITRDAACICTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDTKATN 258
OS	Homo sapiens.	QY	181 IRLRLIRNTLLHLMGKALADPTVTRYYSIKDISIGRCVCVCHGADVCDKADPLDPF 240
PN	WO200198342-A1.	Db	259 VLRLEPRTNTLLHLMGKALADPTVTRYYSIKDISIGRCVCVCHGADVCDKADPLDPF 318
PD	27-DEC-2001.	QY	241 RLQACQNTCCGSCDRCCPGFNQPKPATTTSANECQSCNCHGAYDCYYDPEVDRRN 300
XX		Db	319 RLQCTCQNTCCGSCDRCCPGFNQPKPATANSANECQSCNCHGAYDCYYDPEVDRRN 378
XX	22-JUN-2001; 2001WO-US019929.	QY	301 ASQNDNVYGGGYCLDQHHHTGINCERCLPGFFRAPDQPLDSPHVCRDCESDFTG 360
PR	22-JUN-2000; 2000US-0213156P.	Db	379 ASQSLDGYGGGYCLDQHHHTGNCERCLPGFYRPNHLDSPHVCRNCNCSFTG 438
PR	22-JUN-2000; 2000US-0213161P.	QY	361 TCEDLTGRCYCRPNFTGELCAACAEYTDFFHYVPLPSFPHNDTRQVLPAGQIVNDCN 420
XX	(SMIK ) SMITHKLINE BEECHAM CORP.	Db	439 TCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCVPTFS-SSNDTREQLVLPAGQIVNDCS 497
PA	(SMIK ) SMITHKLINE BEECHAM PLC.	QY	421 AAGTQGNACRDPRLGRVCVKNPFRGAHCLCAPGHGSPCHPCQSSRGVANSLCDPS 480
PA	(GLAX ) GLAXO GROUP LTD.	Db	498 AAGTQGNACRDPRLGRVCVKNPFRGAHCLCAPGHGSPCHPCQSSRGVANSLCDPS 557
XX		QY	481 GQCMRTGTFEGDRCDHCAAGYFHPFLCQLCGSCSPAGTLPPEGCDAGRCOCRPGDGHPCD 540
PI	Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;	Db	558 GQCMRTGTFEGDRCDHCAAGYFHPFLCQLCGSCSPAGTLPPEGCDAGRCOCRPGDGHPCD 617
PI	Murdoch PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;	QY	541 RCLPGYHGYPPCHACADPRGALDOQGVGLCHCRPGMTGATCQSCSGFYGFPSRIBC 600
XX	WPI; 2002-139783/18.	Db	618 RCRPGYHGYPPCHACADPRGALDOQGVGLCHCRPGMTGATCQSCSGFYGFPSRIBC 677
DR	N-PSDB; AAD27805.	QY	601 HCSADGSLHTTCDPTTQCCRPVTLGHCDMCPGAYNPPYCEAGSCHPAGLAPALPAL 660
XX		Db	678 HCSAEGSLHAACDPRSGQSCRPVTLGLRCDTVPGAYNPPYCEAGSCHPAGLAPALPAL 737
PT	Novel secreted and membrane-associated polypeptides and polynucleotides	QY	661 PETAPCMCAHVGSPGSCDRCKPGYGLSASNPETGTRCSCDPRGLTGGVTECO-NGQC 719
PT	useful for preventing, ameliorating or correcting dysfunction or disease	Db	738 PEAQVPCMAHVGSPGSCDRCKPGYGLSASNPETGTRCSCDPRGLTGGVTECO-NGQC 797
PT	including diabetes, cancer, hypertension and growth abnormalities.	QY	720 FCKAHVCGKTCACCKGFFGLDYADYFGCRSCRCDDVGGALGQCEPXTGACRCRNTQGP 779
PS	Claim 1; Page 115-122; 138pp; English.	Db	798 FCKAHVCGKTCACCKGFFGLDYADYFGCRSCRCDDVGGALGQCEPXTGACRCRNTQGP 857
CC	The invention relates to secreted and membrane-associated polypeptides	QY	780 TCSPPAKDHYLPDLHMLRLEEAATPEGHVAFNGFNPLEFENFNSWRGVAHMAIOPRIV 839
CC	and polynucleotides. The sequences of the invention are useful in	Db	858 TCSPPAKDHYLPDLHMLRLEEAATPEGHVAFNGFNPLEFENFNSWRGVAHMAIOPRIV 917
CC	diagnostic assays for detecting diseases associated with inappropriate	QY	840 ARNLNTPDILFRLVFRVNRGTSVNGQISVBEGKLSSTCTNCTEQSQVAFPPSTPAF 899
CC	activity or levels of these polynucleotides, and in identifying their	Db	918 ARNLNTPDILFRLVFRVNRGTSVNGQISVBEGKLSSTCTNCTEQSQVAFPPSTPAF 977
CC	agonists and antagonists that are potentially useful in therapy. The		
CC	sequences of the invention are useful as vaccines for inducing		
CC	immunological responses. The sequences of the invention are useful for		
CC	treating cancers, infections, autoimmune disorders, haematopoietic		
CC	disorders, wound healing disorders, cholesterol ester storage disease,		
CC	inflammation, congenital muscular dystrophy, junctional epidermolysis		
CC	bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,		
CC	viral and bacterial infections, Alzheimer's disease, asthma, arthritis,		
CC	allergies, schizophrenia, sbg44245PROA-associated disorders,		
CC	septicemia, psoriasis, inflammatory bowel disease, transplant rejection,		
CC	graft versus host disease, ischaemia, stroke, acute respiratory disease		
CC	syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,		
CC	brain disorders including parasupranuclear palsy, myotonic dystrophy,		
CC	depression, anxiety disorders and sleep disorders, cardiovascular		
CC	diseases including congestive heart failure and myocardial infarction,		
CC	respiratory diseases including chronic obstructive pulmonary disease,		
CC	acute bronchitis and adult respiratory distress syndrome, liver disorders		
CC	including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral		
CC	and non-viral hepatitis, type II diabetes mellitus, renal disease		
CC	including acute and chronic renal failure, glomerulonephritis, Fanconi's		



QY 900 VTVPQGFGEFFVLPNGIWEAGVLLDYYVLLPSTYYBAALQHVRVTEACTYRPSA 959  
Db 978 ITVPQGFGEFFVLPNGIWEAGVLLDYYVLLPSTYYBAALQHVRVTEACTYRPSA 1037  
QY 960 LHSTENCLVYAHLPDGFPSAAGTEALCRHDSNLPRCPCTEQLSPSHPLATCFQSDVDI 1019  
Db 1038 QOSGDNCLLYTHLPDGFPSAAGTEALCRHDSNLPRCPCTEQLSPSHPLATCFQSDVDI 1097  
QY 1020 QLEMAVPOQGVYLVVEYVGEDSHQBMGVAVHTPQAPQGVNLNHPCCYSSILCRSPARD 1079  
Db 1098 QLOVAVPOQGVYLVVEYVGEDSHQBMGVAVHTPQAPQGVNLNHPCCYSSILCRSPARD 1157  
QY 1080 TOHHLAIFHLDSASIRLTAEOAHFFLHSLVTLVPEEFSTFVPRVFCVSHSGTFNPSS 1139  
Db 1158 TQHLAVFHLDSASVRLTAEOARFFLHSLVTLVPEEFSTFVPRVFCVSHSGTFNPSS 1217  
QY 1140 AACLASREPKPPPIILKDCOVLPPLDPLTQOSQLSPGAPPEGPQPPPTAVDPNAEP 1199  
Db 1218 AACLPBRFPKPPPIILRDCOVLPPLDPLTQOSQLSPGAPPEGPQPPPTAVDPNAEP 1277  
QY 1200 TLLRHPQGVTFVTTQVPTLGRYAFLLHGYQPAHFTFPEVLI INAGRVWQGHANASFCPHG 1259  
Db 1278 TLLRHPQGVTFVTTQVPTLGRYAFLLHGYQPAHFTFPEVLI INAGRVWQGHANASFCPHG 1337  
QY 1260 YGCRITVLCEGOMLVDNDELTVTVRVPGRWLMDYVLI VPEDAYSSYLQEEPLDKS 1319  
Db 1338 YGCRITLVCBQGLLDVTHSELIVTVRVPGRWLMDYVLI VPEDAYSSYLQEEPLDKS 1397  
QY 1320 YDFTSHCATQYHISPSSSSFFCRNAATSLSPYNNALPCGCHGVAVSPCTEPPGGQC 1379  
Db 1398 YDFTSHCATQYHISPSSSSFFCRNAATSLSPYNNALPCGCHGVAVSPCTEPPGGQC 1457  
QY 1380 PCRGHVLGRCSRCATYWGPNCRPCDCCGRLCDELTCGICCPRTVPDCLVCOQPSF 1439  
Db 1458 PCRAHVIGRCSRCATYWGPNCRPCDCCGRLCDELTCGICCPRTVPDCLVCOQPSF 1517  
QY 1440 GCHPLVCEBECNCGSGVQBLDPTCDMSGQCRPNVAGRCDTCAPGFYGYPSCRPC 1499  
Db 1518 GCHPLVCEBECNCGSGVQBLDPTCDMSGQCRPNVAGRCDTCAPGFYGYPSCRPC 1577  
QY 1500 DCHAGTMAVSCDPLTQCHCKENVOGSRCDQCRVGTFLSDAANPKGCTRCFCGATERC 1559  
Db 1578 DCHAGTAPGCDPLTQCHCKENVOGSRCDQCRVGTFLSDAANPKGCTRCFCGATERC 1637  
QY 1560 GNSNLARHFEVDMGFWLLSSDROVPHHRPIELHDLR ---SVADTFSELYWQAP 1615  
Db 1638 RSSSYTROEFVDMGFWLLSSDROVPHHRPIELHDLR ---SVADTFSELYWQAP 1697  
QY 1616 PSYLGDRVSSYGGTLYHVLHSETQRGDIPIPYSRDPDVLQGNQMSIAFLAYPPPGQV 1675  
Db 1698 PSYLGDRVSSYGGTLYHVLHSETQRGDIPIPYSRDPDVLQGNQMSIAFLAYPPPGQV 1757  
QY 1676 HRGOLQVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFQTSYSSSLRVLVLEVAS 1735  
Db 1758 HRGOLQVEGNFRHLETHNPVSREELMMVLAGEQLQIRALFQTSYSSSLRVLVLEVAS 1817  
QY 1736 EAGRGPPASNVELCMCPANYRGSQCAPGYRDTKGLFLGRCVPCQCHGSDRCLPGS 1795  
Db 1818 PAGGALASNVELCMCPANYRGSQCAPGYRDTKGLFLGRCVPCQCHGSDRCLPGS 1877  
QY 1796 GICVGCCHNTGEOCERCRPGFYSSDSNPASBCVSCPCPLAVPSNNADGCVLRNGRTQ 1855  
Db 1878 GVCVDCOHNTEGACERCRPGFYSSDSNPASBCVSCPCPLAVPSNNADGCVLRNGRTQ 1936  
QY 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSQPCDSCNGNDPNMI FSDCDDLPTGACRGCLR 1915  
Db 1937 CLCRPGYAGASCERCAPGFFGNPLVLGSSQPCDSCNGNDPNMI FSDCDDLPTGACRGCLR 1996  
QY 1916 HTTQPHCERCAPGYGNALLPGNCTRCDCSPGCTETCDPOSGRCLCKAGVTGRCDCRLE 1975  
Db 1997 HTTQPHCERCAPGYGNALLPGNCTRCDCSPGCTETCDPOSGRCLCKAGVTGRCDCRLE 2056  
QY 1976 GYFGEQOQGRPCACGPAAGKSGSCHPQSGQCHQCPQTTGQPCLECAPGYWGLPEXGCR 2035

Db 2057 GHFGDGGCRPCACGPAAGKSGSCHPQSGQCHQCPQTTGQPCLECAPGYWGLPEXGCR 2116  
QY 2036 CQCPRGHCDHTGCTCPGLSGRCDTCQQHQHVPVPGKPGGHIHCEVCDHCWVLLD 2095  
Db 2117 CQCPRGHCDHTGCTCPGLSGRCDTCQQHQHVPVPGKPGGHIHCEVCDHCWVLLD 2176  
QY 2096 DLEBAGALLPAIRLOLOGINASSAARHLRLNASTIADLOKLRPPPGPYQAQOQL 2155  
Db 2177 DLEBAGALLPAIRLOLOGINASSAARHLRLNASTIADLOKLRPPPGPYQAQOQL 2236  
QY 2156 BQOQISLQDDTERLGSQ-ATGVOGQAGQLDTESTILGRAQKLLSVRAVGRALNELASR 2214  
Db 2237 BQOQISLQDDTERLGSQ-ATGVOGQAGQLDTESTILGRAQKLLSVRAVGRALNELASR 2296  
QY 2215 MGQSPGDALVPSGEORLWALAEVERLLWMTDRLDGAQAVABAEALAEORLWVQEQ 2274  
Db 2297 TCHLGLANASAPSGEQLRTILAEVERLLWMTDRLDGAQAVABAEALAEORLWVQEQ 2356  
QY 2275 LTSFWEENQSLATHIRDOQAQYESGLMDREALNOAVNTTREAEBELNSRQERKEALQW 2334  
Db 2357 LSSWEEENQSLATHIRDOQAQYESGLMDREALNOAVNTTREAEBELNSRQERKEALQW 2416  
QY 2335 KOELSDQNATLKATLOAASLILGHVSBELQOIQOAKEDLEHLAASLDGAWTPLLKRWQAF 2394  
Db 2417 KOELSDQNATLKATLOAASLILGHVSBELQOIQOAKEDLEHLAASLDGAWTPLLKRWQAF 2476  
QY 2395 SPASKVDLVEAAEAHAKLNQALNLSGIILGINODRFTQRAVEASNAVSSILQAVQAA 2454  
Db 2477 SPASKVDLVEAAEAHAKLNQALNLSGIILGINODRFTQRAVEASNAVSSILQAVQAA 2536  
QY 2455 EDAAGQALQADHTWATVVRQGLVDRQAQALLANSTALEAMQEQORLGLVWAAQOGART 2514  
Db 2537 EDAAGQALQADHTWATVVRQGLVDRQAQALLANSTALEAMQEQORLGLVWAAQOGART 2596  
QY 2515 QLNHWARKNOALAQIQEQAQAMLDSETSEKTAHAKAVAAEALSTATHVQSOLOQGMOK 2574  
Db 2597 QLRDVRACKDQLEAHQIAQAQAVLMDTETSHTAHAKAVAAEALSTATHVQSOLOQGMOK 2656  
QY 2575 NVERWQSOGLQOGLQSDVERDASSVSTLEKTLQALLAKSLRLENGRHNASLALSAN 2634  
Db 2657 NVERWQSOGLQOGLQSDVERDASSVSTLEKTLQALLAKSLRLENGRHNASLALSAN 2716  
QY 2635 IGRVTKLIAQARSAASKVVKVMKNGSGVLRPRDLADLAAYTALKKHEIQTSPVPAPEP 2694  
Db 2717 IGRVTKLIAQARSAASKVVKVMKNGSGVLRPRDLADLAAYTALKKHEIQTSPVPAPEP 2774  
QY 2695 GKNVGDHFLVWGRQATGDMYVSLNOKVHWYRLGKAGPTTSLIDENTIGEQAFAVSI 2754  
Db 2775 GKNVGDHFLVWGRQATGDMYVSLNOKVHWYRLGKAGPTTSLIDENTIGEQAFAVSI 2834  
QY 2755 DRTLOFGHMSVTVEKQWVHEIKGDTVAPSGEGLNLHPDDFVFTVGGYPSNFTPEPLRF 2814  
Db 2835 DRTLOFGHMSVTVEKQWVHEIKGDTVAPSGEGLNLHPDDFVFTVGGYPSNFTPEPLRF 2894  
QY 2815 PLYLGCIEWETLNEEVSILNFEOTFMLDTPVAPKARSKATGDPWLTDSYLDGSGFAR 2874  
Db 2895 PLYLGCIEWETLNEEVSILNFEOTFMLDTPVAPKARSKATGDPWLTDSYLDGSGFAR 2954  
QY 2875 ISFEQFQNTKRFQOELRLVSYNGIIIFPLKQESQFCLAVQEGTFLVIFYDPGSLKXADP 2934  
Db 2955 ISFEQFQNTKRFQOELRLVSYNGIIIFPLKQESQFCLAVQEGTFLVIFYDPGSLKXADP 3014  
QY 2935 LOPPOALTAASKATQVFLLAGNRKRLVVERATVFSVDDNNMLEMADAVYLGVPPEQL 2994  
Db 3015 LOPPOALTAASKATQVFLLAGNRKRLVVERATVFSVDDNNMLEMADAVYLGVPPEQL 3074  
QY 2995 PLSLRQLPSPGSGVRGCIKGIKALGVYDLKRLNTTGISFCGTADLLVGRMTFHGHGFL 3054  
Db 3075 PLSLRQLPSPGSGVRGCIKGIKALGVYDLKRLNTTGISFCGTADLLVGRMTFHGHGFL 3134  
QY 3055 PIALPDVAPITEVTVSGFGFGTQDNLLYTRTSPDGPQVSLREGHVTFLRPMQVETQ 3114

Db 3135 RLALSNVAPLTGNVYSGFPHSAQDSALLYRASPDLGCQVSLQGRVSLQLLRTEVKQT 3194  
 Qy 3115 RVFADGAPHYAFVSNVTGWLYYDDQLQVYKSHERTTLMLOPEPSPRLILGLPVSG 3174  
 Db 3195 AGFADGAPHYAFVSNVTGWLYYDDQLQVYKSHERTTLMLOPEPSPRLILGLPVSG 3254  
 Qy 3175 TFFNFSGICSNVFORLGPORVDFLQNMGSVNVSGCTPAQAIETSS-----RATAQ 3227  
 Db 3255 TIYFSGICSNVFORLGPORVDFLQNMGSVNVSGCTPAQAIETSS-----RATAQ 3314  
 Qy 3228 KVSRRSOPSDLACTTTPMLPGTTODAYQFGGPLPSYLFQVGTSPSHRNRLHLSMLVRPH 3287  
 Db 3315 KASRRSQFARHPACMLPPLRLTRDSYQFGSLSSHLEFVIGILARHNPFLSMHVLPR 3374  
 Qy 3288 AASGGLLSTAPMSGRSPSLVFLNHHGFVAQTESGPGRLQVQSGRQSHRAGQWHRVSRV 3347  
 Db 3375 -SSRGLLFTALRPSPSLALFLSNGHFVLAQMEGLGTRLRAQSRQRSGRWKHSVRV 3433  
 Qy 3348 QMOQIQLVVDGSGTWSQKALHRRVPRPPOPYTLVSGGLPASSYSKLPVSVGFSGLK 3407  
 Db 3434 EKNRILLVTDGARAWSQEGPHRQHGAEHPQPHTLFVGGLPASSHSSKLPVTVGFGCVK 3493  
 Qy 3408 KLOLDKQPLRPTOMGVTPCVSGPLEDGFPGSEGVVTLLEPKAMVYVSLERPL 3467  
 Db 3494 RLRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLULPCAILPDVGLLEVRPL 3553  
 Qy 3468 AAAGLIFELGALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRMHRVAVIM 3526  
 Db 3554 AVTGLIFHLGQARTPYQLQVTEKQLLRADGAGEFSTVTPSVLCLDQWHLAVMK 3613  
 Qy 3527 GRDTLRLEVDQSNHTTGRLESAGSPALLHLSLPSKSTARPELPAVYGCRLKLLING 3586  
 Db 3614 SGNVLRLEVDQSNHTVGPLAAAGAPAPLYLGLPEPMAVQPPWPPAYCCMRRLAVNR 3673  
 Qy 3587 APVNVTSVQIQGAVGMGCPFS 3608  
 Db 3674 SPVATRSVEVHGAGSGCPA 3695  
 RESULT 5  
 ID AAE17309  
 AC AAE17309  
 XX AAE17309;  
 XX 18-APR-2002 (first entry)  
 DE Human laminin alpha protein, sbg417005LAMININ\_ALPHA #1.  
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;  
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;  
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;  
 KW depression; cardiovascular disease; myocardial infarction; renal failure;  
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;  
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;  
 KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;  
 KW neotrophic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;  
 KW haemostatic; vulnerability; anticonvulsant; antineuritic; neuroprotective;  
 KW nephrotropic; hypertensive; vasotrophic; cytostatic; cerebroprotective;  
 KW allergy; laminin alpha protein.  
 OS Homo sapiens.  
 XX  
 XX WO200198342-A1.  
 XX  
 XX 27-DEC-2001.  
 XX  
 XX 22-JUN-2001; 2001WO-US019929.  
 XX  
 XX 22-JUN-2000; 2000US-0213156P.  
 PR  
 XX 22-JUN-2000; 2000US-0213161P.  
 PR

XX (SMIX ) SMITHKLINE BEECHAM CORP.  
 PA (SMIX ) SMITHKLINE BEECHAM PLC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;  
 PI Murdock PR, Smith RE, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX WPI: 2002-139783/18.  
 DR N-PSDB; AAD27804.  
 XX  
 XX Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT useful for preventing, ameliorating or correcting dysfunction or disease  
 PT including diabetes, cancer, hypertension and growth abnormalities.  
 PS Claim 1; Page 107-114; 138pp; English.  
 XX  
 CC The invention relates to secreted and membrane-associated polypeptides  
 CC and polynucleotides. The sequences of the invention are useful in  
 CC diagnostic assays for detecting diseases associated with inappropriate  
 CC activity or levels of these polynucleotides, and in identifying their  
 CC agonists and antagonists that are potentially useful in therapy. The  
 CC sequences of the invention are useful as vaccines for inducing  
 CC immunological response. The sequences of the invention are useful for  
 CC treating cancers, infections, autoimmune disorders, haematopoietic  
 CC disorders, wound healing disorders, cholesterol ester storage disease,  
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis  
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
 CC allergies, schizophrenia, sbg44245PQA-associated disorders,  
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease,  
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,  
 CC depression, anxiety disorders and sleep disorders, cardiovascular  
 CC diseases including congestive heart failure and myocardial infarction,  
 CC respiratory diseases including chronic obstructive pulmonary disease,  
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
 CC and tendinitis, gastrointestinal diseases including intestinal  
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
 CC reproductive diseases including low testosterone and male infertility.  
 CC The present sequence is human laminin alpha protein  
 XX SQ Sequence 3705 AA;

Query Match 79.6%; Score 15815; DB 5; Length 3705;  
 Best Local Similarity 79.1%; Pred. No. 0;  
 Matches 2873; Conservative 279; Mismatches 451; Indels 28; Gaps 9;  
 Qy 1 DLYCKLVGPGVAGGPNQTIQQYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 60  
 Db 79 DLYCKLVGPGVAGGPNQTIQQYCDICTAANSNKAHPVSNADIGTERWQSPPLSRGLE 138  
 Qy 61 YNEVNVTLDLGVFHVAVYVLIKFNANSPRDLVWLERSTDFGHTYQWQFFASSKRDCLER 120  
 Db 139 YNEVNVTLDLGVFHVAVYVLIKFNANSPRDLVWLERSTDFGHTYQWQFFASSKRDCLER 198  
 Qy 121 FGPRTLERITQDDVICTTEYSRIVPLENGETIVSLVNGRPGALNFSPLRDETKATN 180  
 Db 199 FGPRTLERITRDDAAICTTEYSRIVPLENGETIVSLVNGRPGAMNFSPLRDETKATN 258  
 Qy 181 IRLRLRFTNTLLGHLGKALRDPVTTRRYVYVYIKDISIGRCVCHGHADVCDKADPLDFP 240  
 Db 259 VRLRLRFTNTLLGHLGKALRDPVTTRRYVYVYIKDISIGRCVCHGHADVCDKADPLDFP 318  
 Qy 241 RLQCAQHNTCCGSDRCPCGPNQPKPATTTDSANECSNCHGHAYDCYDPEVDRN 300  
 Db 319 RLQCTQHNTCCGTCDCRCPCGPNQPKPATTTDSANECSNCHGHAYDCYDPEVDRN 378



Db 2537 RILCAVQAEDAQAQALQADHWTATVVRGVLVDRQAQLLANSTALEAMLEQEQRLGLV 2596  
Qy 2506 QGRIOAGIOLHNWARKNOLAQIOEAQAMLANDTSETSEKIAHAKAAVAEALSTATHV 2565  
Db 2597 WAALQAGARTQLRDYRAKQDQLEAHIOAAQAMLANDTDETSKKIAHAKAAVAEAQDTATRV 2656  
Qy 2566 QSOLOGMOKNVERWQSLGGLOGQLSVERDASSVSTLEKTLPLLAKLSLENRNVH 2625  
Db 2657 QSOLOQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSLENRNVH 2716  
Qy 2626 NASIALSANTGRVKLIAQARSAAASKVKYSMKNGRSGVLRPRDLADLAAYTALKFHI 2685  
Db 2717 NASIALSASTGRVRELIAQARGAASKVKYKPMKNGRSGVQLRTPRDLADLAAYTALKFYL 2776  
Qy 2686 QSPVAPBPCKNTGDHPLVYMGSRQATGDYGVYSLRNOKVHWYRLGKAGPTTSLSDENI 2745  
Db 2777 QG--PEPEQCGTREDRVTMTNGSRQATGDYGVYSLRNOKVHWYRLGKAGPAVLSDENI 2834  
Qy 2746 GEOFAAASIDRTLQFGHMSVTVKQMVHEIKGDTVAPGSEGLNLNHPDDFVYVGYGYSN 2805  
Db 2835 GEOFAAASVSLDRTLQFGHMSVTVKQMVHEIKGDTVAPGSEGLNLNHPDDFVYVGYGYSN 2894  
Qy 2806 FTFPEPLRFGYLGCIEMETINEEVSILYNEFOTFMDTAVDKPCARSKATGDPMLTDCS 2865  
Db 2895 FTFPEPLRFGYLGCIEMETINEEVSILYNEFOTFMDTAVDKPCARSKATGDPMLTDCS 2954  
Qy 2866 YLDGSGFARISFEKQFQNTKRFDOELRLVSYNGIIFELKQESFCLIAVOEGLVLIFYDF 2925  
Db 2955 YLDGTGFAISFSDQISTTKFQEOELRLVSYNGIIFELKQESFCLIAVOEGLVLIFYDF 3014  
Qy 2926 GSGLUKADPPOPPALFAAKAIOVFLLAGNRKVLVRERATVFSVDQNMLEMDADAY 2985  
Db 3015 GAGLUKAVPLQPPPLTASAKAIQVFLGGRKVLVRERATVFSVDQNMLEMDADAY 3074  
Qy 2986 LGGVPPQLPLSLRQLPSPGSGVRGCIKGKALGVYDLKRLNTTGISFQCTADLLVGR 3045  
Db 3075 LGGVPPQLPLSLRQLPSPGSGVRGCIKGKALGVYDLKRLNTTGVSACTADLLVGR 3134  
Qy 3046 MTFHGHGFLPALPDVAPITTEVYVSGFGRGTQNNLLYRTSPDGPYQVSLREGHTLR 3105  
Db 3135 MTFHGHGFLRALSNVAPLTCNVYSGFGRGTQNNLLYRTSPDGPYQVSLREGHTLR 3194  
Qy 3106 FMNOEVEVTFADGAPHYVAFYVSNVTVGMVLYDDQLQVSKHRTTTPMLQLOPPEPSRL 3165  
Db 3195 LLREVTKTQAGFADGAPHYVAFYVSNVTVGMVLYDDQLQVSKHRTTTPMLQLOPPEPSRL 3254  
Qy 3166 LLGLPVSQTFPHNFGSGCISNVFVQRLRQPVFPLHQMNGSVNVVSGCTPAQIETS--- 3222  
Db 3255 LLGLPVSQTFPHNFGSGCISNVFVQRLRQPVFPLHQMNGSVNVVSGCTPAQIETS--- 3314  
Qy 3223 ----RATAQVSRRSRQPSQDLACTTLPCTIGDAYQFGGLPSYLOFVGISSPHENRL 3278  
Db 3315 PRGLQATARKASRRSRQARHPACMLPPLHRTTTRDSYQFGGSLSHLEFVGIILARHNWP 3374  
Qy 3279 HLSMLVRPHAAASQGLLLSTAPMSGRSPLVFLNMGHFVAQTEGPPRLQVQSRQHSRAG 3338  
Db 3375 SLSMHVLP--SSRGLLFTARLRPGSPSLAFLSNHGFVAQMEGLGTRLAQRQSRSPG 3433  
Qy 3339 QWHRVSVWNGMQQLVVDGSGTQVSKALHRVPRAPRQPYTLVUGCLPASSVSKLPV 3398  
Db 3434 RWHKYSVRWEKNRILVTDGARAWSQEHPRHQGHQHPQHTLVFVGLFPASSHSSKLPV 3493  
Qy 3399 SVGFSGCLKLQLODKQPLRTPTQMVVTPCVSGPLEDGLFPFGSGGVITLDPGATLPDV 3458  
Db 3494 TVGFSGGVRLRLHGRPLGATFRMAGVTPTCLGLEAGLFPFGSGGVITLDPGATLPDV 3553  
Qy 3459 SLELMRPLAAGLIFHLGQALATPYMQLKVLTSQVLLQANDGAGEFSTWTPK-LCDG 3517  
Db 3554 GLELEVRPLAVTGILFHLGQARTPPYQLQVTERQVLLRADDGAGEFSTVTRPSVLCDG 3613  
Qy 3518 EWHRVAVTMGRDTRLELVDTOSNHTTGRLEPSLAGSPALLHGLSPKSSATARPPELAYRG 3577

3614 QWHLAVMKSQNVLRLEVDQAQSNHTVGLFLAAAGAPAPLYLGLPBPMAVQPMFPAYCG 3673  
Qy 3578 CLRKLLINGAPVNTVATVQIOGAVGMGCPSS 3608  
Db 3674 CMRLAVNRSPVAMTRSVVEHVGASGCPA 3704

RESULT 6  
ABB09501  
ID ABB09501 standard; protein; 3600 AA.  
XX ABB09501;  
AC ABB09501;  
XX 01-NOV-2002 (first entry)  
XX Human laminin alpha-5-like NOV1a protein, SEQ ID NO:2.  
DE Human; NOVX; neurological disorder; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; cancer; immune disorder; allergy;  
KW addiction; tuberculous sclerosis; cancer; immune disorder; diabetes;  
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;  
KW thymoiditis; cardiovascular disease; hypertension; reproductive disorder;  
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;  
KW pancreatic cirrhosis; glomerular endotheliosis; bacterial infection;  
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;  
KW atherosclerosis; cell signal processing-related disorder;  
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;  
KW antiinflammatory; immunosuppressive; analgesic; antihypertensive;  
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;  
KW differentiation; proliferation; motility; haematopoiesis; wound healing;  
KW angiogenesis; forensic biology; transgenic animal; drug screening;  
KW gene therapy; NOV1a; laminin alpha-5-like; chromosome 20.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..14  
FT Protein /label= signal\_peptide  
FT Protein 15..3600  
FT Protein /note= "Mature NOV1a protein"  
XX WO200253742-A2.  
XX 11-JUL-2002.  
XX 07-JAN-2002; 2002WO-US000375.  
XX 05-JAN-2001; 2001US-0260018P.  
XX 08-JAN-2001; 2001US-0260360P.  
XX 28-FEB-2001; 2001US-0272411P.  
XX 02-MAR-2001; 2001US-0272817P.  
XX 05-JUL-2001; 2001US-0303231P.  
XX 12-JUL-2001; 2001US-0305060P.  
XX 10-SEP-2001; 2001US-0318405P.  
XX 12-SEP-2001; 2001US-0318700P.  
XX 04-JAN-2002; 2002US-00037417.  
XX (CURA-) CURAGEN CORP.  
XX Kekuda R, Alsbrook JP, Tchernev VT, Liu X, Spytek KA;  
XX Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;  
XX Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;  
XX Rotenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;  
XX Padigar M, Taupier RJ, Miller CE, Eisen A;  
XX WPI; 2002-583619/62.  
XX N-PSDB; ABQ93879.  
XX Novel polypeptides and nucleic acids homologous to transmembrane  
XX receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
XX treating cancer, atherosclerosis, neurological, skin and autoimmune  
XX disorders.

PS	Claim 1c; Page 14-15; 323pp; English.				
XX	The invention relates to 24 novel human proteins designated NOV1-NOV14				
CC	(AB09501-AB09524), collectively referred to as NOVX proteins, and				
CC	nucleic acids encoding them (AB093879-AB093902). NOVX proteins, and				
CC	nucleotides are useful in the treatment, diagnosis or prevention of NOVX-				
CC	associated disorders or in the manufacture of a medicament for treating				
CC	such disorders, with specific applications described for each of the 24				
CC	NOVX proteins, based on their homology to known proteins. Various				
CC	disorders are associated with NOVX proteins including neurological				
CC	disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),				
CC	pain, behavioural disorders, addiction, tubercular sclerosis, cancers				
CC	(e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders				
CC	(e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,				
CC	various forms of arthritis, diabetes, thyroiditis, cardiovascular disease				
CC	(e.g., hypertension), reproductive disorders, endometriosis,				
CC	incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,				
CC	cirrhosis, glomerular endoteliosis, polycystic kidney disease, endocrine				
CC	disorders, obesity, bacterial infections and particularly cardiomyopathy,				
CC	atherosclerosis, cell signal processing-related disorders and disorders				
CC	of metabolic pathway regulation. NOVX nucleic acids and polypeptides may				
CC	be used to identify cellular receptors or downstream effectors which				
CC	binds to a NOVX protein, and are also useful as targets for the				
CC	identification of small molecules that modulate or inhibit processes such				
CC	as neurogenesis, cell differentiation, cell motility, cellular				
CC	proliferation, haematopoiesis, wound healing and angiogenesis. NOVX				
CC	nucleic acid sequences can be used to identify a cell or tissue type and				
CC	are useful as a source of primers or probes for forensic biology and for				
CC	identifying and cloning NOVX homologues in other cell types. Cells				
CC	comprising NOVX nucleic acids are useful for producing non-human				
CC	transgenic animals which are useful for studying the function and				
CC	activity of NOVX proteins and for identifying and evaluating modulators				
CC	of NOVX activity. The present sequence represents the laminin alpha-5-				
CC	like protein NOV1a. The gene encoding NOV1a is located on chromosome 20				
XX					
SQ	Sequence 3600 AA;				
	Query Match 74.3%; Score 14771; DB 5; Length 3600;				
	Best Local Similarity 74.8%; Pred. No. 0;				
	Matches 2739; Conservative 275; Mismatches 472; Indels 178; Gaps 26;				
QY	1 DLYCKLVGFGVAGGDPNQTIOGYDCICTAANSKNAHPVNAIDGTERWQSPPLRSGLE 60				
DB	58 DLYCKLVGFGVAGGDPNQTIOGYDCICTAANSKNAHPVNAIDGTERWQSPPLRSGLE 117				
QY	61 YNEVNVTLDLGVHAYVYLIFKANSRPDLVLERSTDFGTYQFWQFFAASKRDCLER 120				
DB	118 YNEVNVTLDLGVHAYVYLIFKANSRPDLVLERSTDFGTYQFWQFFAASKRDCLER 177				
QY	121 FGPRTLERITODDDVICTEYRIVPLENGEIVWSLVNRPDALNFSYSPILLRDTKATN 180				
DB	178 FGPQTLERITRDAAICTEYRIVPLENGEIVWSLVNRPDALNFSYSPILLRDTKATN 237				
QY	181 IRLRFLRITNTLLGHLGKALRDPVTTRRYYSIKDISIGRCVCHGHADVCDAKPLDPF 240				
DB	238 VLRFLRITNTLLGHLGKALRDPVTTRRYYSIKDISIGRCVCHGHADVCDAKPLDPF 297				
QY	241 RLQCAQHNTCGGSDRCPCGNQOPFKPATDTSANECQSNCHGHAYDCYYDPEVDRRN 300				
DB	298 RLQCTQHNTCGGTCDRCPCGNQOPFKPATDTSANECQ-CBECYGHATDCYYDPEVDRR 356				
QY	301 ASQNDQNVVGGGVCLDCOHHHTTGNCERCLPGFFRAPDQLDSPHVCRPCDCSDFTDG 360				
DB	357 ASQSLDGTVGGGVCLDCOHHHTTGNCERCLPGFFRSPNHLDSPHVCRGNCESDFTDG 416				
QY	361 TCEDLTGRCYCRPNFTGELCAAEGYTDFFHCYPLPSPPHNDTEQVLPAGQIVNCDN 420				
DB	417 TCEDLTGRCYCRPNFSGERCDCVCAEGTGFPSY-REHLPGNDTEQVLPAGQIVSCDCS 475				
QY	421 AAGTQGNACKDPRLRGCKENFPGACELCAPGHFSPCHPCOCSS---PGVANSLCD 477				
DB	476 AAGTQGNACKDPRVRGRCLCKENFGOTHCELCAFGYFGGC-PASVPALEWPMPTAVTLTQ 534				
QY	478 PESQCMCRGTG-----FSGDRCDHCALOYFHFFPL-CQLCGGSPAGTLPEGCDDEAG 526				
DB	535 ASAGAENASRGPHVIAVPPATFTLSASH-----PLRSVAVCGGSPAGTLPEGCDDEAG 586				
QY	527 RCQCRCPDFDCHDCLPLGYPVDPCHACACDPRGALDQOCGVGGLCHCRPGMTGATCOE 586				
DB	587 RCLQCPFAFGHCDRCRPGVYHGFNCACTCDPRGALDQ-CGAGGLCHCRPGYTGATCOE 646				
QY	587 CSPGFYGFPCIPCHCSADGSLHTTC-----DPTTGQCRCP-RVTGL-H-CMVCVPGAYN 639				
DB	647 CSPGFHGFPS-----CPATALLKAPCTQPTVPGVSAAGFVRGCGVTHVCPVPTTSPTA 701				
QY	640 FPYCEAGSCHPAGLAPANPALPETQAPCMRAHVEGPSDCRCKPGVWGLSASNEPGCTRC 699				
DB	702 KPLFTAGSCHPAGLAPVDPALPEVSPCMCRANHVEGPSDCRCKPGVWGLSASNEPGCTRC 761				
QY	700 SCDPRGLTGGVTCQNGQCFCAHVGKTCACAKGQFFGLDYADYFGCRSCRCDVGGAL 759				
DB	762 SCDLRGLTGGVAECQGTGQCFCKPHVCGQACASKDGGFFGLDQADYFGCRSCRCIDGAL 821				
QY	760 GQCEPTGTACRCRPNTOGTCSBPADKHVLPDLHMRLELEBAATPEGHAVFEGNPLE 819				
DB	822 GQCEPTGTACRCRPNTOGTCSBPADKHVLPDLHMRLELEBAATPEGHAVFEGNPLE 881				
QY	820 FENFMRGYAHMAIQPRIVARLNVTSFDFLRLVFRVYVNRGSTSVNGQISVREBGLSSC 879				
DB	882 FENFMRGYAHMAIQPRIVARLNVTSFDFLRLVFRVYVNRGAMSVSRVREGRSATC 941				
QY	880 TNCTEQSQVAFPPSTEPAFVTVQPGFGFPVNLPGINALLVEAGVLLDYVLLPSTY 939				
DB	942 ANCTAQSQVAFPPSTEPAFVTVQPGFGFPVNLPGINALLVEAGVLLDYVLLPSTY 1001				
QY	940 YEALLQHRVTEACTVAPSALHSTENCLVYAHPLDGFPSAAGTEALCRHNSLPRCPT 999				
DB	1002 YEALLQHRVTEACTVAPSALHSTENCLVYAHPLDGFPSAAGTEALCRHNSLPRCPT 1061				
QY	1000 EQLSPSHPLATCFGSDVDIOLEMAVPOQYVLYVEYVEDSHQEMGVAVHTPOAPAQQ 1059				
DB	1062 EQLSPSHPLATCFGSDVDIOLEMAVPOQYVLYVEYVEDSHQEMGVAVHTPOAPAQQ 1121				
QY	1060 GVLNLHPCYSSILCRSPARDTQHHLAIFHLDSEASIRLTAEQAHFHLSVTLVPEBFT 1119				
DB	1122 GLLSHLCLTSTLCRGRTARDQHLAVFHLDSASVLTAEQARFFLGHVTLVPEBFP 1181				
QY	1120 EFVEPRVFCVSSHGTENPSSAACLAGRFPKPPQFIILKDCQVLPPLPDLPLTQSQELSPG 1179				
DB	1182 EFVEPRVFCVSSHGTENPSSAACLAGRFPKPPQFIILKDCQVLPPLPDLPLTQSQELSPG 1241				
QY	1180 APPEGPQRPPTAVDPNAEPTLHHPQGTVFTTQVPTLGRYAFLLHGYQVHPSFPEVE 1239				
DB	1242 MSPAGPRPPTAVDPNAEPTLHHPQGTVFTTQVPTLGRYAFLLHGYQVHPSFPEVE 1301				
QY	1240 LINGGRIWQGHANASFCFHGYGCRITLVLCBQTMLDVTDNELTIVTVRVPGRWMLDYVL 1299				
DB	1302 LINAGRVWQGHANASFCFHGYGCRITLVLCBQTMLDVTDNELTIVTVRVPGRWMLDYVL 1361				
QY	1300 IVPEDAYSYSYLOEPLDKSYDFISHCATQGYHISFSSSPFCFNAATSLSYFNNGALP 1359				
DB	1362 WPENVYSFYGLREEPLDKSYDFISHCAAGGYHISFSSSLFCRNAASLSLFYNNGARP 1421				
QY	1360 CGCHEVAVSPTCEPFGGQPCRGHVGRCSCATGYWGFPCNCRPCDCGALCDELITGO 1419				
DB	1422 CGCHEVAVSPTCEPFGGQPCRGHVGRCSCATGYWGFPCNCRPCDCGALCDELITGO 1481				
QY	1420 CIPPTVTPDCLVQCPQSPFGCHPLVGCBECSGPGVQBELTDPDTCMDMSGQCRCPNVA 1479				
DB	1482 CIPPTVTPDCLVQCPQSPFGCHPLVGCBECSGPGVQBELTDPDTCMDMSGQCRCPNVA 1541				
QY	1480 GRCDTCAPGFYGPSCRPCDCHEAGTMAVSCDPLTGQCHCKENVOGRSCDQCRVTFSL 1539				
DB	1542 GRCDTCAPGFYGPSCRPCDCHEAGTMAVSCDPLTGQCHCKENVOGRSCDQCRVTFSL 1601				
QY	1540 DAANPKGCTKCFGFGATRCGNSNLARHFDVMEGVWLLSSDRQVVPHEHRPEIELLHAD 1599				

1602 DAAMFKCTRCFCGATERCRSSYTHQBFVDMEGVLLSTDRQVPHRQPTMELRAD 1661  
1600 LR-----SVADTFSELYWQAPSPSYLGDVSYSGTGLHYELHSETORGBDIFIPYBSRPDVL 1655  
1662 LRHVPEAVPEAFPELYWQAPSPSYLGDVSYSGTGLHYELHSETORGBDIFIPYBSRPDVL 1721  
1656 QGNQMSAFLEAYPPQVHRGQLOLVEGNFRLETHNPVSREELMMVLAGELOQIRA 1715  
1722 QGNQMSITFLEPAYPTFGHVRHGQLOLVEGNFRLETHNPVSREELMMVLAGELOQIRA 1781  
1716 LFSQSSSVSLRRVYVLEVASAGPPASNVELCMCFANVYRGDSQCECAPYYRDTKGLF 1775  
1782 LFSQISSAVFLRRVALEVASPAGOCALASNVELCLCPASVYRGDSQCECAPFYRDVKGLF 1841  
1776 LGRVCPCQCHSDRCLPGSGICVGCCHNTEGOCERCRCRPFVSSDPSNPASCVSCPCP 1835  
1842 LGRVCPCQCHSDRCLPGSGVCV-COHNTGAEHCRCQAGFVSS-RDDPSACVSCPCP 1899  
1836 LAVPSNNFADGCVLRNGRTQCLCRPGYAGASCERCAPFGFNPLVLGSSQCPDCSNGD 1895  
1900 LSVFESN-----RCAPGFGFNPLVLGSSQCPDCSNGD 1932  
1896 PNMTFSDCDPLTGACRGLRHTTTPHCERCAPFGYGNALLPGNCTRCDCSPCCGTETCDPQ 1955  
1933 PNLLFSDCDPLTGACRGLRHTTTPRCBEICAPFGYGNALLPGNCTRCDCSTPCGTEACDPH 1992  
1956 SGRLCLKAGVTGQRCDRLEGYFGFEGCQCRPCACGPAAGKSECHPQSQCHCQCPGTTG 2015  
1993 SGHCLCLKAGVTGRCDCRQEGHFGDGGCRPCACGPAAGKSECHPQSQCHCQCPGTTG 2052  
2016 PQCLECAPYWGKPEKGRCCRCQPRGHCDPTHGCTCPGGLSBERCDTCSQHQVVPKG 2075  
2053 PQCRECAPYWGKPEKGRCCRCQPRGHCDPTHGCTCPGGLSBERCDTCSQHQVVPKG 2112  
2076 PGHGIHCEVCHDCVLLDDLEBAGALLPAIRELOGINASSAAWALHRLNASTADL- 2134  
2113 PVGSHIHEVCHDCVLLDDLEBAGALLPAIHEOLGINASSAAWALHRLNASTADLQ 2172  
2135 -----QSKLRPPGPRVQAQOQTLLEQOQSIQOQTERLGSQ 2172  
2173 VLSVLAFFPPQGPVQAFTRFLPQSLRSPGLPRHETAQOQLEVLQOQSTSLF-----PQ 2225  
2173 ATGVQQAQGLDWTETSLGSAQKLESVRAVGALNELASRMQCGSPGALVPSGEQLR 2232  
2226 AVGTRDQASQQLATGATEATLGHAKTLAAIRAVDRTLSELMSQTHGLANASPSGEQLL 2285  
2233 WALLAEVERLLWDMTRDLGAQGAVAEALABAQRLMARVQEQLTSEFWEENQSLATHIRDQ 2292  
2286 RTLAEVERLLWEMEARDLGAPQAAAEALAAQARVLARVQEQLSLSEENQALATQTRDR 2345  
2293 LAQTESGLMDLREALNQAVNTTREAELHNSHQERVKEALQKQELSDNATLKATLQAA 2352  
2346 LAQHEAGLMDLREALNRAVDATREAQELNSRQERLEALQKQELSRDNATLQATLHAA 2405  
2353 SLILGHVSEILQGIQDAK-EDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVEAAEABA 2411  
2406 RDTLASVFRLLLEGISPLKQELERLASLDGARTPLLQRMQTFSPAGSKLRLVEAAEABA 2465  
2412 QKINQALNLSGIIILGINQDRFIORAVEASNAYSIILOAVQAAADAAQALROASRTWEM 2471  
2466 QOLGQALNLS-IILDVNQDELTORATEASNAYSRILOAVQAAADAAQALQOQADHTWOT 2524  
2472 VVORGLAAGAROLLANSALSETILGHQGRIGLAQ-----GRLOAGIQLHNVWARKNQL 2526  
2525 VVORGLVDRQAQOLLANSALSEAMLOEQORLGLCEWPMGALRPAGTQLRDVYAKDQL 2584  
2527 AAQIQEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSQLOQMKNVERWQSLGGL 2586  
2585 EAHIAQAQAMLAMDTGETSKIAHAKAVAAEADQATATRVQSQLOQMKNVERWQOYEG 2644  
2587 QOQDLSQVERDASSSVSTLEKTLPLQAKLSLENRGVHNASLALSANIGRVKLIQAAR 2646

2645 RQDLGQAVLDAGSAVSTLEKTLPLQAKLSLENRGVHNASLALSANIGRVKLIQAAR 2704  
2647 SAASK-VKVSXMKFNGRSGVRLRPDRDLADLAAYTALKFHQSPVAPAPBPBGKNTGDHFVLY 2705  
2705 GAASKVVKVPKFNKRGSGVRLRPDRDLADLAAYTALKFHQSPVAPAPBPBGKNTGDHFVLY 2762  
2706 MGSROATGDYMGVSLRNQKHWYVRLKAGAGTTLSIDENIGEOFAAIVSIDRTLQFGHMSV 2765  
2763 MGSROATGDYMGVSLRDKKVHWYVQLGEGAGPAVLSIDEDIGEOFAAIVSIDRTLQFGHMSV 2822  
2766 TVEKOMVHEIKGDTVAPGSEGLNHPDDFVYVGGYPSNFTPEPRFRFCYGLGCIEMET 2825  
2823 TVERQMIQETGDTVAPGAGELNHPDDFVYVGGYPSNFTPEPRFRFCYGLGCIEMET 2882  
2826 LNEEVVSYLYNEFEQTFMFLDTAVDKPCARSKATGDPWLTDGSLDGSFGARISFEKQFSNTK 2885  
2883 LNEEVVSYLYNEFEQTFMFLDTAVDKPCARSKATGDPWLTDGSLDGSFGARISFEKQFSNTK 2942  
2886 RPDQELRLVSYNGIIFFLKQESQFLCLAVQSGTLVLFVDFGSLGKKADPQPPQALTAAS 2945  
2943 RPEQELRLVSYNGIIFFLKQESQFLCLAVQSGTLVLFVDFGSLGKKADPQPPQALTAAS 3002  
2946 KAIQVFLLAGNRKRVLVRERATVFSVDQDNMLEMADAYLGGVPPPEQLPSLRLQFPSPG 3005  
3003 KAIQVFLLAGNRKRVLVRERATVFSVDQDNMLEMADAYLGGVPPPEQLPSLRLQFPSPG 3061  
3006 GSVRCIGIKGALKYKVDLKRINTTIGSGTADLLVGRMTFHHGHGELPLALPDVAPIT 3065  
3062 GSVRCIGIKGALKYKVDLKRINTTIGSGTADLLVGRMTFHHGHGELPLALPDVAPIT 3121  
3066 EYVYSGFGRGTQDNMLLYRTSPDGYQVSLRSGHVTLRFMNQEVETQRFADGAPHV 3125  
3122 GNYVSGFGRGTQDNMLLYRTSPDGYQVSLRSGHVTLRFMNQEVETQRFADGAPHV 3181  
3126 AFYSNVTGWLYVDDQQLVKSHERTTLMLOLQPEPSRLLGLPVSQTFHNSGCTSN 3185  
3182 AFYSNATGWLYVDDQQLVKSHERTTLMLOLQPEPSRLLGLPVSQTFHNSGCTSN 3241  
3186 VVQBLRGPQRFVDLHONMGSVNYSGCTPAQLTETSATOKVSRRSRQSQDLACTTP 3245  
3242 VVQBLRGPQRFVDLHONMGSVNYSGCTPAQLTETSATOKVSRRSRQSQDLACTTP 3301  
3246 WLPGTITDAYQPGGFLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPMSGRSP 3305  
3302 PHLRTTRDSYQPGGSLSHLEBFVGILARHN-----VSUWEXNRILLVTDGAPAWSQE 3332  
3306 SLVFLNHHGFVAQTEGPGPRLOVQSRHAGQVHRSVRWGMQIOQLVVDGSGQTSQK 3365  
3333 -----VSUWEXNRILLVTDGAPAWSQE 3355  
3366 ALHHRVPRAERPPYTLVSGGLPASSYSKLPVSVFSGCLKKQLDQKQPLRTPTQMVGV 3425  
3356 GPHRCHQGAEPHQPHTLFGGLPASSHSKLPVTVFSGCVKRLRHLGRPLGAPTRMAGV 3415  
3426 TFCVSGPLEDGLFFPGSGSVTLELPKAKMPVSVLESMRPLAAAGLIFHLGQALATPYM 3485  
3416 TFCILGPLEAGLFFPGSGSVTLELPKAKMPVSVLESMRPLAAAGLIFHLGQALATPYM 3475  
3486 QLKVLTEQVLLQANDGAGEFSTWVTYTPK-LCDGRWHRVAVINGRDTLRELVDTQSNHTTG 3544  
3476 QLOVLPRQVLLRADGAGEFSTVTRPSVLCDDGQWHLAVMKSGNVLRELVDAQSNHTVG 3535  
3545 RUPESLAGSPALLHLGSLPKSSTARPELPAYRGCLKLLINGAPVNVYVTAQVQAGVGR 3604  
3536 PLLAAAGAPAPLYLGLPEPMAVQFPFAYCGCMRRRLAVNRSPVAMTRSVREVHGAAGAS 3595  
3605 GCPS 3608  
3596 GCPS 3599

ID ABB09503 standard; protein; 3597 AA.

AC ABB09503;

XX 01-NOV-2002 (first entry)

DT Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.

XX Human; NOVX; neurological disorder; Alzheimer's disease;  
 XX Huntington's disease; Parkinson's disease; pain; behavioural disorder;  
 XX addition; tuberculous sclerosis; cancer; immune disorder; allergy;  
 XX autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;  
 XX thyroiditis; cardiovascular disease; hypertension; reproductive disorder;  
 XX endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;  
 XX pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;  
 XX polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;  
 XX atherosclerosis; cell signal processing-related disorder;  
 XX metabolic pathway regulation disorder; cytostatic; neuroprotective;  
 XX antifungal; immunosuppressive; analgesic; antiatherosclerotic;  
 XX dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;  
 XX differentiation; proliferation; motility; haematopoiesis; wound healing;  
 XX angiogenesis; forensic biology; transgenic animal; drug screening;  
 XX gene therapy; NOV1c; laminin alpha-5-like; chromosome 20.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1. .14  
 FT Peptide /label= Signal\_peptide  
 FT Protein 15. 3597  
 FT /note= "Mature NOV1c protein"

XX W0200253742-A2.

XX 11-JUL-2002.

XX 07-JAN-2002; 2002WO-US000375.

XX 05-JAN-2001; 2001US-0260018P.

XX 08-JAN-2001; 2001US-0260360P.

XX 28-FEB-2001; 2001US-0272411P.

XX 02-MAR-2001; 2001US-0272817P.

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XX 10-SEP-2001; 2001US-0318405P.

XX 12-SEP-2001; 2001US-0318700P.

XX 04-JAN-2002; 2002US-00037417.

XX (CURA-) CURAGEN CORP.

XX Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;

XX Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAV, Li L;

XX Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;

XX Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;

XX Padigaru M, Taupier RJ, Miller CE, Eisen A;

XX WPI; 2002-583619/62.

XX N-PSDB; ABQ93881.

XX Novel polypeptides and nucleic acids homologous to transmembrane  
 XX receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
 XX treating cancer, atherosclerosis, neurological, skin and autoimmune  
 XX disorders.

XX Claim 1c; Page 20-21; 323pp; English.

XX The invention relates to 24 novel human proteins designated NOV1-NOV14  
 XX (AB09501-AB09524), collectively referred to as NOVX proteins, and  
 XX nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and  
 XX nucleotides are useful in the treatment, diagnosis or prevention of NOVX-  
 XX associated disorders or in the manufacture of a medicament for treating  
 XX such disorders, with specific applications described for each of the 24  
 XX NOVX proteins, based on their homology to known proteins. Various

CC disorders are associated with NOVX proteins including neurological  
 CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
 CC pain, behavioural disorders, addition, tuberculous sclerosis, cancers  
 CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
 CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
 CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
 CC (e.g., hypertension), reproductive disorders, endometriosis,  
 CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
 CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine  
 CC disorders, obesity, bacterial infections and particularly cardiomyopathy,  
 CC atherosclerosis, cell signal processing-related disorders and disorders  
 CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may  
 CC be used to identify cellular receptors or downstream effectors which  
 CC binds to a NOVX protein, and are also useful as targets for the  
 CC identification of small molecules that modulate or inhibit processes such  
 CC as neurogenesis, cell differentiation, cell motility, cellular  
 CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX  
 CC nucleic acid sequences can be used to identify a cell or tissue type and  
 CC are useful as a source of primers or probes for forensic biology and for  
 CC identifying and cloning NOVX homologues in other cell types. Cells  
 CC comprising NOVX nucleic acids are useful for producing non-human  
 CC transgenic animals which are useful for studying the function and  
 CC activity of NOVX proteins and for identifying and evaluating modulators  
 CC of NOVX activity. The present sequence represents the laminin alpha-5-  
 CC like protein NOV1c. The gene encoding NOV1c is located on chromosome 20

XX Sequence 3597 AA;

Query Match 74.0%; Score 14706.5; DB 5; Length 3597;  
 Best Local Similarity 74.5%; Pred. No. 0;  
 Matches 2729; Conservative 274; Mismatches 482; Indels 177; Gaps 25;

QY 1 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANKAKHPVSNADGTERWQSPPLSRGLE 60  
 DB 58 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANKAKHPASNAIDGTERWQSPPLSRGLE 117  
 QY 61 YNEVNTLDLGQVPHVAYVLIKFANSRPRDLVLERSTDFGHTYQPMQFPASSKRCDLER 120  
 DB 118 YNEVNTLDLGQVPHVAYVLIKFANSRPRDLVLERSTDFGHTYQPMQFPASSKRCDLER 177  
 QY 121 FGPTLERTQDDDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDEFTKATN 180  
 DB 178 FGPTLERTITRDAACITTEYSRIVPLENGEIVVSLVNGRPGAWNFYSPLLRDEFTKATN 237  
 QY 181 IRLRFLRTNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADYCDADKDPDPF 240  
 DB 238 VRLRFLRTNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADYCDADKDPDPF 297  
 QY 241 RLQCAQHTCGSCDRCRCCFQFNQPKPATNSANECSNCCHGHAYDCYDPEVDRN 300  
 DB 298 RLQCTCOHTCGTCRCCFQFNQPKPATNSANECSNCCHGHAYDCYDPEVDRR 356  
 QY 301 ASQNDNVYGGVCLDCQHTTCINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDG 360  
 DB 357 ASQSLDGTQGGVCLDCQHTTCINCERCLPGFYRSPNHPDLSPHVCRGCNCESDFTDG 416  
 QY 361 TCEDLTGRCYCRPNFTGELCAACAGVTDPHCYPLPSFFPHNDTREQVLPAQIVNCCDN 420  
 DB 417 TCEDLTGRCYCRPNFSGRCDVCAEGFTGFPSCY-REHLFONDTRQVLPAQIVSDDCS 475  
 QY 421 AAGTQGNACRDPRLGRVCVKPNFRGAHCELCAFGHGPSCHPQCQSS---PGVANSLCD 477  
 DB 476 AAGTQGNACRDPVRGRLCKXPNFQGTFCELCAFGYGPCC-PASVPALEWPMATVLTQ 534  
 QY 478 PESGQCMCRTG-----FEGDRCDHCAVGYHFPL-CQLCGCSPAGTLPBGCDGAG 526  
 DB 535 ASAGAEMASRGPHVIAVPPATFTLSASH-----FLRSVAVCGSPAGTLPBGCDGAG 586  
 QY 527 RCQCRPGFGHCDRCLPGVHYGPDCHACACDPGALDQCGVGLCHCRPGNTGATCOE 586  
 DB 587 RCLCOPEFAGPHCDRCRPGVHYGFGFNCAACTCDPRGALDQCGVGLCHCRPGNTGATCOE 646  
 QY 587 CSPGPGYFPSPICPHCGSADGSLHTTC-----DPTTGTQCRPRVTGLHCDMCPVGAFFPY 642



647 DB CSPGFHGFPS-----CPATALLKAPCTQPTVPGVGSAAAGP-VRGCGVTRVCPVPTTSPT 700  
643 QY CEAGSCHPAGLAPANPALPETOACMCRAHVEGSPCDRCXPGYWGLSASNPBEGCTRCSGD 702  
701 DB AKJALATLPVWPVDPALPEAQVPCMCRAHVEGSPCDRCXPGYWGLSASNPBEGCTRCSGD 760  
703 QY PRGTLGGVTECO-NGNOCFCARHVGCTKCAACKDGFGLDYADYFGCRSCRCDVGGALGO 761  
761 DB LRGTLGGVABEQGTGQCFKPHVCGACASCKDGFGLDQADYFGCRSCRCDIGGALGO 820  
762 QY GCEPKTGACRCRPNQPTGPTCEPAKHVLPDLHMRLELEBAATPEGHAVRFGNPLEFE 821  
821 DB SCEPRTGVCRCRPNQPTGPTCEPAKHVLPDLHMRLELEBAATPEGHAVRFGNPLEFE 880  
822 QY NFSVRGVAHMAIOPRIVARLVNTPSPLFRVPRVNRGSGTVNGQISVREBKGKLSCTN 881  
881 DB NFSVRGVAHMAIOPRIVARLVNTPSPLFRVPRVNRGSGTVNGQISVREBKGKLSCTN 940  
882 QY CTEOSQVAPPPSTEPAFVTVPQRFGEPPFVLPNGIOWALLVBAEGVLLDVVLLPSTYYE 941  
941 DB CTAQSQVAPPPSTEPAFVTVPQRFGEPPFVLPNGIOWALLVBAEGVLLDVVLLPSTYYE 1000  
942 QY AALLOHVRTEACTYRPSNALSSTENCLVYVHLLPLDGFPSAAGTALCRHDSLSRBPCTEQ 1001  
1001 DB AALLOHVRTEACTYRPSNALSSTENCLVYVHLLPLDGFPSAAGTALCRHDSLSRBPCTEQ 1060  
1002 QY LSPSHPLIATCFGSDVDIQTLEMAVPOQYQVYLVVYVYVGEDSHQEMGVAVHTPQAPQGV 1061  
1061 DB LSPSHPLIATCFGSDVDIQTLEMAVPOQYQVYLVVYVYVGEDSHQEMGVAVHTPQAPQGV 1120  
1062 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1121  
1121 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1180  
1122 QY LSPSHPLIATCFGSDVDIQTLEMAVPOQYQVYLVVYVYVGEDSHQEMGVAVHTPQAPQGV 1181  
1181 DB LSPSHPLIATCFGSDVDIQTLEMAVPOQYQVYLVVYVYVGEDSHQEMGVAVHTPQAPQGV 1240  
1182 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1241  
1241 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1300  
1242 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1301  
1301 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1360  
1302 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1361  
1361 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1420  
1362 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1421  
1421 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1480  
1422 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1481  
1481 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1540  
1482 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1541  
1541 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1600  
1542 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1601  
1601 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1660  
1602 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1657  
1661 DB LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1720  
1658 QY LNLHPFCYSSICRSPARDTQHILAI FHLDSBASRLTABQAHFPLHSVTLVPVEESTEF 1717

1721 DB NQMSITFLEPAYPTPGHVHRGQLQVEGNFRHTTNTVSRLELMVVLASLEQLIRALF 1780  
1718 QY SQTSSSVLSLRVVLVASEAGRGPASVVELCMCPANVYRGDSOCBACAGYVYRDKGLFLG 1777  
1781 DB SOISSAVELRRVALLVASEAGRGPASVVELCMCPANVYRGDSOCBACAGYVYRDKGLFLG 1840  
1778 QY RCVPQCCGHSDRCCLFSGGICVGCQHNTEGDCQCRCPGFPVSSDFSNPASCPCPCPLA 1837  
1841 DB RCVPQCCGHSDRCCLFSGGICVGCQHNTEGDCQCRCPGFPVSSDFSNPASCPCPCPLA 1898  
1838 QY VPSNNFADGCVLNRGRTQCLCRPGVAGASCRCAPGFPNGNPLVLGSSCQPCDCSNGDPN 1897  
1899 DB VPSNNFADGCVLNRGRTQCLCRPGVAGASCRCAPGFPNGNPLVLGSSCQPCDCSNGDPN 1931  
1898 QY MTFSDCDPLTGACRCCLRHHTTTPHCHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSG 1957  
1932 DB LTFSDCDPLTGACRCCLRHHTTTPHCHCERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSG 1991  
1958 QY RCLXAGVTGQRCDRCLEGYFGFEGCQCRCPACGPAKSGECPHOSQCHCQCPGTTGPO 2017  
1992 DB HCLXAGVTGQRCDRCLEGYFGFEGCQCRCPACGPAKSGECPHOSQCHCQCPGTTGPO 2051  
2018 QY CLECAFGYWGVLPEKRCRCQCPGRHCDPHTGCTCPGLSGERCDTCSQQHQVVPVPGKPG 2077  
2052 DB CRECAFGYWGVLPEKRCRCQCPGRHCDPHTGCTCPGLSGERCDTCSQQHQVVPVPGKPG 2111  
2078 QY GHGHCVCDCVCHVLLDDLERAGALLPAIREQLOGINASSAAWRLHRLNASTADL--- 2134  
2112 DB GHGHCVCDCVCHVLLDDLERAGALLPAIREQLOGINASSAAWRLHRLNASTADL--- 2171  
2135 QY OSKLRPPGPRYQAAQQLTLEQOQISLSQOQTERLGSQAT 2174  
2172 DB SVLAFPPQPGVQVATFPLPQSQRLSPGPHETAQQLVLEQQSTSLP-----PQAV 2224  
2175 QY GVOGAGQLLPTTESTLGRAQKLLSVAVRAGALNELASRMGQSGPGDALVPSGEURLWA 2234  
2225 DB GTRDQASQLLACTEATLGHAKTLLAAIRAVDRITSELMSQTHGLGLANASAPSGEQLRT 2284  
2235 QY LAEVEILLDMVTRDGLGAGVAAEALAEAOALMARVOEQLTSFWEENQSLATHRDOLA 2294  
2285 DB LAEVEILLDMVTRDGLGAGVAAEALAEAOALMARVOEQLTSFWEENQSLATHRDOLA 2344  
2295 QY QYESGIMDLREALNOAVNTTREAEBELNSRQERYKEALQWQOELSDQNTATKATLQAASL 2354  
2345 DB QYESGIMDLREALNOAVNTTREAEBELNSRQERYKEALQWQOELSDQNTATKATLQAASL 2404  
2355 QY ILGHVSELLQIDQAK-EDLEHLLASLDGANTPLIKRMOAFSPASSKVDVLEAEAAHQAQ 2413  
2405 DB ILGHVSELLQIDQAK-EDLEHLLASLDGANTPLIKRMOAFSPASSKVDVLEAEAAHQAQ 2464  
2414 QY LNQLAINLSGIITLGINDRFIQRAVEASNAVSSIIQAVQAAEDAAQALQASRTWEMVY 2473  
2465 DB LNQLAINLSGIITLGINDRFIQRAVEASNAVSSIIQAVQAAEDAAQALQASRTWEMVY 2523  
2474 QY QRLGAAGAPOLLANSALBETILGHQGRGLAQ-----GRICAAAGIOLHNYWARKNOLAA 2528  
2524 DB QRLGAAGAPOLLANSALBETILGHQGRGLAQ-----GRICAAAGIOLHNYWARKNOLAA 2583  
2529 QY QIOEQAQMLAMDTSTSEKIAHAKVAAEALSTATHVQSQQGMQKNVERWQSQGLGLOQ 2588  
2584 DB QIOEQAQMLAMDTSTSEKIAHAKVAAEALSTATHVQSQQGMQKNVERWQSQGLGLOQ 2643  
2589 QY QDLSQVERDASSSVTLTKTLPOLLAKLSRLNENGVHNASLANSINIGRVKRLIAQARSA 2648  
2644 DB QDLSQVERDASSSVTLTKTLPOLLAKLSRLNENGVHNASLANSINIGRVKRLIAQARSA 2703  
2649 QY ASK-VKVMKNGRSGVRLRPRDLADLAATALKFHIQSPVPAPEPGKNTGDHFPVLYMG 2707  
2704 DB ASK-VKVMKNGRSGVRLRPRDLADLAATALKFHIQSPVPAPEPGKNTGDHFPVLYMG 2761  
2708 QY SRQATGDYMGVSLRNQKRVHVRVLRGKAGPTTSLIDENTIGEOPFAAVSIDORTQFGHMSVTV 2767  
2762 DB SRQATGDYMGVSLRNQKRVHVRVLRGKAGPTTSLIDENTIGEOPFAAVSIDORTQFGHMSVTV 2821

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QY 2768 EKQVHEIKGDTVAPGSEGLLNKHPDDVFYVGGYPSNFTTPEPIRPFYGLGCIEMETLN 2827
DB 2822 EQMIQETKGTAVAPGAEGLLNKHPDDVFYVGGYPSFTTPEPIRPFYGLGCIEMETLN 2881
QY 2828 EKVSLYNEFEOTFMDLTDVADKCAKATGDPWLDGSGYFARISFEKOPSTKRF 2887
DB 2882 EKVSLYNEFEOTFMDLTDVADKCAKATGDPWLDGSGYFARISFEKOPSTKRF 2941
QY 2888 DQELRLVSYNGIIFELKQBSQFLCLAVQGTTLVLYDFGSLGKADPLQPPQALTAASKA 2947
DB 2942 EQELRLVSYNGIIFELKQBSQFLCLAVQGTTLVLYDFGSLGKADPLQPPQALTAASKA 3001
QY 2948 IQVFLLAGNRKVLVREVERATVPSVDQNMLEADAYILGGYPPQOLPLSIRQLPPSGS 3007
DB 3002 IQVFLLAGNRKVLVREVERATVPSVDQNMLEADAYILGGYPPQOLPLSIRQLPPSGS 3060
QY 3008 VEGCKIGIKALGYVDLKRLLNTTIGSFCTADLLVGRWTMTFHGFLPLALPDVAPIREV 3067
DB 3061 VEGCKIGIKALGYVDLKRLLNTTIGSFCTADLLVGRWTMTFHGFLPLALPDVAPIREV 3120
QY 3068 VYSGFGFRGTQNNLLYRTSDPGYQVSLRSGHVTLPFMQEVETQRFADGAPHYVAF 3127
DB 3121 VYSGFGFRGTQNNLLYRTSDPGYQVSLRSGHVTLPFMQEVETQRFADGAPHYVAF 3180
QY 3128 YSNVTGVWLYVDLQOLVKSHERTTLMLOLQPEEPSRLLLGLPVSGTFHNFSGCISNVF 3187
DB 3181 YSNVTGVWLYVDLQOLVKSHERTTLMLOLQPEEPSRLLLGLPVSGTFHNFSGCISNVF 3240
QY 3188 VQRLGFRQVFDLQNMGSVNVSVGCTPAQLIETSRATQVRSRSPQSDLACTPWL 3247
DB 3241 VQRLGFRQVFDLQNMGSVNVSVGCTPAQLIETSRATQVRSRSPQSDLACTPWL 3300
QY 3248 PGTIQDAYQFGGLPSYLOFVGISPSHRNRLHLSMLVRPHASQGLLLSTAPMSGRSPSL 3307
DB 3301 LRTTRDSYQFGSLSHLSEFVGLAHNRN----- 3329
QY 3308 VLFLNHHGHEVAQTGEGPRLQVRSRQSRAGQWHVSVRWGMQOIQLVVDGSGTWSQAL 3367
DB 3330 -----VSVRWKXNRIILLVTDGARAWSRGP 3354
QY 3368 HURVPAERPPQYTLVSGGLPASSYSSKLPVSVGSGCLKKLODKQPLRTQMVGTP 3427
DB 3355 HRQHQAEHPQHTLFFVGLPASHSSKLPVTVGSGCVKRLRHLRGLGAPTRMAGVTP 3414
QY 3428 CVSGPLEDGLFPFGSGGVITLPLKAKMPYVLSLEMRPLAAAGLIFHLGQALATPYMQL 3487
DB 3415 CILGPLEAGLFPFGSGGVITLPLKATLPDVGLEVRPLAVTGLIFHLGQARTPPYLQL 3474
QY 3488 KYLTEQVILLQANDGAGEFTWTYK-LDGRHVRVAVIMGRDTRLRLVDQSNHTTGL 3546
DB 3475 QVLPQVLLRADDGAGEFTSVTRPSVLCQGWHRFLAVKSGNVLRLVEDAQSNHTVGL 3534
QY 3547 PSLAGSPALLHGLSLPKSSSTARPELPAYRGCLRLKILLGAPVNTASVOIQAGVGMRCG 3606
DB 3535 LAAAGAPAPLYLGGLPPEMAVQPPWPPAYCGCWRRLAVNRSPVATRSVEVHGAVGASGC 3594
QY 3607 PS 3608
DB 3595 PA 3596

RESULT 8
ABB81598
ID ABB81598 standard; protein; 2743 AA.
XX
AC ABB81598;
XX
DT 19-SEP-2002 (first entry)
DE
DE Human laminin alpha 5 2743 N-terminal amino acid sequence SEQ ID NO:36.
XX
XX Laminin alpha 5; laminin 10; vulnerable; cell growth; differentiation;
KW
```

```
KW tissue repair development; laminin; healing; vascular tissue;
KW re-endothelialization; vascular injury; cell attachment; cell stasis;
XX proliferation; migration.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..35
XX Protein 36..2743
XX /label= signal
XX /label= laminin_alpha_5
XX
XX WO200250111-A2.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-US051035.
XX
XX 21-DEC-2000; 2000US-0257449P.
XX
XX 28-MAR-2001; 2001US-0279282P.
XX
XX 13-NOV-2001; 2001US-00279282.
XX
XX (BIOS-) BIOSTRATUM INC.
XX
XX Tryggvason K, Doi M, Thyboll J;
XX
XX MPI: 2002-557650/59.
XX
XX N-PSDB; ABO72930.
XX
XX New human laminin-10 proteins, useful for accelerating the healing of
XX vascular tissue, improving the biocompatibility of grafts, or for
XX promoting re-endothelialization at the site of vascular injuries.
XX
XX Disclosure; Page 223-231; 231pp; English.
XX
XX The present invention describes human laminin alpha 5. Also described is
XX an isolated laminin 10. Laminin 10 has a vascular phenotype. Laminins are
XX useful in maintaining cell/tissue phenotype as well as promoting cell
XX growth and differentiation in tissue repair development. Specifically,
XX laminin 10 can be used for accelerating the healing of vascular
XX tissue, improving the biocompatibility of grafts useful for treating such
XX injuries, for promoting re-endothelialization at the site of vascular
XX injuries, and promote cell attachment and subsequent cell stasis,
XX proliferation, differentiation, and/or migration. The present sequence
XX represents the 2743 N-terminal amino acid sequence of human laminin alpha
XX 5, which is used in the exemplification of the present invention
XX
XX Sequence 2743 AA;
XX
XX Query Match 62.28; Score 12354.5; DB 5; Length 2743;
XX Best Local Similarity 82.48; Pred. No. 0;
XX Matches 2198; Conservative 172; Mismatches 290; Indels 7; Gaps 4;
XX
XX QY 1 DLVCKLVGGPVAGDPNQTIQGOYCDICTAANSKAPVSNADGTERMWQSPPLSRGLE 60
DB 79 DLVCKLVGGPVAGDPNQTIQGOYCDICTAANSKAPVSNADGTERMWQSPPLSRGLE 138
QY 61 YNEVNTLDLQGVFHVAVYLIKFNANSPRDLWLERSTDFGHTYQWQFASKRDCLER 120
DB 139 YNEVNTLDLQGVFHVAVYLIKFNANSPRDLWLERSTDFGHTYQWQFASKRDCLER 198
QY 121 FGPRTLEITODDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYSLLRDFTKATN 180
DB 199 FGPRTLEITODDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYSLLRDFTKATN 258
QY 181 IRLRLFRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 240
DB 259 VRLRLFRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 318
QY 241 RLQACQHNCTGSCDRCCEGNCQKPAATTDANECOSCNCHGHAYDCYDPEVDRN 300
DB 319 RLQCTQHNCTGSCDRCCEGNCQKPAATTDANECOSCNCHGHAYDCYDPEVDRN 378
```

tissue repair development; laminin; healing; vascular tissue; re-endothelialization; vascular injury; cell attachment; cell stasis; proliferation; migration.

Homo sapiens.

Key Location/Qualifiers  
Peptide 1..35  
Protein 36..2743  
/label= signal  
/label= laminin\_alpha\_5

WO200250111-A2.  
27-JUN-2002.  
21-DEC-2001; 2001WO-US051035.  
21-DEC-2000; 2000US-0257449P.  
28-MAR-2001; 2001US-0279282P.  
13-NOV-2001; 2001US-00279282.

(BIOS-) BIOSTRATUM INC.  
Tryggvason K, Doi M, Thyboll J;  
MPI: 2002-557650/59.  
N-PSDB; ABO72930.

New human laminin-10 proteins, useful for accelerating the healing of vascular tissue, improving the biocompatibility of grafts, or for promoting re-endothelialization at the site of vascular injuries.

Disclosure; Page 223-231; 231pp; English.

The present invention describes human laminin alpha 5. Also described is an isolated laminin 10. Laminin 10 has a vascular phenotype. Laminins are useful in maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair development. Specifically, laminin 10 can be used for accelerating the healing of vascular tissue, improving the biocompatibility of grafts useful for treating such injuries, for promoting re-endothelialization at the site of vascular injuries, and promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The present sequence represents the 2743 N-terminal amino acid sequence of human laminin alpha 5, which is used in the exemplification of the present invention

Sequence 2743 AA;  
Query Match 62.28; Score 12354.5; DB 5; Length 2743;  
Best Local Similarity 82.48; Pred. No. 0;  
Matches 2198; Conservative 172; Mismatches 290; Indels 7; Gaps 4;

QY 1 DLVCKLVGGPVAGDPNQTIQGOYCDICTAANSKAPVSNADGTERMWQSPPLSRGLE 60  
DB 79 DLVCKLVGGPVAGDPNQTIQGOYCDICTAANSKAPVSNADGTERMWQSPPLSRGLE 138  
QY 61 YNEVNTLDLQGVFHVAVYLIKFNANSPRDLWLERSTDFGHTYQWQFASKRDCLER 120  
DB 139 YNEVNTLDLQGVFHVAVYLIKFNANSPRDLWLERSTDFGHTYQWQFASKRDCLER 198  
QY 121 FGPRTLEITODDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYSLLRDFTKATN 180  
DB 199 FGPRTLEITODDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYSLLRDFTKATN 258  
QY 181 IRLRLFRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 240  
DB 259 VRLRLFRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 318  
QY 241 RLQACQHNCTGSCDRCCEGNCQKPAATTDANECOSCNCHGHAYDCYDPEVDRN 300  
DB 319 RLQCTQHNCTGSCDRCCEGNCQKPAATTDANECOSCNCHGHAYDCYDPEVDRN 378





1074 QY RSPARTQHHLAIFHLDSIASIRLTABQAHFFLHSLVTLVPIVEEPSTEFVPRVFCVSSHG 1133  
1075 QY RSPARTQHHLAIFHLDSIASIRLTABQAHFFLHSLVTLVPIVEEPSTEFVPRVFCVSSHG 1133  
998 DB RSVADIMBRIANIELTADQLKHMARFLHQCIIPIEBEYABEYRQVQHCIAIY 1057  
1134 QY TNPSSAACLAGRFPKPPQFIILKQCQVLPPLPDLPLTQSOELSPGAPPEQPQRPPTAV 1193  
1058 DB RFVQSATCVSLAHTPPPTALILDVLSGRPF-PHLP-----QQSSPSVDV 1101  
1194 QY DNABEFTLHRHOGTVFTTQPTLGRVAFLLHGYQVHPBPFPVEVLINGRIWQHANA 1253  
1102 DB LFG---VTLKAFONQVTLGRVPHLGRVYVVFYHFOAAHPTFPQVSDGWSRAGSFHA 1158  
1254 QY SPCPHGYGRTLVLCBQGTMLDVTNDELTVTVRVEGRWMLDYLVIIPEDAYSSYLQ 1313  
1159 DB SPCPHVLCGRDOVIAEQIEFOISPEVAATVKVPEKSLVLRVLPVPAENVDYQILHK 1218  
1314 QY EPLDKSYDPIFSCATOGYHISPPSSPFCRNAATSLFYNNGALPCGCEHGVASTCE 1373  
1219 DB KSMDSLEIFITGCKNSFLDPTASRCPKNSARSLVAFYHKGALPCECHTGTATGPHCS 1278  
1374 QY PFGQPCRGHVIGRDCSRATGYWGFNCRPCDCGRLCDELGTQCICPPRTVPPDCLV 1433  
1279 DB PEGQPCPCPNVIGROCTRCATGHYFPRCKPCSCGRRLCEMTGQRCPPRTVPPQCEV 1338  
1434 QY CQPSFGCHPLVGCCEKNSGPGVOELTDPCTCDMDSGOCRCRPNVAGRCDCATCAPGYGY 1493  
1339 DB CETHSPFPMAGCEGNCRRGTTEAAMPEDCRDSGOCRCRPNVAGRCDCATCAPGYGY 1398  
1494 QY PSRCPDCHEAGTMASVCDPLTGCQCKENVOGSRCDQCRVGTFSLDAANPKGCTRCFCF 1553  
1399 DB PECVPCNCRDTEGVCDDPGTGCACLCKENVEGTECNVCRGSPHLPANLKGCTSCFCF 1458  
1554 QY GATERGCSNLARHBFVDMEGHVLSSDROVVPHREPEIELLHDLARSVADTSELYWQ 1513  
1459 DB GVNQCHSHKRTKRFVDMGLHSETADRVIDVPSFNGSNMVADELQEPATIHSSASW 1518  
1614 QY APPSYLGRVSYGGTLYHLSHETQRGDIFIPYERDPVVLQGNQMSIAFLELAYPPG 1673  
1519 DB APTSYLGRVSYGGTLYHLSHETQRGDIFIPYERDPVVLQGNQMSIAFLELAYPPG 1577  
1674 QY QVHRGOLQVEGNFHLTHNPVSEELMVLGLQLOLQALPSQTSYSSVSLRVLV 1733  
1578 DB RUHGHVHVVEGNFHRASRAPVSEELMVLGLQLOLQALPSQTSYSSVSLRVLV 1637  
1734 QY ASEAGRGPPASVVELCMCPANRYGSCQECAPGYRDTKGLGRVPCQCHGSHDRCLP 1793  
1638 DB ASDTSGRIALAVEICACPPAYAGDSQCGSPGYRDKHGLYTKGCVPCNCGHSHQCD 1697  
1794 QY GSGICVGCQHTTEGQCRCPGVSSDPSNPASPCVSCRCPLAVPSNADGCVLNGR 1853  
1698 DB GSGICVGCQHTTEGQCRCPGVSSDPSNPASPCVSCRCPLAVPSNADGCVLNGR 1751  
1854 QY TQCLCRPGYAGASCRCAPGFGNPLVLGSSCQPCDCSGNDPNMIFSDCDPLTGACRCG 1913  
1752 DB VRCCKAGYGTQCBRCAPGYFNGPKFGGSCQPCSCNSG----- 1792  
1914 QY LRHTGPHCERCAPGYGNALLPGNCTCDSCPGTETCDPQSGRCICKAGVTGQRCDCR 1973  
1793 DB ----- 1792  
1974 QY LEGYFGEQOCRCRPAKAGSECHPQSGQCHQCPGTTGPQCLECAPGYMGLPEKGC 2033  
1793 DB -----QLGSC----- 1798  
2034 QY RRCQCRGHCDPHTGCHTCPPGLSERCDCQSQOHQVVPKPGHGHIEVCDHCVLL 2093  
1799 DB -----PLTGDCI-----NOEPKSSPAE-----ECDDCSCVMTL 1828  
2094 QY LDDLERAGALLPAIREQLQGINASSAAWARLHRLNASTADIQSKLRBPPGFRYQAA----- 2149  
1829 DB LNDLATMGEQLRLVKSQQLQSASAGLLEQHRHMETQAKLRLNQL-----NYRSALSNH 1883

2150 QY -QOQLOTLBOOSISLOODTERLGSCQATGVQGAQGLD-----TTSTLGRAQKLLSVRA 2203  
1884 DB GSKISGLRELTDLNQEETLOEKAQ-VNSKRAQTLNNVNRATQSAKELDKIKNVIRN 1942  
2204 QY VGRALNELASRMGQSPGDALVPSEQLR-WALAEVERLLWDMETRDILGAQAVAEALA 2252  
1943 DB VHIILLKQISGTDGECNN---VPSGDFREW--AEAQMMRELNRNFRGKHLREAEADR 1996  
2263 QY EAQRLMARVQEQILSFWEENGSLATHIRDOLAQVSEGLMDLREALNOAVNTTREAELNS 2322  
1997 DB ESQILNLRITWKTQHQENGLANSIRDSLSEYAKLSDJRLARLQAAQAQKANGLNQ 2056  
2323 QY RNOERKVEALQW-KELS--QDNATLKATLOAAALILGHVSELQGIQDOAKEDLEHLAAS 2379  
2057 DB EN-ERALGAIOQVKEINSLOSDFTKYLTTADSSLLQTNIA--LQLMKSKQKEYKLAAS 2113  
2380 QY LDGAWTPLLKMQAPSPASSKVDIWEAAEAHAKNLQALNLSGIIILGINQDRIOQAVE 2439  
2114 DB LNEARQELSDKVRRELSRAGKTSILVEAEERHARSLQELAKOLEIKKNASGDELVRCAVD 2173  
2440 QY ASNAYSSILOAVQAEADAAGALQASRTWEMVQVQRLAAGARQOLLANSALAEETILGHQ 2499  
2174 DB AATAYENILNAKAEADAANRAASASBSALQTVIKEDLPRAKATLSSNSDKLLNEAKMTQ 2233  
2500 QY GRLGLAQGRLOAAGIQLHNWARKNOLAAQIOEAQACMLAMDTSSEK----- 2547  
2234 DB KKL-----KQEVSPALNNLOOTLNI VTVQKE-----VIDTLTLTLDGHLGIRQDID 2281  
2548 QY -IAHAKAAVAAEALSTATHVQSQGQKXVVERQSGQLGQGLQSDQVDERDASSVSTL 2605  
2282 DB AMISSAKMVRKANDITDVLGDLNPIQTDVERIKDYVGRTONEDPKKALTADNNSVNL 2341  
2606 QY EKTLPOLLAKLSRLNRENVHNASLA---LSANTGRVYKLIQAARSAASAKVYKSMKFNGR 2661  
2342 DB TNKLPLDLWRKIESI-----NQQLPLIGNSDNMDRIRLIIQOARDAASKVAVPMRPNKG 2395  
2662 QY SGVRLRPPRDLADLAAYATLAKPHIQSPVPAPEPKNTGDHFLVYMGSRQATDYMVGSLR 2721  
2396 DB SGVEVLENDLEDLKGVTSLFLQRPNSRENG--TENMFVYVYLGKNDASRDYIGVAVV 2453  
2722 QY NQKVHMYVRLKAGPPTLSIDENIGE-----PAAYSIDRTLOQGHWSVTVEKQVHEI 2775  
2454 DB DQQLTCVYNLDR-EAELOVDQILTKSETKEAVMDRVKFORIYQPARLNT----- 2503  
2776 QY KGDIVA-----SGLLNLHPDDFVYVGGYPSNFTPPPEPLFPFPGYLCIEM 2823  
2504 DB KGATSSKPEPGVYDMGDRNSNTLLNDPENWVYVGGYPPDPKLPRLSPFPYKGCIEL 2563  
2824 QY ETLNEEVSLYNEFBQTFMLDTAVDKPCARSKATCDPMLTDGSLYLDGSGPARISFEKQFSN 2883  
2564 DB DDLNENVLUSLNFKKTNLNTTEVEPCRRKEB-----SKNTEGTYGARVTOQH-AP 2617  
2884 QY TKRFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLYDFDGSGLKK-----ADPLQPPQ 2939  
2618 DB IPTFGQITQTTVDRLGLFFAENGDRFISLNIEDGKLMVRYKLSLSELPKRGVGDAIN--- 2674  
2940 QY ALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNML---EMAD--AYLGGVPEQL 2994  
2675 DB --NGRDSIQI-----KIGKLRKMINVDVQNTIIDGEVDFSTYLLGI----- 2718  
2995 QY FLSLRQLPP-SGGSVRGCIKIGIKALGYVLDLRLN-TTGISFGCTADLLVGRWTMTHGHG 3052  
2719 DB PIATRERENISTAPFRGCMKNLK---KTSGVRLNDTVGTVKKCEDWKLVRASFSRGG 2775  
3053 QY ---FLPLALPDVAIPITVYVSGFGFRGTODNNLLYRTSPDGPYQVSLRREGHVTLRFMNQ 3109  
2776 DB QLSFTDGLPP-----THLQNSFGQTFQSGILLDHQHTWRNLQVLEDEYIELTSDS 2831  
3110 QY E---VETORFADGAPHYVAFYNNVTGVLYVDQQLQVKSHERTTTPMLQLOPEEPSRL 3166  
2832 DB GPFIKSPQTYMDGLLHVSVISNSGLRLIDQLL-----RNSKRLKHISSRSQSLR 2885  
3167 QY LGGLPVSGTFHFGSCISNVFVQELRGPQRVFDLHQNWGSVNTVSV-GCT-----P-AQLIE 3220

2886 LGG-----SNFEGCISNVFQRLSLSPVLDLTSNLSKRDVSLGCGSLNKPFPMLLK 2938  
3221 TSRTAQKVSRRSQPSDLACTTWPGLCTIDAYQFGGPLP-----SYLQFVGISPSH 3274  
2939 GSTRNKTKTFINQLQDTPVASPRSVKWDQAC---SPLKPTQANGALQFGDIPISH 2995  
3275 RNRLHLSMLVRPHA-----ASQGLLLSTAPMSGRSPSLVFLNHFHFFVAQTEGPGP 3325  
2996 LLFKLPQELLKPRSQFVDMQTTSSRGLVFHTGT---KNSFMALYLSKRLVFLALGTGDK 3052  
3326 RLQVSRQHSRAGQHRVSVRMGMQOICLVVDGSSQTSQKALHHRVPRAEPRQPVTLSVG 3385  
3053 KLRIKSEKCNKDGKWHVTVFGHDGKRLVVDGL-----RAREGSLPGNSTISIR 3102  
3386 -----GLPASSYSSKLPSVGFSGGLKKLQLDKPLRTPTQMGVTPCVSGPLEDGLFPP 3440  
3103 APVILGSPSPGKPSLPTN-SFVGCLKNFQLOSKPLTTPSSSGFVSSCLGGPLEKGIYFS 3161  
3441 GSEGVVTELPKAKMPYVLEMLRPLAAGLIFHLGQALATPYQLKVLTE--QVILQA 3498  
3162 BEGHRVTLAHSVLLGPEFKLVFSIRPSLTGTLIHIG---SFGKHLCVYLEAGKVTASM 3218  
3499 NDGAGFSTWVTPK--LCDGRHWRVAVTMGRDTRLRLEVDTSQNTHTTGLRLPESLAGSPAL 3556  
3219 DSGAGTSTSVT-PKQSLCDGQWHSVAVTIKQHLHLELDTDSSTYTAGQIPPPASTQBP 3277  
3557 LHLGSLPKSSTAR--PELPAYRGKRLKLLINGAPVNVTVASVOIQAVGMRGCP 3607  
3278 LHLGAPANLTILRIPVWKSFFGCLRNHVNHPVPTVEALEVQGFVSLNGCP 3330

RESULT 10  
ABB09504  
ID ABB09504 standard; protein; 1640 AA.  
XX ABB09504;  
XX ABB09504;  
DT 01-NOV-2002 (first entry)  
XX Human laminin alpha-5-like NOVIid protein, SEQ ID NO:8.  
XX Human; NOVI; neurological disorder; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;  
KW addition; tuberous sclerosis; cancer; immune disorder; allergy;  
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;  
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;  
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;  
KW pancreatitis; cirrhosis; endocrine disorder; obesity; cardiomyopathy;  
KW polycystic kidney disease; glomerular endotheliosis; bacterial infection;  
KW atherosclerosis; cell signal processing-related disorder;  
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;  
KW antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;  
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;  
KW differentiation; proliferation; motility; haematopoiesis; wound healing;  
KW angiogenesis; forensic biology; transgenic animal; drug screening;  
KW gene therapy; NOVIid; laminin alpha-5-like; chromosome 20.  
XX Homo sapiens.  
OS  
XX  
XX WO200253742-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 07-JAN-2002; 2002WC-US000375.  
XX  
XX 05-JAN-2001; 2001US-0260018P.  
PR 08-JAN-2001; 2001US-0260360P.  
PR 28-FEB-2001; 2001US-0272411P.  
PR 02-MAR-2001; 2001US-0272817P.  
PR 05-JUL-2001; 2001US-0303231P.  
PR 12-JUL-2001; 2001US-0305060P.  
PR 10-SEP-2001; 2001US-0318405P.

12-SEP-2001; 2001US-0318700P.  
04-JAN-2002; 2002US-00037417.  
(CURA-) CURAGEN CORP.  
Kekuda R, Alsbrook JP, Tchernev VT, Liu X, Spytek KA;  
Pattarajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CM, Li L;  
PI Gorman L, Edinger S, Schiore P, Ellerman K, Malyankar U;  
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;  
PI Padigaru M, Taupier RJ, Miller CE, Eisen A;  
XX  
XX WPI: 2002-583619/62.  
DR N-PSDB, ABQ93882.  
XX  
XX Novel polypeptides and nucleic acids homologous to transmembrane  
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
PT treating cancer, atherosclerosis, neurological, skin and autoimmune  
PT disorders.  
XX  
XX Claim 1c; Page 23; 323pp; English.  
XX  
XX The invention relates to 24 novel human proteins designated NOVI-NOVI4  
XX (ABB09501-ABB09524), collectively referred to as NOVI proteins, and  
XX nucleic acids encoding them (ABQ93879-ABQ93902). NOVI proteins, and  
XX nucleotides are useful in the treatment, diagnosis or prevention of NOVI-  
XX associated disorders or in the manufacture of a medicament for treating  
XX such disorders, with specific applications described for each of the 24  
XX NOVI proteins, based on their homology to known proteins. Various  
XX disorders are associated with NOVI proteins including neurological  
XX disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
XX pain, behavioural disorders, addiction, tuberous sclerosis, cancers  
XX (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
XX (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
XX various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
XX (e.g., hypertension), reproductive disorders, endometriosis,  
XX incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
XX cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine  
XX disorders, obesity, bacterial infections and particularly cardiomyopathy,  
XX atherosclerosis, cell signal processing-related disorders and disorders  
XX of metabolic pathway regulation. NOVI nucleic acids and polypeptides may  
XX be used to identify cellular receptors or downstream effectors which  
XX binds to a NOVI protein, and are also useful as targets for the  
XX identification of small molecules that modulate or inhibit processes such  
XX as neurogenesis, cell differentiation, cell motility, cellular  
XX proliferation, haematopoiesis, wound healing and angiogenesis. NOVI  
XX nucleic acid sequences can be used to identify a cell or tissue type and  
XX are useful as a source of primers or probes for forensic biology and for  
XX identifying and cloning NOVI homologues in other cell types. Cells  
XX comprising NOVI nucleic acids are useful for producing non-human  
XX transgenic animals which are useful for studying the function and of NOVI  
XX activity. The present sequence represents the laminin alpha-5- like  
XX protein NOVIid. The gene encoding NOVIid is located on chromosome 20  
XX  
XX Sequence 1640 AA:  
Query Match 30.78; Score 6092; DB 5; Length 1640;  
Best Local Similarity 72.7%; Pred. No. 0;  
Matches 1197; Conservative 156; Mismatches 278; Indels 16; Gaps 5;  
QY 1970 CDRLEGYFGEQCGCRPCACGPAAGKSGECPQSGCHQCPGTTPQCLECAPGYWGLP 2029  
DB 1 CDRQEGHFNGCGGCRPCACGPAAGKSGECPQSGCHQCPGTTPQCRECAPGYWGLP 60  
QY 2030 EKGRCRCQPRGHCDPHTGHTCTCPGLSGERCCTCSQHQHVPVPGKPGHIGCEVCDHC 2089  
DB 61 EQGRCRCQCPGRCDPHTGRCNCPGLSGERCCTCSQHQHVPVPGKPGHIGCEVCDHC 120  
QY 2090 VVLLDLELAGALLPAIRELOQGINASSAAWRLHRLNASIADLOSKLRPPGPRYQAA 2149  
DB 121 VVLLDLELAGALLPAIRELOQGINASSAAWRLHRLNASIADLOSKLRPPGPRYQAA 180  
QY 2150 QQLQTLFQQSISLQDPTERLGSATVQGGAGQLDITTESTLGRAQKLVSVAVGRLN 2209

Db 181 QLEVLQQSTSLQCDARRLGGQAVGTRDQASQLLACTEATLGHAKTLAAIRAVDRTLS 240  
Qy 2210 ELASRMGGSPGDALVPSGEQLRWALAEVERLLWDMFTDLGACGAVAEAEAEALQRLMA 2269  
Db 241 ELSMOTGHGLANASAPSGEQLRTLAVERLLWEMEARDLGAPAAAEAEALAAQKLLA 300  
Qy 2270 RVQQLTSFWEENOSLATHRDQLAQVYESGLMDLREALNCAVNTTREAEBELNSRNOERVK 2329  
Db 301 RVQQLSLEENQALATQDRDLAQHAGLMDLREALNCAVNTTREAEBELNSRNOERLE 360  
Qy 2330 EALQWKBELSDNATLKATQAASLIILGHVSELQIGIQDQAKEDLEHLAASLDGAWTPLLK 2389  
Db 361 EALQKBELSDNATLQATLHAARDTTLASVFRLLHSLDQAKBELRLAASLDGARTPLLQ 420  
Qy 2390 RMQAFSPASSKVDLVEAEBAHQKLNQALNLSGIIILGINODRFIQAEVANSAYSSILQ 2449  
Db 421 RMQTFSPAGSKRLRVEAEBAHQKLNQALNLSGIIILVDNODRLTORAIEASNAYSRILQ 480  
Qy 2450 AVQAAEDAAAGALQARQARTWEMVYVQGLAAGAROLLANSALBETTLGHQGRGLAQGR 2509  
Db 481 AVQAAEDAAAGALQAOADHTWATVVRQGLVDRQAQLLANSTALBEAMLQEQORGLVWAAL 540  
Qy 2510 QAAGIQLHNWARKNQLAAQIQEAOAMLANDTSETSKIAHAKAVAAEALSTATHVQSOL 2569  
Db 541 QGARTQLRDVRAKXQDLQEAHIQAACANLAMDDETSTSKIAHAKAVAAEALSTATHVQSOL 600  
Qy 2570 QGMOKNVERWOSQLGGLOQDLSOVERDASSVSTLEKTLPOLAKLSRLNENGVNASL 2629  
Db 601 QAMQENVERWOGQVGLRGQDLGAVLDAGHSVSTLEKTLFOLLAKLSILENENGVNASL 660  
Qy 2630 ALSANIGRVKLIQAASAKSKVKVMKFNRSRVRPRDLADLAAYTALKFHTQSPV 2689  
Db 661 ALSASIGRVRELIAQARGAASKVKVPMKFNRSRQVLRTPRDLADLAAYTALKFYLG-- 718  
Qy 2690 PAPPGKNTGDHFLVNGSRQATGDYNGVSLRNQKVMYRIGKAGPTTSLIDENIGEOF 2749  
Db 719 PEPEPGQOTDRFVYNGSRQATGDYNGVSLRDKKVMYVQLGAGPAVLSDIEDIGEOF 778  
Qy 2750 AAVSIDRTLQFGHMSVTEKOMVHEIKGDTVAPGSEGLNLHPDDFFVYGGYPSNFTPP 2809  
Db 779 AAVSLDRTLQFGHMSVTEKOMVHEIKGDTVAPGAEGLNLHPDDFFVYGGYPSNFTPP 838  
Qy 2810 EPLRFPGLGCIEMETNEEVSYLNFEQTFMDDTAVDKPCASKATGDPMLDGSVLDG 2869  
Db 839 PLLRFPFGYRGCIEMDTNEEVSYLNFEQTFMDDTAVDRPCASKSKTGDPMLDGSVLDG 898  
Qy 2870 SGFARISPEKQFNKTFQDLRLVSYNGIIFFLKQBSQFLCLAVQEGTLVLFYDFGSG 2929  
Db 899 TGFARISPDQSITTKRFEQELRVSYSGVLFLLKQSQFLCLAVQBSLVLLYDFGAG 958  
Qy 2930 KKADPLOPPQALTAASKAIQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGV 2989  
Db 959 KKAVPLOPPPLTSASKAIQVFLLAGSRKRVLRVERATVYSVEQDNLDLADAYILGV 1018  
Qy 2990 PPEQLPLSLROLFPSSGSGVRGCIKIGIKALGYDLKRLNTTGISFGCTADLLVGRMTTFH 3049  
Db 1019 PPDQLPSLRLWLPFTGSGVRGCVKIGIKALGYDLKRLNTTGVSACTADLLVGRMTTFH 1078  
Qy 3050 GHGFLPALPDVAPITEVYSGFGFRGTQDNLLIYRTSPDGPYQVSLREGHTVLRPMNQ 3109  
Db 1079 GHGFLRLALSNVAPLTGNVYSGFGFHSQASALLIYRASPDGLCQVSLQQGRVSLQLRT 1138  
Qy 3110 EVETQRYFADGAPHVAFYSNVTCGWLVDQOLVKSHERTTLMLOPEEPSRLILGG 3169  
Db 1139 EVKTQAGFADGAPHVAFYSNATGWLVDQOLVKQMPHGRPPPELOPQEGEPRLILGG 1198  
Qy 3170 LPVSGTTHNFSGCISNVFQRLRQFQVFDLQHNQMSVNVSGCTPAQLIETS----- 3222  
Db 1199 LPESGTIYFSGCISNVFQRLRQFQVFDLQHNQMSVNVSGCTPAQLIETS----- 1258  
Qy 3223 RATAQKVSRRRQSQDLACTTTPMLPGTIQDAVQFGPLPSYLOFVCISSHNRLHLSM 3282  
Db 1259 QATARKASRRSRQPARHPACMLPPLHRLTRTDSYQFGGSLSHLEFVGILARHNWPSLSM 1318

3283 LVRPHAAQSGILLSTAPMSGRSPSLVLFNLHGHFVAQTEGPGPRLQVQSRQHSRAGQWHR 3342  
Db 1319 HVLPR-SRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLTRLRAQSRQSRSPGRWHK 1377  
Qy 3343 VSVRGMQOIQLVVDGSGOTWSQKALHHRVPRAERPQPYTLVSGGLPASYSKSLPVSYGF 3402  
Db 1378 VSVRMEKRIILLVDGARANQSQEGPHRQHQAEHPQHTLVFGGLPASHSKSLPVTVG 1437  
Qy 3403 SGCLKKLDQDQPLRTPTQMGVTPCVSGPLEDGLFFPGSGGVVTLLELPKAMPYVLSLEL 3462  
Db 1438 SGCVRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLDPVGL 1497  
Qy 3463 EMRPLAAAAGLPHLQALATPYMQLKVLTEOVLLQANDGAGEFSTWVTPK-LCDGRWHR 3521  
Db 1498 EVRPLAVTGLIFHLQARTPYLQL-----QVLLRADDDGAGEFSTVTRPSVLCDDQWHR 1552  
Qy 3522 VAVIMGRDTLRLVDVTQSNHTTGRPLPESLAGSPALLHLSLPKSTARPPELPAYRGCLR 3581  
Db 1553 LAVMKSNGVLRLEVDQAQSNHTVGPLLAAAAGAPLPLGLPEPMAVQPNPPAYCGCMR 1612  
Qy 3582 LLINGAPYNTVASVOIQGAVGMRGCP 3608  
Db 1613 LAVNRSPVAMTRSEVHGAVGASGCPA 1639

RESULT 11  
AAM39009  
ID AAM39009 standard; protein; 1601 AA.  
XX AAM39009;  
XX  
DT 22-OCT-2001 (first entry)  
XX Human polypeptide SEQ ID NO 2154.  
XX  
DE Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW Peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
DR N-PSDB; AAI58165.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.  
XX



PS	Example 4; SEQ ID NO 2154; 10078pp; English.	
XX	The invention relates to human nucleic acids (AA157798-AA161369) and the	
CC	encoded polypeptides (AA38642-AA42213) with neurotropic,	
CC	immunopressant and cytostatic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localised neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilisation of the activities such as: immune system suppression,	
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and	
CC	C.N.S disorders. Note: The sequence data for this patent did not form	
CC	part of the printed specification	
XX		
XX	Sequence 1601 AA;	
XX	Query Match 29.5%; Score 5871.5; DB 4; Length 1601;	
XX	Best Local Similarity 72.5%; Pred. No. 0;	
XX	Matches 1161; Conservative 155; Mismatches 275; Indels 11; Gaps 4;	
QY	2015 GPQCECAPGYVGLPEKGCRCOCPCRGCHDPTHGCTCPPLGSGRCDCSCQOHOVPVPG 2074	
DB	2 GPQCECAPGYVGLPEKGCRCOCPCRGCHDPTHGCTCPPLGSGRCDCSCQOHOVPVPG 61	
QY	2075 KPGCGHICEVCDHCVLLDDLERAGALLPAIRBQLOGINASSAAWRLHRLNASIADL 2134	
DB	62 GPVGHSHICEVCDHCVLLDDLERAGALLPAIRBQLOGINASSAAWRLHRLNASIADL 121	
QY	2135 QKLRPPGPVQAAQOLTLQCSISLODTERLGSQATGVQGAQGLDTESTLGRA 2194	
DB	122 QSLRSPGPRHETAQQLVLEQSTLSLQGDARRLGGQAVGTRDQASLLAGTEATLGA 181	
QY	2195 QKLESVRVAGNALNLSRMGGSPCDALVPSGEQLRWALAEVERLLDMRTRDLGAQ 2254	
DB	182 KYLLAAIRAVDTLSLMSQTHGLANASRSGQLLTAEVRLWEXEARLDGAQ 241	
QY	2255 AVAEELABARQIMARVQSLTSFWEENOSLATHIRDQAQVSGIMDLREALNOAVNTT 2314	
DB	242 AAEEELAAARQIMARVQSLTSFWEENOSLATHIRDQAQVSGIMDLREALNOAVNTT 301	
QY	2315 REAEELNSORVKEALQKSELSDNATLTKATLQASLLIIGHVSELLQGLDQAKEDE 2374	
DB	302 REAEELNSORVKEALQKSELSDNATLTKATLQASLLIIGHVSELLQGLDQAKEDE 361	
QY	2375 HLAASLDGAWTFLPKEMQAFSPASSKVDLVEAAEAHAQKLNQALNLSGIILGINQDRFI 2434	
DB	362 RLAAASLDGAWTFLPKEMQAFSPASSKVDLVEAAEAHAQKLNQALNLSGIILGINQDRFI 421	
QY	2435 QRAVENASYSILQAVQAEADAAGALFOASRTWEMVYVORGLAAGALLANSALBET 2494	
DB	422 QRAVENASYSILQAVQAEADAAGALFOASRTWEMVYVORGLAAGALLANSALBET 481	
QY	2495 ILGHQGRGLGAQRLQAAGIQLHNYWARKNQAAQIQEAQAMLANDTSETSEKIAHAKAV 2554	
DB	482 MLQEQORGLVWALQAGTQLRDVRAKQDLQEAHIQAAQAMLANDTSETSEKIAHAKAV 541	
QY	2555 ABAELSTATHVQSLQGMQKQVVERQSLGGLQGGDLSDVERDASSVSTLEKTLIPOLLA 2614	
DB	542 ABAEQDTATRVQSLQGMQKQVVERQSLGGLQGGDLSDVERDASSVSTLEKTLIPOLLA 601	
QY	2615 KLSRLNRRGVHNASLALSANIGRVRKLIQAARSAASKVKVSMKFNRRSGVRLRPRDLAD 2674	
DB	602 KLSRLNRRGVHNASLALSANIGRVRKLIQAARSAASKVKVSMKFNRRSGVRLRPRDLAD 661	
QY	2675 LAAYTALKPHIQSPVAPPEPGKNTGDHFLVLYNGSQATGDYNGVSLRNQKHVWYRLSKA 2734	
DB	662 LAAYTALKPHIQSPVAPPEPGKNTGDHFLVLYNGSQATGDYNGVSLRNQKHVWYRLSKA 719	
QY	2735 GPTTILSIDENIGEQFAAVSIDRTLQFGHMSVTVRQMVHEIKGDTVAPGSEGLNLNHPDD 2794	
DB	720 GPAVLSIDENIGEQFAAVSIDRTLQFGHMSVTVRQMVHEIKGDTVAPGAGGLNLRPDD 779	
QY	2795 FVFVGGYVGNFTPPPEPLRPPGVLGCIEMETLNEEVVSLNPNBQTMFLDPAVDPKPARSK 2854	
DB	780 FVFVGGYVGNFTPPPEPLRPPGVLGCIEMETLNEEVVSLNPNBQTMFLDPAVDPKPARSK 839	
QY	2855 ATGDPMLTDSYLDGGGFARISFEKQFNSNTRKPDQELRLVSYNGIIFFLKQESQFCLAV 2914	
DB	840 STGDPMLTDSYLDGGGFARISFEKQFNSNTRKPDQELRLVSYNGIIFFLKQESQFCLAV 899	
QY	2915 QEGTLVLFYDGSGLKKADPLOPQALTAASKAIOVFLLAGNKRVLVVRVERATVSVDO 2974	
DB	900 QEGTLVLFYDGSGLKKADPLOPQALTAASKAIOVFLLAGNKRVLVVRVERATVSVDO 959	
QY	2975 DNMLEMADAYLLGGVPEQPLSLRLOLFPSSGSGVRCIKGKALGYVDLKRLLNTTGISF 3034	
DB	960 DNMLEMADAYLLGGVPEQPLSLRLOLFPSSGSGVRCIKGKALGYVDLKRLLNTTGISF 1019	
QY	3035 GCTADLLVGRVTFHGHGFLPLADPVAITEVYVYSGFGRGCTQDNNLLVYRSPDGPYQ 3094	
DB	1020 GCTADLLVGRVTFHGHGFLPLADPVAITEVYVYSGFGRGCTQDNNLLVYRSPDGPYQ 1079	
QY	3095 VSLREGHVTILRFMNQEVETQVFADGAPHYVAVFVSNVTGVWLVYVDDLOQLVKSHERTPM 3154	
DB	1080 VSLREGHVTILRFMNQEVETQVFADGAPHYVAVFVSNVTGVWLVYVDDLOQLVKSHERTPM 1139	
QY	3155 LQIQPEPSKLLGGLPVSGTFFNFSGCISNVFVQRLRGQRVDFLHONMGSVNVVSGCT 3214	
DB	1140 LQIQPEPSKLLGGLPVSGTFFNFSGCISNVFVQRLRGQRVDFLHONMGSVNVVSGCT 1199	
QY	3215 PAQLIETS-----RATAKVSRRSRQPSODLACTTTPMTPGTIQDAYQFGGPLPSYLOF 3267	
DB	1200 PAQLIETS-----RATAKVSRRSRQPSODLACTTTPMTPGTIQDAYQFGGPLPSYLOF 1259	
QY	3268 VGISPSHRNLHLSMLVRPHAAQGLLLSTAPVSGRSPSLVFLFNHGHFVAQTEGPGPRL 3327	
DB	1260 VGISPSHRNLHLSMLVRPHAAQGLLLSTAPVSGRSPSLVFLFNHGHFVAQTEGPGPRL 1318	
QY	3328 QVQSOHRSRAGQHRVSVRGMQIQLVVDGSGTQSKALHHRVPRAPERQPVYTLVSGGL 3387	
DB	1319 QVQSOHRSRAGQHRVSVRGMQIQLVVDGSGTQSKALHHRVPRAPERQPVYTLVSGGL 1378	
QY	3388 PASSYSSKLPVSVGFSGLKLLQDLQPLRTPTQMVGVTPCVSGPLEDGLFFPGSGVVT 3447	
DB	1379 PASSYSSKLPVSVGFSGLKLLQDLQPLRTPTQMVGVTPCVSGPLEDGLFFPGSGVVT 1438	
QY	3448 LELPKAKMPVSVLEENRPLAAAGLIFHLQALATPYMQLKVTEQVLLQANDGAGEFST 3507	
DB	1439 LELPKAKMPVSVLEENRPLAAAGLIFHLQALATPYMQLKVTEQVLLQANDGAGEFST 1498	
QY	3508 WVTYPK-LCDGRVHRVAVIMGRDTRLVDTQSNHTTGRPLPESLAGSPALLHLGSLPKSS 3566	
DB	1499 WVTYPK-LCDGRVHRVAVIMGRDTRLVDTQSNHTTGRPLPESLAGSPALLHLGSLPKSS 1558	
QY	3567 TARPFLPAYSGCLRKLINGAPVNVVTSVQIQAGVNRGCPSS 3608	
DB	1559 TARPFLPAYSGCLRKLINGAPVNVVTSVQIQAGVNRGCPSS 1600	
XX	RESULT 12	
XX	ABB64954	
XX	ID ABB64954 standard; protein; 3712 AA.	
XX	AC ABB64954;	
XX	DT 26-MAR-2002 (first entry)	
XX	DE Drosophila melanogaster polypeptide SEQ ID NO 21654.	
XX	KW Drosophila; developmental biology; cell signalling; insecticide;	
XX	KW pharmaceutical.	

OS	Drosophila melanogaster.	QY	478	PESQCMCRITGFEGRCDHCHALGYFHPFLCOLCGCSFAGTLPEGCD-EAGRCQCRPGFDG	536
XX		Db	509	VTTGECCLTNFGDNCERCKGHYFNFTGYSYCDNDQGTSEISECNKQGCICREGF	568
XX		QY	537	PHCDRLPGVGHYDPDCHACACDREGALDQCGVGLCHCRPGNTGATCQCSCPGFYGPPS	596
PD	27-SEP-2001.	Db	569	PRCQCLPGFYNYPDPCPCNSSTGSAITCDNTGKCNCLNPNFAGKQCTICTAGYYSYDP	628
XX		QY	597	CIPCHCSADGSLHTTCDPTTGQCRPRVTGLHCDMCPGAYNPPYCEASGCHPAGLAP-	655
XX		Db	629	CLPCHCDSHGSGVSCN-SDGQCLCPNFDGRQDCSKGFGYFNPPSCDCNCDAGVIDK	687
PA	(PEKE ) PE CORP NY.	QY	656	-ANPALPETQAPCMCRAHVSGPCDRCKPGVWGLSASNPEGCTRCSCDPRGTGLGVTECQ	714
XX		Db	688	FAGGSPVVGELCKCKERVGTGRI CNECKPLYNNINISNTEGEICDCTDGTISALDTCT	747
XX	Venter JC, Adams M, Li PWD, Myers EW;	QY	715	G-NQGCFCCKAHVCGKTCACACXGDFGLDYADYFCRCRCRCDVGGALGQCGCEPKTGACRCR	773
DR	WPI; 2001-656860/75.	Db	748	SKSGCPCKPHTQGRQCQCKRGTDFLDSASLFGCKDCSDVGGWSQVCDKISQCKCH	807
XX	N-PSDB; ABL09057.	QY	774	PNTOGPTCSEPAKHLYLPDLHMLLELEAATPGHVRFGFNPLEFENFESMRGVAHMVA	833
PT	New isolated nucleic acid detection reagent for detecting 1000 or more	Db	808	PRITGLACTQPLTTHFTLHQFYEDGSLPGGTQVRDYDEAAPFGFSKSGYVFNNA	867
PT	genes from Drosophila and for elucidating cell signaling and cell-cell	QY	834	IQPRIVARLNVTSPLFRLVRYVNRGSTSNGOISVREECKLSSTCTNCTEQSQPVAFPP	893
PT	interactions.	Db	868	IONDVRENVVFKSSLYRILVRYNPNANVTATISVTSNPLE-----VDQHVKVLQP	922
PS	Disclosure; SEQ ID NO 21654; 21pp + Sequence Listing; English.	QY	894	STEPAFVTV--PQPGCEPFVNLPGIALLVEA-EGVLLDYVLLPSTYEAALLQHRVT	950
XX	The invention relates to an isolated nucleic acid detection reagent	Db	923	TSEPFVTVAGPLGVKPSAIVLDPRYVFTTKANKNMWLDYFVLLPAAFYAAGLTHRIS	982
CC	capable of detecting 1000 or more genes from Drosophila. The invention is	QY	951	EACTVRPSALSTENCILVYAHLPDGFPSAAGTEALCRHNSLRPCPTLEQLSPSH----	1006
CC	useful in developmental biology and in elucidating cell signalling and	Db	983	NPC-----ELGNMELCRHYKASVEFSPAATPFVI--GENSKPTNPVETVTDDEHLQIV	1035
CC	cell-cell interactions in higher eukaryotes for the development of	QY	1007	-----PPLATCFGSDVDIQLEMAVPOGQYLVVEYGE-----DSHQMGVAVHTQRA	1056
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	Db	1036	SHVEDIPVLS---GQNELHYIVDPGRSGYFVIDYISDRNFPDSYI---INUKLNDP	1089
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	QY	1057	PQGVNLNHPGYSLSRSPARDTQHLLAIFHLDE--ASIRLTA---EQAHFPLHSLVT	1111
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-	Db	1090	DSEISVLYPLCYLTICETSVNEDGMEKS-FYINKEDLPVILISADIEDGSRPFIISVA	1148
CC	ABB72072). The sequence data for this patent did not form part of the	QY	1112	VPVEEFSFEVFEVFCVSSHGTFNPSAACLASRFPKPPQPIILKOCQVLPDPDPLT	1171
CC	printed specification, but was obtained in electronic format directly	Db	1149	IPVDQMSIDYINPSPVCVI-----HDQCATKFRSVP-----DSKKIEFTD----	1191
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences	QY	1172	QSQELSPCAPBEGPQPRPTAVDPNAEPTLL-RHQGTWVFTTQV-----PTLGRYAFLLH	1226
XX	Sequence 3712 AA;	Db	1192	HEDRIATNKPYY-----ASLDERVKLVHLDSQNEATIVIESKVDTAKPNL--FVILVK	1242
QY	Query Match	QY	1227	GYQPVHPSFPYEVVLINGGR-IWQGHANASFCPHGYGCTRLVLCGQTMVDVTDNLTVTV	1285
Db	Best Local Similarity	Db	1243	YYQPSHPKYQVYVYTLTAGKNQYDGKFDIQHCPSSSGCRGVIRPAGESFEI-DDEFKFTI	1301
QY	Matches 1226; Conservative 595; Mismatches 1528; Indels 569; Gaps 122;	QY	1286	RVPEGRWMLDYLIVPEDAYSSVLOEPLDKSVDFISHCATQGYHISPSSSSPFCRNA	1345
Db		Db	1302	TDRSQVMLDYLVVVPLQYNDLLVEETFDQTKFQIONCHDHPHILT-HVADDFCKS	1360
QY	1 DLYCKLVGVPVAGDPN-QTIOGQYCDICTAANSNKAHPVSNNAIDGTERWQSPPLSRGL	QY	1346	ATSLSLFYNNAGALPCGCEHVGAVSPTCEPFGGQCPGRGHVIGRDCRCATGYWGFNCRP	1405
Db	51 ELYCKLVGANTEDHDIDYSVIQGVQVCDYCDPTVPERNHPPENNAIDGTEAWQSPPLSRGM	Db	1361	VPSLTADYNSGALPCNCDYAGSTSFECFPGGQCPKPNVIERTCGACRSRYGFPDCKP	1420
QY	60 EYNEVNTLDLGVFHVAVYLIFANSRPRDLAVLERSDFGHTYQWQFFASKRDCLE	QY	1406	CDC-GARLCDBELTGQCICFPRTVPDCLVCPQSGCHPLVGCCECNCGSGGVQELDTPT	1464
Db	111 KFEVNTIINFEQHFVAYLFIKMGNSRPRGLTLEKSTDYGTWTFWQHFSPTPADCT	Db	1421	CKCPNSAMCEPTEGCMCPFNVI GDLCEKAPNTYGFHQVIGCEBACNPNMGIAN-GNSQ	1479
QY	120 RFGPRTLERITQDDDVICTEYSRIVPLENGEIVSLVNGRPGALNFSYSPLLRDTKAT	QY	1465	CDMSDQCRCPNVAGRRCDDTCAPGYGYPSCRPCDCHCACTMASVCCDPLTGQCHKENV	1524
Db	171 YFGKDTYKPI-TRDDDVICTEYSKIVPLENGEIPVMLLNERPSSYFNSTVLQEWTRAT	Db	1480	CDLFGTCECQNTTEGRACDVCSNGYFNFPFCEQCSCHKPGTELEVCDKIDGACFCCKNV	1539
QY	180 NLRRLRTNLLHNGKALRDPVTTRYVYYSIKDISIGRCVCHGHADVCDKADPLDP	QY	1525	QGSRCQCRVGTFTSLDAANPKGCTRCFCFGATERCG-----NSNLARH-----BEVD	1571
Db	231 NVRIRLRTKNLGLHLSVARQDPTVTRRYFYSIKDISIGRCVCMGHADTCDVKDKSP				
QY	240 FR-LQCAQCHNTCCGSDRCPCPNQOPKWPATPDSANECCSCNCHGHAYDYCYDPEVDR				
Db	291 VRILACRQHTCGIQNCECCPGFEQKKWRQNTNARPFNCEPCNCHGSHNECKYDEEVNR				
QY	299 RNAQONQNVYGGGVCLDQHHGTGNCERCLPGFFRAPDQPLDPSHYCRDCSDST				
Db	351 KGLSLDTHGHYDGGGVQCONQHNVTGNCNKRKPKYTRPKGHNWNETDVCSQCQDYFS				
QY	359 DGTCEDTGRCYCRPNFTGELCAACAEGYTDFPHCYPLPSPPHNDTREQVLPAQIVNCD				
Db	411 TGHCEETGNCERAAQPPSCDSCAYGYGPNP-----RE-----CE				
QY	419 CNAAGTGNACRKPRLGRVCKNPNFRGAHCELCAQFPHG-PSCHPQCCSPGVANSLCD				
Db	450 CNLNGTNGYHCEAERG-QQCFCKINFAQYKQCAEGYGFPECKACECNKIGITNDCN				

Db 1540 VGRDCCQVDGYINLQESPNDCCTTCFCGKTSRCDSDAVLRVYVYVLLKXHSITTPPEPHE 1599  
Qy 1572 MEGWLLSDRQVWPHHRPEL-----LHAD--LRSVADTFSELYWQAPSYLG-----1620  
Db 1600 ES-----IKPDMVPVPAD-----EILLNETLKADFTLREVND-----ERPAIFVGLDYL 1644  
Qy 1621 ----DRVSSYGGTLYHVELHSETQGDIFIPYESRDPVVLQGNQMSIAFLAFLAYPPGGQVH 1676  
Db 1645 LNCNWHISAYGGDLAYTLFTSGPDKYI---VAPDVILFSEHNALVHTSYEQPSRNEPF 1701  
Qy 1677 RQQLQVLEGNFRHLEPHNVSREELMMVLAGELOIQIRALFSQTSSSVSLRVVLEVAE 1736  
Db 1702 TNKRVNIVESNFQTI-SGKPVSRADFMVLRDLKVFIRANYWEQTLVTHLSDVYLTLADE 1760  
Qy 1737 AGRGPASN---VELCMCPANYRGDSCQACAGYVYRDTKGLFLGRCVPCOCHGHRDCLP 1793  
Db 1761 DADGTGEYQFLAVERCSPGSGHSCDCACAGYVYRDPSPGGYVPCPCNGHSETCDC 1820  
Qy 1794 GSGICVGCQHTGDCQCRCPGFVSSDPSPASPCVPCPCPLAVPSNPNFADGCVLRNGR 1853  
Db 1821 ATGICSKQHGTEGDCRCCVSGYGNATNGTPGDCMICACPLPDSNNFATSCBISBSG 1880  
Qy 1854 TQ--CLCRGYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNDNMIFSDCDPLTGACR 1911  
Db 1881 DQTHCECKPGYTPRCESCANGFYGPESIGQVCKPCECGNINPEDQGS--CDTITGECL 1939  
Qy 1912 GCLRHTTGHCRCAPFGYNALLPNCNTRCPCSTGTCQDPSQGRCLCKAGVTVGQRCD 1971  
Db 1940 RCLNNTFGAACNLCAFGYDAIKLNCQSCDCDDLTGTCDPFGVGVCTCHENVIGDRCD 1999  
Qy 1972 RCLGVFGFQCGOCPKPCAGPAAKSECHPOSGQCHQCPGTGQCLCAFGYVGLPEK 2031  
Db 2000 RCKPDHYFESGVGCRACDGAASNTQCDPHTGHCACKSGVTGRCQDCAVDHMKYKD 2059  
Qy 2032 GCRRCOCPRGH-----CDPHTGHTCPCPGLSGBRCDTSCQHQVPPGKPGHGHCEVC 2086  
Db 2060 GCTPCNCGYSRGFCNGNTGKQCLPGVIGDRCDACPNRW---VLKDEG---CQBC 2112  
Qy 2087 DHCWVLLDDLERAGALLPAIREQLOGINASSANWARLRLN-----ASIALDQSLRRP 2141  
Db 2113 NNCHALLDVTMRMYQIDSV---LDFNSVTLAFTSOKLANYDQALDELEPKVKLLDP 2169  
Qy 2142 PGPYQAQOQLTLEQSQISLQODTERLGSQATGVQOGQGLDITTESTLGRAQKLLSV 2201  
Db 2170 -----NSVDLSFKKANSLESDAKSYAKVQNTLANAFDIRERSSTLGNITVAY---2220  
Qy 2202 RAVGRALNELASRMGQSGDALVPGEQRLRWALAEVERLLMDMTRDLGAQGAABAEAL 2261  
Db 2221 -----DEAVKSAQAKAEIASVEALSKNLE-----AAASTKIDAAAL 2256  
Qy 2262 AEQRLMARVQ-----EOLTSFWEENQSLATHIRDO---LAQYESGLMDLRE 2305  
Db 2257 EQACHILGQINGTISILTNEQVLEKARKLYEYVTLVLPKAKNKSIALKNNDIGESPD 2316  
Qy 2306 ALNCAVNTTREABELNSRQERYKEALQWKQELSQDNATLKATLOA-----A 2352  
Db 2317 HLEDLFWS--EASQAKSADVERNRVANQAFDNSKFTVSEQKLAQEKNIKAGNFLING 2375  
Qy 2353 SLILGHVSELLQSIDQAKEDLEHLAASLDGAWTPLLKRWQAFSPASSKVDLYEAAEBAHAQ 2412  
Db 2376 DLTLNQINQKDLNRDALNELNSFNKNVD---BELPVEDQHKEDALTDQAE-----Q 2426  
Qy 2413 KLNQALAINLSGIILG-INODRFTQRAVEASNAYSSILQVQAAEDAAQALRQASRTWM 2471  
Db 2427 KAELALKAQDLAAQYTDMTASAEPAIKAAATYSGIVEAVEAAQKLSQDAISAAGNATDK 2486  
Qy 2472 ----VQVQGLAA--GARQLLANS--SALRETLHGQRLGLAOGELQAGLOAGQLHNWARKNQ 2525  
Db 2487 TDGIEERAHLDATGSTDLLQARQSLQKVQDDLEPRLNASAGKVQ-----KISAVNNA 2539  
Qy 2526 LAAQIOBAQAMLANDTSETSEKI--ALAKAVAAEALSTATHVQSQLOQMOKNVERMOSQLG 2584

Db 2540 TEHLQKDKINKLDOLPAESORDMKNNSNANASDALBILKNVLEILPVSQVOTPELEKAH 2599  
Qy 2585 G-----LQGDLSQVER---DASSSVSTLEKTLQQLAKLSLENRGVHNASIALSANI 2635  
Db 2600 GINEDLDLTNKDYSQANKQLDDVEGVSVKLSE-----LAEDIEEQHRVGSQSRQLGQEI 2654  
Qy 2636 GRVKLJAQARSAAKVKUSMKNGSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPG 2695  
Db 2655 ENLKAQVEAARQANSIKGVNFKPSTILELKTPEKTKLATNTNSTYFRITTEPS-----2710  
Qy 2696 KNTGDHVLVYM---SRQATGYMGVSLRNQKVHWYRLGKAGPTTLSDENI--GEQF 2749  
Db 2711 -----GFLLYLGNDKNTAQKNDFVAEIVNGYPILTIDLGN--GPERITSDKYVADGRWY 2764  
Qy 2750 AAVSIDTLQFGHMSVTVKQMVHEIKGDTVAPGSEGLN-----LHPD--DFVYVGGYP 2803  
Db 2765 QAV--VDR--MGPNAKLTIREELFN---GDVVBHSKSGYLEGSONILHVDKXSLFVGGYP 2818  
Qy 2804 --SNFTPEPLRPFGYLGCIEMETLNEEVSLYNF-----BOTMLDITAVDKPC 2850  
Db 2819 GISDFNAPDPLTNSFSGDIEDLKIGDESGLVFNWVYVDDNDQAGAREDRVLEKKFVTG 2878  
Qy 2851 ARSKATGDPMLTDGSLYLDGSGFARISPEKQFSNTKRPDQBLRLVSVNGIILFFLKQESQFL 2910  
Db 2879 LRPKXGVVQLNATSNLKSRSIQFSF-----KADKO-----TSNGLLFFYGRDKHYM 2926  
Qy 2911 CLAVQEGTLVLFYDFGSLKKAQPLQPPQALTAASKAIQVFLLAGNKRKRV-----LVRV 2964  
Db 2927 SIEMIDGAIFNLSLGE-----GGVQ-----SGSQDRNDNQWHKQVA 2965  
Qy 2965 ER-----ATVFSVDQNMLEMDAYLGGVPE--QLPLSLRLQLFPFSGSV 3008  
Db 2966 ERENENGLLKVDIVISRTNAPLEADLEPKRLRYFGCHPRRLNTSISLQPNFD-----3020  
Qy 3009 RGCTKGKALKGYVDLKLRLNT--TGISFGCTADLLVGRMTFHHGELPLALPDVAPITEV 3067  
Db 3021 -GCIDNVINGVVDLYEYVYTGGEVGECSAKSTVVSYPAPHEYFLRMNVSDDNLHV 3079  
Qy 3068 VYSGFGRGTQDNKLLYRTSPD--GPYQVSLREGHVTLRFM--NQYETQVRFADGAPHY 3124  
Db 3080 V---LHKFTQPGVLYFAANHDOSSITGLSQDGLLKANSQSLVIDRILLNDEGDHV 3136  
Qy 3125 VAFVSVNTGWLVDQLOLVKSHERTTLMLOLP--EERSRLLLGCLP-----VSG 3174  
Db 3137 VTVOHTQOGLRLTVDD---VDNKRGLSP---QPLILEGGDIFFAGLPONYRTPRNALA 3188  
Qy 3175 TFHNFSGCISNVFORLRLGQPVDFDL---HQNMGSVNVSVGC-----3213  
Db 3189 SLAYFVGCISDVTVN-----EEIINFANSAEKKNNGIN---GCPPHVLAYPESLVPSVYP 3240  
Qy 3214 -----TPAQL 3218  
Db 3241 SGDNEVSPWSNADTLPLKPDIESTLPTPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTSP 3300  
Qy 3219 I-----ETSRTATQVRRSRQSPQ---DLACTTTPMLPTIOD---AYQFGGCLPSY 3264  
Db 3301 VIDEKELEAKTPQKI-LTTPPAKMLNLPDSERCKLPEQNFVDFTFEGYRFYGLREQR 3359  
Qy 3265 LQFVGISPSHENRHLNLRPHAAASQGLLSTAPMSGRSPSLVFLNHHGHVFAQTGPGP 3324  
Db 3360 LQINSLPVKVRERHDIGISPRTERPN--GLLI--VAGSKQRDDFIAYVLLDGRVTVYER--VG 3416  
Qy 3325 PRLO--VQSRQHSRAGQWHRVSVWGMQOQLVVDGSGTWSQKALHHRVPAERPOP---3379  
Db 3417 AQLQAKITTEAELNDGTWHTVTVRQTKVSLLDKLEQPGSVDLN-----AESAPVLA 3471  
Qy 3380 --YTLISVGLL-----PASSYSKSLPVSVGSGCLKKLQLDKQPLRTPQMVGTTPC 3428  
Db 3472 VELPYLGGVKNKFLSESVKNLTDFTKTEVPY---FNGCLKNKIKFDAMBLETPPEEFGVVP 3528  
Qy 3429 VSGPLEDLFPFGSEGVVTELEPKAKMPYVSLEMLPLAAGLIF--HLQOALA-----3481  
Db 3529 -SEQVERGLFENNOKAFYKIFDHFVGVGTEMKISDFRPRDNGLLTFSVHGKNKSYAILLEV 3587

QY 3482 --TFYMLKVLTEQVLLQANDGAGEFSTWVTP---KLCGRWHRVAVIMGRDTLRLVLD 3536  
Db 3588 DNTLYFTVKDNLKIV-----STNYKLPNNESEFCDGKTRNVQAKSKFVINIAD 3637  
QY 3537 -TOSHTTGLPESLAGSPALLHGS-----LPKSSSTARPELPAYRGCLRLKLLINGAPV 3589  
Db 3638 FISSNPGVNEGVSIVTTRNPLFLGGHVAPORAPGKTKK-----SPKGCISKVEVNQRM 3693  
QY 3590 NVTASVQIQGAVGMRGCP 3607  
Db 3694 NITPNM-VVGDIWQGYCP 3710

RESULT 13

ADE09114  
ID ADE09114 standard; protein; 1486 AA.  
AC ADE09114;  
XX  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Novel protein-related contig polypeptide sequence #180.  
XX  
XX novel gene; novel protein; tissue marker; molecular weight marker;  
XX novel chromosome marker; genetic disorder; contig.  
XX Unidentified.  
OS  
XX WO2003054152-A2.  
PN  
XX  
XX 03-JUL-2003.  
XX  
XX 10-DEC-2002; 2002WO-US039555.  
XX  
XX 10-DEC-2001; 2001US-0339739P.  
PR 11-DEC-2001; 2001US-0339453P.  
PR 14-MAR-2002; 2002US-0365091P.  
PR 14-MAR-2002; 2002US-0365384P.  
PR 12-APR-2002; 2002US-0372381P.  
PR 12-APR-2002; 2002US-0372615P.  
PR 22-APR-2002; 2002US-00128558.  
PR 24-APR-2002; 2002US-0376045P.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Drmanac RT, Wang Z;  
PI Ma Y, Wang D, Chen R, Xu C, Boyle B;  
XX WPI; 2003-569235/53.  
XX  
XX New polynucleotides, useful for expressing recombinant proteins for  
PT analysis, characterization or therapeutic use, or as markers for tissues  
PT in which the corresponding protein is preferentially expressed.  
XX  
XX Disclosure; SEQ ID NO 2658; 1177pp; English.  
XX  
XX The invention comprises the amino acid and coding sequences of novel  
CC proteins. The DNA and protein sequences of the invention are useful as:  
CC markers for tissues in which the corresponding protein is preferentially  
CC expressed; as molecular weight markers on gels; as chromosome markers or  
CC tags; to identify chromosomes or to map related gene positions; and to  
CC compare with endogenous DNA sequences in patients to identify potential  
CC genetic disorders. The present amino acid sequence was used in the  
CC exemplification of the invention.  
XX  
XX Sequence 1486 AA;  
SQ

Query Match 20.0%; Score 3968.5; DB 7; Length 1486;  
Best Local Similarity 45.4%; Pred. No. 3.8e-218;  
Matches 737; Conservative 208; Mismatches 490; Indels 189; Gaps 18;

QY 1 DLVCKLVGGPVAGDPNQTIQGOYCDICTAANSKKAHPVSNADIGTERRWQSPPLSGLE 60  
Db 43 ELYCKLVGGPAPGS-GHTIQGFCDCNSEDPRKAHPVNAIDGSRWQSPPLSGTG 101  
QY 61 YNEVNTLDLQGVPHVAYVLIKFANSRPPDLWLWLERSTDFGHTYQPMQFASRKCDCLER 120  
Db 102 YNRVNTLDLQGLPHVAYVLIKFANSRPPDLWLWLERSTDFGHTYQPMQFASRKCDCLE 161  
QY 121 FGPTRLERITODDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSP-LLRDFTKATN 180  
Db 162 FGREANMAVTRDDDLVCTYSRIVPLENGEVVSLVNGRPGAKNFTFSTLRGVGNK 221  
QY 181 IRLAFLRLNTLLHLMGKALRDPVTTRYYYSIKDISIGGRVCVCHGADVCDADPLDPF 240  
Db 222 HPLAFLRLNTLLHLSKAQRDLSTRYYYSIKDTAIGGCVCNCHAEVCNINNPEKLF 281  
QY 241 RLQACQHNTCGSDRCRCPNQPKPATTSANECQNCNCHGHAYDCVYDEVEDRN 300  
Db 282 R--CECQHHTCGTCDRCCTGYNQRRWRPAWEGSHESCEACNCHGHASNCIYDPVREQ 339  
QY 301 ASQNDNVYGGGVCLDCQHHHTGINCERCLPGFRAPDOPDLSPHYCRPCDCESDFTDG 360  
Db 340 ASLNTQIYAGGVGCINCQHNNTAGVCEQCAKYRYPGVVPDADGICPCSCPEHADG 399  
QY 361 TCEDLTGRCYCRPNFTBELCAACAEYTDPPHCYPLSPFPHNDTREQLVPAQIIVNDCN 420  
Db 400 -CEQSGRCHCKPNFHDNCEKCAIGY-NFPVCLRIPIFPVSTPSSDPVAGDIKGCDCN 457  
QY 421 AAGTQGNACRDPRLGRVCCKPNFRGAHCELCAFGHGPSCHPCQCSPPGVANSLCDPES 480  
Db 458 L----- 458  
QY 481 GQCMRTGFEGRDCHCALGYFHPFLCQLGCSFAGTLPEGCDRAGRCQRPFGDGHCD 540  
Db 459 -----EGVLPEICDAHGRCLCRPGVEGRCD 484  
QY 541 RCLPGYHGYDCHACADPRGALDQCGVGLCHCRPNTGATCQECSPGYGFPSPCIPC 600  
Db 485 -----TCRSGYSPIQAC 499  
QY 601 HCSADGSLHTTCDPTTGQCRCPRTVGLHCDMCPGAYNFFPYCBAGS--CHPAGLAHPN 658  
Db 500 WCSALGSYQMPGSSVTGQCECRPGVTGQRCDRLCSGAYDFPHCPQSSSACDPAGTINWL 559  
QY 659 ALPETOAPCMCAHVEGSCDRCKPGYGLSASPEGCTRCSDPRGLGGVTSC-QQNG 717  
Db 560 GY-----CQCKLHVEGPTCSRCLLYWNLDKENPSCGCKCHKGGTVSGTGECRQDG 613  
QY 718 QCFCKAHVCGKTCMAACKDGFGLDYADYFGCRSCRDVGGALGQGCCEPKTGACRCRPTQ 777  
Db 614 DCHCKSHVGGSDCTCEDGYFALEKSNYFGCGQCDIGGALSSNCSGSPGVCCREHW 673  
QY 778 GPTCSEPAKHVLPDLHMRLEBEATPEGHAVRFGNPLEFENFSGVHMAIQPR 837  
Db 674 GKVCORPENNYFPDLHMKYEIEDGSTPNGRDLRFGDFLAFPEFSGVQAQVAVQND 733  
QY 838 IVARLNV--TSPDLPLRVRYNRGSTSVNGOISVREBEGKLSSTCTNCTEQSQPVAFPPST 895  
Db 734 VRITLVKSGSLFRVILRVNPGTEAVSGHIIYPSWGA-----QSKELIFLSK 786  
QY 896 EPFAVTVQRFGEFVNLNPGIALLVEAGVLDYVLLPSTYEAALLQHRVTEACTY 955  
Db 787 EPFAVTLPGNGFADPFSTPGMWACIKAEGLVLDYLLPRDYEAASDLQVTEPCAY 846  
QY 956 RPSALHSTENCLVAAHLPLDGFPSAAGTEALCRND--NSLPRPCPTEQLSPSHPPPLATCF 1013  
Db 847 ---AGPPQENCLLYOHLFPVTRFPCTRCEA--RHFLLDGEPRPVAVROPTAHPVWVDLS 901  
QY 1014 GSDVDIQLEMAVPOQGYVLVVEYVGDSHQMVGAVHTPORAPQGVNLNHPDYSILC 1073  
Db 902 GREVELHLRVIPQGVYVWVVEYSTEAAQLFVVDANVKSSGSLAGQVNIYSNYSVLC 961  
QY 1074 RSPARDTQHLAI FILDSEASIRLTAEQAHFLLHSVTLVPVEEFPSTEFVPRVFCVSSHG 1133

962 RGAVIDHMSRIAMVELLTADIQKHGMARFLLHQVCIIPIEYSAEYVRPQVHCIA SVG 1021  
 1134 TNPSSAACLASRFPKPPQPIILKQCVLPPLPDDIPLTOSQELSGAPGEGPQPPPTAV 1193  
 1022 RFVNSQATCVSLAHETPPTALLDLVLSGRFF-PLHP-----QQSGPSVDV 1065  
 1194 DPAEPTLLRHPOGTIVFTQVPTLGRYAFLLHGGQPVHPSPFVEYLNGGRIMQGHANA 1253  
 1066 LFG---VTLKAPQNVTLGRVPHLGRYVFIHFYQAAHPTTPAQVSDGQWPRAGS FPA 1122  
 1254 SPCPHGYGRTLVLCGGQTMVDNDELVTVRVPEGRWLDYVLIVPEDAYSSSYLOE 1313  
 1123 SFCPHVLCGRDQVIVXGQIEFDISEPEVAATVKVPEGKSLVLRVLVWPAENYDYOILHK 1182  
 1314 EPLDKYDIISHCATOGYHISPSSSPFFCNRNATSLSFYNGALPCGCHVEGAVSPICE 1373  
 1183 KSMKSLSEITTCGKNSFYLDQTSRFPCKNSARSLVAFYHKGALPCECHPTGATGPHCS 1242  
 1374 PFGQGPCRHVIGRDCSRCATGYWGFNCG---RPGDCGARLCEDELTCGICCPRTVPDPDC 1431  
 1243 PEGGSAHAFPTSGGSAAPVQOATYGFPRCKPKPCSCGRRLCEEMTGQCRCPRTVRPQC 1302  
 1432 LVCQPOSFCHPLVGCENCSGPGVQELTDFPCDMSQCCRCRPNVAGRRCDTCAPGFY 1491  
 1303 EVCEHSHSLHPVAGCEGNCSSRGRTIEAMPFCRDEDSGCCGCKPRITGRQCDRCASGFY 1362  
 1492 GYPSCRPCDCHEAGTWASVCDPLTGQCHCKENVQSGRCDQCVGTFSLDAAKPKGCTRCF 1551  
 1363 GFPECVPCNCRDCTEPFGVCDPTGACLCCKENVGTECNVCREGSPHLDPANLKGCTSCF 1422  
 1552 CPGATERCGNSNLARHEFVDMEGWLLSSDRQVPHHEHREPEIELHLADLRSVADTFSELY 1611  
 1423 CFGVNNQCHSSHRRKRTKFDVLMGLHLETDADVDPVSVFPGNSWVADLQELPATIHAS 1482  
 1612 WQAP 1615  
 1483 WQAP 1486  
 RESULT 14  
 AAM50358  
 ID AAM50358 standard; protein; 953 AA.  
 AC AAM50358;  
 XX AAM50358;  
 DT 18-FEB-2002 (first entry)  
 DE Human laminin-15 alpha 5 chain.  
 KW Laminin-15; human; retina; eye; therapy; ophthalmological;  
 KW antiinflammatory; rod dystrophy; rod-cone dystrophy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200183516-A1.  
 XX 08-NOV-2001.  
 PD 01-MAY-2001; 2001WO-US013943.  
 PF 01-MAY-2000; 2000US-0200863P.  
 PR 01-MAY-2000; 2000US-0200863P.  
 XX (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 XX Burgeson RE, Brunken W, Champliand M, Hunter D;  
 PI WPI; 2002-041478/05.  
 XX N-PSDB; AAI70817.  
 DR Novel substantially pure preparation comprising laminin having laminin  
 PT chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders

PT XX such as retinitis pigmentosa, macular degeneration, retinal detachment.  
 PS Disclosure; Fig 2A; 59pp; English.  
 CC The present sequence is that of the alpha 5 chain of human laminin-15, a  
 CC novel member of the laminin family that is produced in the retina. The  
 CC retina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2,  
 CC gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed  
 CC within the inter-photoreceptor matrix and in the outer plexiform layer,  
 CC and may serve to stabilise retinal synapses. The invention provides  
 CC laminin-15 preparations and cells comprising a nucleic acid encoding the  
 CC laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of  
 CC producing laminin-15. The laminin-15 preparation is used in claimed  
 CC methods of: increasing retinal immunophotoreceptor matrix stability;  
 CC increasing the stability of retinal photoreceptor compounds, especially an  
 CC outer segment, inner segment or synapse; increasing retinal adhesion;  
 CC treating a disorder associated with retinal degeneration, especially rod  
 CC dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration  
 CC and retinal detachment; increasing the stability of synapses of the  
 CC central nervous system or peripheral nervous system; stimulating an  
 CC neuroregeneration, axon outgrowth or synapse formation; preparing an  
 CC implant, e.g. a catheter, artificial joint, retinal implant, timed  
 CC releasing device, neural cell growth guide or artificial tissue, by  
 CC coating with the laminin-15 preparation; and increasing photosensitivity  
 CC by implanting a tip coated with the laminin-15 preparation into an eye.  
 CC The laminin may be recombinant, and the 3 chains co-expressed in the same  
 CC cell or expressed in different cells  
 XX Sequence 953 AA;

Query Match 17.6%; Score 3488.5; DB 5; Length 953;  
 Best Local Similarity 70.9%; Pred. No. 6.6e-191;  
 Matches 677; Conservative 105; Mismatches 162; Indels 11; Gaps 4;  
 QY 2662 SGVRLRPRDLADLAATALKHFIQSPVAPPEKQNTGDHFVLYMGSROATGYMGVSLR 2721  
 DB 1 SGVQLRTPRLADLAATALKFVLLQ--PEPEPQGGTEDFRVYMGSRQATGYMGVSLR 58  
 QY 2722 NOKVHVYRLKGAGPTTSLIDENIGEOFAAVSIDRTLOFGHMSVTVKQMVHEIKGDTVA 2781  
 DB 59 DKVHVYVQLGEAGPAVLSDIDEGEQFAAVSLDRTLOFGHMSVTVKQMVHEIKGDTVA 118  
 QY 2782 PGSEGLNLNLHPDDFVYVGYGYPNSFTPPPLRPPGYLGCITEMETLNEEVVSLNFBOTFM 2841  
 DB 119 PGAEGLNLNLRPDDFVYVGYGYPSTFTPPPLRPPGYRGCIEMDTLNEEVVSLNFBOTFM 178  
 QY 2842 LDTAVDKPCARSKATGDPWLTDGSLDGSQGFARISPEKQFSNTKRPDQELRLVSYNGIIF 2901  
 DB 179 LDTAVDRPCARSKSTGDPWLTDGSLDGTGFARISFDSQISTTKRFEQELRLVSYSGVLP 238  
 QY 2902 FLKQESQFLCLAVQEGTLVLFYDFGSLKKADPLQPPQALTAASKAIQVFLLAGNRKRVL 2961  
 DB 239 FLKQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPLTSASKAIQVFLLAGNRKRVL 298  
 QY 2962 VRVERATVFSVDONMLEMADAYVLLGGVPPPEQLPLSLRQLFPGSGSVRGCIKGKALKGY 3021  
 DB 299 VRVERATVYSVEQNDLELADAYVLLGGVPPPDQPPSLRWLFPPTGGSVRGCVKIGALKGY 358  
 QY 3022 VDLKRLNTTGISFGCTADLLVGRMTTFHGHGFLPLALPDVAPITEVYVYSGFGRGTQDNN 3081  
 DB 359 VDLKRLNTTGVSACTADLLVGRAMTFHGHGFLRLALSNVAPLTGNYVYSGFGRHSAQDSA 418  
 QY 3082 LLYRTSPDGPYQVSLREGHVTILRFMQVETQRFADGAPHYVAFVSNVTGWLYVDDQ 3141  
 DB 419 LLYTRASPDGLCQVSLQCGVSLQLLRETVKTQAGFADGAPHYVAFVSNVTGWLYVDDQ 478  
 QY 3142 LQLVKSHERTTPEMLQLOPEBPSRLLLGGLPVSGTFHNFSGCISNVFQRLRGPGORVFDLH 3201  
 DB 479 LQVKNKPHRGPPPELOPQPEGPRLLLGGLPESGTIYNFSGCISNVFQRLRGPGORVFDLQ 538  
 QY 3202 QNMGSVNVVSGCTPAQLIETS-----RATAKVSRSRSPQSDLACTTWPMLPGTIQDA 3254  
 DB 539 QNLGSVNVVSGCAPALQATPGLPGRGLQATARKASRSRQPARHPACMLPPLHTRTRDS 598

QY 3255 YQFGGPPSLVQFVIGISPSHRNRLHLSMLVVRPHAAAGQGLLLSTAPMSGRSPSLVLFNNG 3314  
DB 599 YQFGGSLSSLEFVIGILARHNWPSLSMHVLP-R-SRGLLFTARLRPGSPSLALFLSNG 657  
QY 3315 HFVAQTGPGPRQLQVQSRQSRAGQHRVSVRWGMQIQLVDSQTSWQKALHHRVPRA 3374  
DB 658 HFVAQMEGLTRLAQRQSRQSRGRWHKVSVRKEKRILLVTDGARANQSGGPHRQOGA 717  
QY 3375 ERQPYTLVGGLPASSYSKLPVSVGFSCGLKKQLQDKQPLRTPQMVGVTPCVSGPBLE 3434  
DB 718 EHPQPHTLFVGGLPASSSHSKLPVTVGFGSCVRLRLHGRPLGAPTRMAGVTPCILGPLE 777  
QY 3435 DGLFFPGSEGVVTLLEPKAKMPVYSLEMRPLAAGLIFHLGQALATPVMQLKVLTQOV 3494  
DB 778 AGUFPFGGCVITLLEPCALPLDVGLEVRPLAVTGLIFHLQOARTPPYLQLOVTEKQV 837  
QY 3495 LLQANDGAGBFSTWVTPK-LCDGRWHRVAVINGRDLRLVDTQSNHTTGRLPESLAGS 3553  
DB 838 LLRADDCGAGBFSTVTPSVLQDQWHLAVMSGNVRLVEDVAQSNHTVPLPLAAAGA 897  
QY 3554 PALLHGLSPKSTARELPAYRGCLRLKLLINGAPVNTVASVOICAGVMRGCPGS 3608  
DB 898 PAPLYLGLPEPMAVQPPWPAYCGCMRLAVNRSPVANTRSVVRGAVGASGCPA 952  
RESULT 15  
ID ABB09502 standard; protein; 908 AA.  
XX AC ABB09502;  
XX DT 01-NOV-2002 (first entry)  
XX DE Human laminin alpha-5-like NOV1b protein, SEQ ID NO:4.  
XX KW Human; NOVX; neurological disorder; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;  
KW addiction; tuberous sclerosis; cancer; immune disorder; allergy;  
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;  
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;  
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;  
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;  
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;  
KW atherosclerosis; cell signal processing-related disorder;  
KW metabolic pathway regulation disorder; cytotoxic; neuroprotective;  
KW antiinflammatory; immunosuppressive; analgesic; antithrombotic;  
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;  
KW differentiation; proliferation; motility; haematopoiesis; wound healing;  
KW angiogenesis; forensic biology; transgenic animal; drug screening;  
KW gene therapy; NOV1b; laminin alpha-5-like; chromosome 20.  
XX OS Homo sapiens.  
XX PN WO200253742-A2.  
XX PD 11-JUL-2002.  
XX PF 07-JAN-2002; 2002MO-US000375.  
XX PR 05-JAN-2001; 2001US-0260018P.  
PR 08-JAN-2001; 2001US-0260360P.  
PR 28-FEB-2001; 2001US-0272411P.  
PR 02-MAR-2001; 2001US-0272817P.  
PR 05-JUL-2001; 2001US-0303231P.  
PR 12-JUL-2001; 2001US-0305060P.  
PR 10-SEP-2001; 2001US-0318495P.  
PR 12-SEP-2001; 2001US-0318700P.  
PR 04-JAN-2002; 2002US-00037417.  
XX (CURA-) CURAGEN CORP.  
XX PA Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;  
PI

PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;  
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;  
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;  
PI Padigaru M, Taupier RU, Miller CE, Eisen A;  
XX WPI; 2002-583619/62.  
DR N-PSDB; ABO93880.  
XX Novel polypeptides and nucleic acids homologous to transmembrane  
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
PT treating cancer, atherosclerosis, neurological, skin and autoimmune  
PT disorders.  
XX Claim 1c; Page 17; 323pp; English.  
PS The invention relates to 24 novel human proteins designated NOV1-NOV14  
CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and  
CC nucleic acids encoding them (ABQ33879-ABQ3902). NOVX proteins and  
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-  
CC associated disorders or in the manufacture of a medicament for treating  
CC such disorders, with specific applications described for each of the 24  
CC NOVX proteins, based on their homology to known proteins. Various  
CC disorders are associated with NOVX proteins including neurological  
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
CC pain, behavioural disorders, addiction, tuberous sclerosis, cancers  
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
CC (e.g., hypertension), reproductive disorders, endometriosis,  
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine  
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,  
CC atherosclerosis, cell signal processing-related disorders and disorders  
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may  
CC be used to identify cellular receptors or downstream effectors which  
CC binds to a NOVX protein, and are also useful as targets for the  
CC identification of small molecules that modulate or inhibit processes such  
CC as neurogenesis, cell differentiation, cell motility, cellular  
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX  
CC nucleic acid sequences can be used to identify a cell or tissue type and  
CC are useful as a source of primers or probes for forensic biology and for  
CC identifying and cloning NOVX homologues in other cell types. Cells  
CC comprising NOVX nucleic acids are useful for producing non-human  
CC transgenic animals which are useful for studying the function and  
CC activity of NOVX proteins and for identifying and evaluating modulators  
CC of NOVX activity. The present sequence represents the laminin alpha-5-  
CC like protein NOV1b. The gene encoding NOV1b is located on chromosome 20  
SQ Sequence 908 AA;  
Query Match 16.7%; Score 3325; DB 5; Length 908;  
Best Local Similarity 70.8%; Pred. No. 1.5e-181;  
Matches 646; Conservative 99; Mismatches 154; Indels 14; Gaps 4;  
QY 2704 LYNGSRQATGDMGVSLRNQKHVYRLGKAGPTTLSDENIGQFAAVSDRTLQFGHM 2763  
DB 1 MYNGSRQATGDMGVSLRDKKXVHYQLGEAGPAVLSDIDIGQFAAVSDRTLQFGHM 60  
QY 2764 SVTVKQMVHEIKGDTVAPGSEGLNLHPDDFVFGVGGYPSNFTPEPLRFPGLGCIEM 2823  
DB 61 SVTVRQMIQETKGTDTVAPGAGLLNLPDDFVFGVGGYPTFTFPLLRFPFGYRGCIEM 120  
QY 2824 ETLNEEVSVLNFEQTFMLDITAVDKPCARSKATGDPWLTGDSYLDGSGFAISFKQFSN 2883  
DB 121 DTLNEEVSVLNFEQTFMLDITAVDRPCARSKGTGDPWLTGDSYLDGTFGFAISFDSQIST 180  
QY 2884 TKRFQDELRLVSYNGIIFFLKQESOFCLAVQEGTLVLFYDFGSLGKKADLPQPQALTA 2943  
DB 181 TKRFQDELRLVSYNGVLFLLKQSQFCLAVQBSGLVLLYDFGAGLKKAVLPQPPPLTS 240  
QY 2944 ASKAIQVFLLAGNRKRVLRVERATVFSVDQNNMLEMADAYVLGGVPPPEQPLSLRQLFP 3003  
DB 241 ASKAIQVFLGGSRKRVLRVERATVYSVEQNDLELADAYVLGGVPPDQLPPLSLRWLFP 300

Search completed: May 18, 2004, 14:41:46  
Job time : 135.708 secs



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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:30:58 ; Search time 27.4981 Seconds  
(without alignments)  
6824.493 Million cell updates/sec

Title: US-10-037-182-4  
Perfect score: 19876  
Sequence: 1 DLYCKLVGSPVAGSDPNQTI.....QKALQTHAXPSVPLLMH 3635

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pgp:\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pgp:\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pgp:\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pgp:\*  
5: /cgn2\_6/ptodata/2/iaa/6CTUS COMB.pgp:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pgp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19876	100.0	3635	US-09-845-583A-2	Sequence 2, Appli
2	3488.5	17.6	953	US-09-845-583A-4	Sequence 4, Appli
3	3096	15.6	3084	US-09-562-702A-12	Sequence 12, Appli
4	3096	15.6	3106	US-09-562-702A-10	Sequence 10, Appli
5	3010.5	15.1	3089	US-09-562-702A-4	Sequence 4, Appli
6	3010.5	15.1	3110	US-09-562-702A-2	Sequence 2, Appli
7	3005.5	15.1	3111	US-08-460-309-4	Sequence 4, Appli
8	3005.5	15.1	3111	US-08-125-077-4	Sequence 4, Appli
9	3005	15.1	3088	US-09-562-702A-8	Sequence 8, Appli
10	3005	15.1	3110	US-09-562-702A-6	Sequence 6, Appli
11	3005	15.1	3110	US-09-561-709B-7	Sequence 7, Appli
12	2727	13.7	3075	US-08-460-309-5	Sequence 5, Appli
13	2727	13.7	3075	US-08-125-077-5	Sequence 5, Appli
14	2171.5	10.9	1792	US-09-561-818A-4	Sequence 4, Appli
15	2171.5	10.9	1800	US-09-561-818A-8	Sequence 8, Appli
16	2171.5	10.9	1816	US-09-561-818A-2	Sequence 2, Appli
17	2171.5	10.9	1824	US-09-561-818A-6	Sequence 6, Appli
18	2149.5	10.8	1713	US-08-600-982-24	Sequence 24, Appli
19	2149.5	10.8	1713	FCT-US94-10261A-24	Sequence 24, Appli
20	2112.5	10.6	1792	US-09-561-818A-12	Sequence 12, Appli
21	2112.5	10.6	1816	US-09-561-818A-10	Sequence 10, Appli
22	1668.5	8.4	1799	US-09-845-583A-6	Sequence 6, Appli
23	1612	8.1	1798	US-09-561-709B-11	Sequence 11, Appli
24	1605	8.1	1765	US-09-562-702A-16	Sequence 16, Appli
25	1605	8.1	1765	US-09-561-818A-14	Sequence 14, Appli
26	1605	8.1	1786	US-09-562-702A-14	Sequence 14, Appli
27	1605	8.1	1786	US-09-561-818A-14	Sequence 14, Appli

28	1605	8.1	1786	4	US-09-561-709B-9	Sequence 9, Appli
29	1600	8.0	1798	4	US-09-845-583A-8	Sequence 8, Appli
30	1584	8.0	1725	4	US-09-562-702A-20	Sequence 20, Appli
31	1584	8.0	1725	4	US-09-561-818A-20	Sequence 20, Appli
32	1584	8.0	1786	4	US-09-562-702A-18	Sequence 18, Appli
33	1584	8.0	1786	4	US-09-561-818A-18	Sequence 18, Appli
34	1579.5	7.9	1761	4	US-09-561-709B-1	Sequence 1, Appli
35	1462.5	7.4	1587	4	US-09-845-583A-10	Sequence 10, Appli
36	1462.5	7.4	1587	4	US-09-561-709B-3	Sequence 3, Appli
37	1347.5	6.8	1572	4	US-09-562-702A-32	Sequence 32, Appli
38	1347.5	6.8	1572	4	US-09-561-818A-28	Sequence 28, Appli
39	1347.5	6.8	1605	4	US-09-562-702A-30	Sequence 30, Appli
40	1347.5	6.8	1605	4	US-09-561-818A-26	Sequence 26, Appli
41	1327.5	6.7	1576	4	US-09-562-702A-24	Sequence 24, Appli
42	1327.5	6.7	1576	4	US-09-561-818A-24	Sequence 24, Appli
43	1327.5	6.7	1584	4	US-09-562-702A-28	Sequence 28, Appli
44	1327.5	6.7	1609	4	US-09-562-702A-22	Sequence 22, Appli
45	1327.5	6.7	1609	4	US-09-561-818A-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1  
US-09-845-583A-2  
; Sequence 2, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-2

Query Match	100.0%	Score	19876	DB	4	Length	3635	
Best Local Similarity	100.0%	Pred. No.	0					
Matches	3635	Conservative	0	Mismatches	0	Indels	0	Gaps
0;								
Qy	1	DLYCKLVGSPVAGSDPNQTIQQYCDICTAANSKHAHPVSNADCTERWQSPPLSRGLE	60					
Db	1	DLYCKLVGSPVAGSDPNQTIQQYCDICTAANSKHAHPVSNADCTERWQSPPLSRGLE	60					
Qy	61	YNEVNVTLDLGOVHVAVYVLIKFPANSPRDLWLVERSTDFGHTYQPMQOFFASSKDDCLER	120					
Db	61	YNEVNVTLDLGOVHVAVYVLIKFPANSPRDLWLVERSTDFGHTYQPMQOFFASSKDDCLER	120					
Qy	121	FGPRLERITQDDVICITEYSRIIVPLENGEIVSLVNGRPGALNFYSYPLLRDFTKATN	180					
Db	121	FGPRLERITQDDVICITEYSRIIVPLENGEIVSLVNGRPGALNFYSYPLLRDFTKATN	180					
Qy	181	FLRLRLRNTLLHLMGKALRDPVTTRYYSIKDSTIGGRCVCHGHADVCDAXDPLDPF	240					
Db	181	FLRLRLRNTLLHLMGKALRDPVTTRYYSIKDSTIGGRCVCHGHADVCDAXDPLDPF	240					
Qy	241	RLQACQNTCGGSDRCPCPGFNQPKPATTTDSANEQSCNCHGHAYDYCYDVEVDRN	300					
Db	241	RLQACQNTCGGSDRCPCPGFNQPKPATTTDSANEQSCNCHGHAYDYCYDVEVDRN	300					
Qy	301	ASQNDVNYGGVCLDCQHTTTCINGERCILPGFERAPDQLDSPHYCRPCDCESDFTDG	360					
Db	301	ASQNDVNYGGVCLDCQHTTTCINGERCILPGFERAPDQLDSPHYCRPCDCESDFTDG	360					

Qy	361	TCBDLTGRCYCRNFTGELCAAAGYTDPPHCYPLPSPPHNDTRQVLPAGQIVNCDN	420
Db	361	TCBDLTGRCYCRNFTGELCAAAGYTDPPHCYPLPSPPHNDTRQVLPAGQIVNCDN	420
Qy	421	AAGTQGNACKDPRLGRCVCKPNFRGAHCBELCAPGFHGPSCHPCQCSSPGVANS.LCDPES	480
Db	421	AAGTQGNACKDPRLGRCVCKPNFRGAHCBELCAPGFHGPSCHPCQCSSPGVANS.LCDPES	480
Qy	481	GQCMRTGFGEDRCDHCALGYHFHPLCOLCGSPAGTLPBGCDGACRCQCRPGFDGPHCD	540
Db	481	GQCMRTGFGEDRCDHCALGYHFHPLCOLCGSPAGTLPBGCDGACRCQCRPGFDGPHCD	540
Qy	541	RLPGVGHYDPCACACDPRGALDQCGVGGLCHCRPGNTGATCQCSQPGFYGFPSCI PC	600
Db	541	RLPGVGHYDPCACACDPRGALDQCGVGGLCHCRPGNTGATCQCSQPGFYGFPSCI PC	600
Qy	601	HCSADGSLHTTCDPTTQCRPRVTGLHCDMCPGAYNPPYCEAGSCHPAGLAPANPAL	660
Db	601	HCSADGSLHTTCDPTTQCRPRVTGLHCDMCPGAYNPPYCEAGSCHPAGLAPANPAL	660
Qy	661	PETQAPCMCAHVEGSPCDCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQGNQCF	720
Db	661	PETQAPCMCAHVEGSPCDCKPGYWGLSASNPEGCTRCSDPRGTLGGVTECQGNQCF	720
Qy	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDOGALGQCGCEPKTGACRCRPNTOGPT	780
Db	721	CKAHVCGKTCACAKDGFGLDYADYFGCRSCRCDOGALGQCGCEPKTGACRCRPNTOGPT	780
Qy	781	CSEPAKHVLPDLHMELELEEAATPEGHVRGEPNPLEFENFSWGYAHMAIQPRIVA	840
Db	781	CSEPAKHVLPDLHMELELEEAATPEGHVRGEPNPLEFENFSWGYAHMAIQPRIVA	840
Qy	841	RLNVTSPLFRLVRYNRGSTSVNGQISVREBGLSSCTNCTEQSQPVAFPSTEPAFV	900
Db	841	RLNVTSPLFRLVRYNRGSTSVNGQISVREBGLSSCTNCTEQSQPVAFPSTEPAFV	900
Qy	901	TVPORGEFEPVLPNGI WALLVEABGVLLDYVLLPSTYYEALLGHRVTEACTYRPSAL	960
Db	901	TVPORGEFEPVLPNGI WALLVEABGVLLDYVLLPSTYYEALLGHRVTEACTYRPSAL	960
Qy	961	HSTENCLVYAHLPDGFPSAAGTEALCRHDSNLPFCPTQLSPSHPP.LATCFGSDVDIQ	1020
Db	961	HSTENCLVYAHLPDGFPSAAGTEALCRHDSNLPFCPTQLSPSHPP.LATCFGSDVDIQ	1020
Qy	1021	LEMAVPOGQVYLVEVYVGEDSHQEMGVAHTPQAPQOQVNLHPCPYSSLCRSPARDT	1080
Db	1021	LEMAVPOGQVYLVEVYVGEDSHQEMGVAHTPQAPQOQVNLHPCPYSSLCRSPARDT	1080
Qy	1081	QHHLAI FHLDEASIRLTAAQAHFFLHSVTLVPVEBPFSTEFVPRVFCVSSHGTNPSSA	1140
Db	1081	QHHLAI FHLDEASIRLTAAQAHFFLHSVTLVPVEBPFSTEFVPRVFCVSSHGTNPSSA	1140
Qy	1141	ACLASRFPKPPQPIILKDCQVLPPLDPLTQSQELSPGAPPPEGQPRPPTAVDPNAEPT	1200
Db	1141	ACLASRFPKPPQPIILKDCQVLPPLDPLTQSQELSPGAPPPEGQPRPPTAVDPNAEPT	1200
Qy	1201	LLRHPQGTWTTQVPTLGRYAFLLHGYQVHPSPFVVEVLNGRIWGHANASFCPHGY	1260
Db	1201	LLRHPQGTWTTQVPTLGRYAFLLHGYQVHPSPFVVEVLNGRIWGHANASFCPHGY	1260
Qy	1261	GCRTLVLCGQTMLDVTDNELTVTVRVPGEGRWMLDYVLIVPEDAYSSSYLQEBPLDKSY	1320
Db	1261	GCRTLVLCGQTMLDVTDNELTVTVRVPGEGRWMLDYVLIVPEDAYSSSYLQEBPLDKSY	1320
Qy	1321	DFISHCATQGHISFSSSSSPCRNAATSLSFYNNGALPCGCHVEGAVSPCTCFPGQCP	1380
Db	1321	DFISHCATQGHISFSSSSSPCRNAATSLSFYNNGALPCGCHVEGAVSPCTCFPGQCP	1380
Qy	1381	CRGHVIGDSCRCATGYWGFNCRPCDCGARLDCDELGTGQCICPPRTVPPDCLVCQPSFG	1440
Db	1381	CRGHVIGDSCRCATGYWGFNCRPCDCGARLDCDELGTGQCICPPRTVPPDCLVCQPSFG	1440

Qy	1441	CHPLVGEECNCSGPGVOELTDPDTCMDSDGQCRCPNVAGRRCDTCAFGYGVPSCRPCD	1500
Db	1441	CHPLVGEECNCSGPGVOELTDPDTCMDSDGQCRCPNVAGRRCDTCAFGYGVPSCRPCD	1500
Qy	1501	CHEAGTMAVCDPLTGTQCHCKENVOGSRCDQCRVGTFTSLDAANPKGCTRCFCFGATBRG	1560
Db	1501	CHEAGTMAVCDPLTGTQCHCKENVOGSRCDQCRVGTFTSLDAANPKGCTRCFCFGATBRG	1560
Qy	1561	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTTFSELYWQAPPSYL	1620
Db	1561	NSNLARHEFVDMEGWLLSSDRQVVPHEHRPEIELLHADLRSVADTTFSELYWQAPPSYL	1620
Qy	1621	DRVSYYGTLHYELHSETQRGDIPIPYESRPDVVVLQGNQMSIAFLELAYPPPGVHRGQL	1680
Db	1621	DRVSYYGTLHYELHSETQRGDIPIPYESRPDVVVLQGNQMSIAFLELAYPPPGVHRGQL	1680
Qy	1681	QLVEGNFRHLETHNPVSRREELMVLGLQIQRALFSQTSSSVSLRRVVLVASEAGRG	1740
Db	1681	QLVEGNFRHLETHNPVSRREELMVLGLQIQRALFSQTSSSVSLRRVVLVASEAGRG	1740
Qy	1741	PPASNVELCMCPANRYGDSQCECAPGYVRTDKGLFLGRCPVCQCHGSHDRCLPGSGICVG	1800
Db	1741	PPASNVELCMCPANRYGDSQCECAPGYVRTDKGLFLGRCPVCQCHGSHDRCLPGSGICVG	1800
Qy	1801	COHNTGDOCHRCRCPGVSSDPSNPASPCVSCPLAVPSNPNFADGVLNRGTQCLCRP	1860
Db	1801	COHNTGDOCHRCRCPGVSSDPSNPASPCVSCPLAVPSNPNFADGVLNRGTQCLCRP	1860
Qy	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNNIFSDCDPLTGACRCGLRHTTGP	1920
Db	1861	GYAGASCERCAPGFFGNPLVLGSSCQPCDCSGNGDPNNIFSDCDPLTGACRCGLRHTTGP	1920
Qy	1921	HCERCAPGYNALLPGNCTRCDCSPGTETCDQSGRCCLCKAGVTGORDCCLGEGFGF	1980
Db	1921	HCERCAPGYNALLPGNCTRCDCSPGTETCDQSGRCCLCKAGVTGORDCCLGEGFGF	1980
Qy	1981	EOCGRCACGPAKSGSECHPGQSGQCHQCPGTTGPQCLECAPGYWGLPEKGCRCRCQCP	2040
Db	1981	EOCGRCACGPAKSGSECHPGQSGQCHQCPGTTGPQCLECAPGYWGLPEKGCRCRCQCP	2040
Qy	2041	GHCDPHTGHTCPPGLSGERCDTCSQOHQVVPKPGHGHCHVCVLLDLDLERA	2100
Db	2041	GHCDPHTGHTCPPGLSGERCDTCSQOHQVVPKPGHGHCHVCVLLDLDLERA	2100
Qy	2101	GALLPAIREQLOGINASSAAWARLHRLNASIADQSKLRPPGPRYQAAQLOTLQOQSI	2160
Db	2101	GALLPAIREQLOGINASSAAWARLHRLNASIADQSKLRPPGPRYQAAQLOTLQOQSI	2160
Qy	2161	SLQODTERLGSQATGVQOQAGQLDTESTTLGRAQKULESVRAVGRALNELASRMGQSP	2220
Db	2161	SLQODTERLGSQATGVQOQAGQLDTESTTLGRAQKULESVRAVGRALNELASRMGQSP	2220
Qy	2221	GDALVPSGEOLRWALAEVERILLWMDRTDLGAQGAFAEAEAEQRLMARVQEOQLTSFE	2280
Db	2221	GDALVPSGEOLRWALAEVERILLWMDRTDLGAQGAFAEAEAEQRLMARVQEOQLTSFE	2280
Qy	2281	ENQSLATHIRDQLAQYESGLMDLREALNQA VNTTREAELNSRNOERVKELQWKQELSQ	2340
Db	2281	ENQSLATHIRDQLAQYESGLMDLREALNQA VNTTREAELNSRNOERVKELQWKQELSQ	2340
Qy	2341	DNATLKATLOASLILGHVSELLOGIDQAKEDLSLASLDGANTPLLRKMQAFSPASSK	2400
Db	2341	DNATLKATLOASLILGHVSELLOGIDQAKEDLSLASLDGANTPLLRKMQAFSPASSK	2400
Qy	2401	VDLVEAAEAHAQKLNQALNLSGIILGINQDRFTIQRAVEASNAYSSILQAVQAAEDAAQ	2460
Db	2401	VDLVEAAEAHAQKLNQALNLSGIILGINQDRFTIQRAVEASNAYSSILQAVQAAEDAAQ	2460
Qy	2461	ALRQASRTWEMVQGLAAGARQLANSSALFEETILGHQGLAQGLQAGLQHNW	2520
Db	2461	ALRQASRTWEMVQGLAAGARQLANSSALFEETILGHQGLAQGLQAGLQHNW	2520
Qy	2521	ARKNQLAAQIOBAQAMLANDTSETSEKIAHAKAAEALSTATHVQSQLOQMKNVWRWQ	2580

Db	2521	ARKNQLAQAQOEQAQMLAMDTSETSEKIAHAKAVAAEALSTATHVQSQLOQMKNVERWQ	2580
Qy	2581	SQGLGQGDLSQVERDASSVSLEKTLPLQLAKLSRLNRRGNVGHNASLALSANIGRVK	2640
Db	2581	SQGLGQGDLSQVERDASSVSLEKTLPLQLAKLSRLNRRGNVGHNASLALSANIGRVK	2640
Qy	2641	LIAQARAASAKVKVSMKFNCSGVRLRPPRLADLAAYTALKFHIQSPVAPPEPKNTGD	2700
Db	2641	LIAQARAASAKVKVSMKFNCSGVRLRPPRLADLAAYTALKFHIQSPVAPPEPKNTGD	2700
Qy	2701	HFVLYMGSQRATGDMYGSVLNRQVHVYRLGKAGPTTILSIDENIQEQFAAVIDRTLOF	2760
Db	2701	HFVLYMGSQRATGDMYGSVLNRQVHVYRLGKAGPTTILSIDENIQEQFAAVIDRTLOF	2760
Qy	2761	GHSVTVVEKQWHEIKDTPVAPSGEGLNLNHPDDFVYVGGYPSNTPPEPLRFPYLG	2820
Db	2761	GHSVTVVEKQWHEIKDTPVAPSGEGLNLNHPDDFVYVGGYPSNTPPEPLRFPYLG	2820
Qy	2821	IEMETLNEEVVLYNPFQTFMLTAVDKPCARSKATGDPMLTDGSLDGSGFARISFEKQ	2880
Db	2821	IEMETLNEEVVLYNPFQTFMLTAVDKPCARSKATGDPMLTDGSLDGSGFARISFEKQ	2880
Qy	2881	FSNTRKPDQELRLVSYNNGIIFFLKQBSQFICLAVQEGTLVFDYFGSLKKADPLOPPQA	2940
Db	2881	FSNTRKPDQELRLVSYNNGIIFFLKQBSQFICLAVQEGTLVFDYFGSLKKADPLOPPQA	2940
Qy	2941	LTAASKAIQVFLLAGNKKVLYVVERATVPVSODNNLEADAYLGGVPPCOLPLSLRQ	3000
Db	2941	LTAASKAIQVFLLAGNKKVLYVVERATVPVSODNNLEADAYLGGVPPCOLPLSLRQ	3000
Qy	3001	LFPSGGSVRCIKGKIKALGKYVDLKLNTTGTISFGCTADLLVGRWTMTFHGHGFLPLALPD	3060
Db	3001	LFPSGGSVRCIKGKIKALGKYVDLKLNTTGTISFGCTADLLVGRWTMTFHGHGFLPLALPD	3060
Qy	3061	VAPITEVYVSGFGRGTQDNLLYYRTSPDGPYQVSLRGHVTLRPMNQEVETQRFADG	3120
Db	3061	VAPITEVYVSGFGRGTQDNLLYYRTSPDGPYQVSLRGHVTLRPMNQEVETQRFADG	3120
Qy	3121	APHYVAFYSNVTVGWLIVDDQLOLVKSHERTTPEMLQLOPPEPSRLLLGGLPVSGTFHNFS	3180
Db	3121	APHYVAFYSNVTVGWLIVDDQLOLVKSHERTTPEMLQLOPPEPSRLLLGGLPVSGTFHNFS	3180
Qy	3181	GCTSNVFPQRLRGPQRFVDLHQNMGSNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL	3240
Db	3181	GCTSNVFPQRLRGPQRFVDLHQNMGSNVSVGCTPAQLIETSRATAQKVSRRSRQPSQDL	3240
Qy	3241	ACTTPTMLPGTIODAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM	3300
Db	3241	ACTTPTMLPGTIODAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLSTAPM	3300
Qy	3301	SGRSPSLVFLFNHGHVTAQTEGPGPLQVQSRQHSRAGQWHRVSVRWGMQOQLVVDGSG	3360
Db	3301	SGRSPSLVFLFNHGHVTAQTEGPGPLQVQSRQHSRAGQWHRVSVRWGMQOQLVVDGSG	3360
Qy	3361	TWSQKALHHRVPAERPOQVTLTVSGGLPASSYSKLPVSVSGCLKKLOLQKQPLRPTT	3420
Db	3361	TWSQKALHHRVPAERPOQVTLTVSGGLPASSYSKLPVSVSGCLKKLOLQKQPLRPTT	3420
Qy	3421	QMVGVTPCVSGPLEDGLFPFGSEGVVTLPLKAKMPYVLSLEMRPLAAAGLIFFHLGQAL	3480
Db	3421	QMVGVTPCVSGPLEDGLFPFGSEGVVTLPLKAKMPYVLSLEMRPLAAAGLIFFHLGQAL	3480
Qy	3481	ATPYMQLKVLTEQVLIQANDGAGEFTWTYTKLCDGRHWRVAVIMGRDRTLEVDVTQSN	3540
Db	3481	ATPYMQLKVLTEQVLIQANDGAGEFTWTYTKLCDGRHWRVAVIMGRDRTLEVDVTQSN	3540
Qy	3541	HTTGRLPESLAGSPALLHLSLPKSTARPELPAYRGCLRKLLINGAPVNVITASVQIOGA	3600
Db	3541	HTTGRLPESLAGSPALLHLSLPKSTARPELPAYRGCLRKLLINGAPVNVITASVQIOGA	3600
Qy	3601	VGNRGCPSTLALSKQGKALTQRHAKPSVPLLWH	3635

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Db      3601  VGNRGCPSTGLALSQKGKALQTHAKPSVSPLLWH  3635

RESULT 2
US-09-845-583A-4
; Sequence 4, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583A-4

Query Match      17.6%; Score 3488.5; DB 4; Length 953;
Best Local Similarity 70.9%; Pred. No. 6.2e-262;
Matches 677; Conservative 105; Mismatches 16; Indels 11; Gaps 4;

QY      2662  SGVRLRPDRDLADLAAYTALKFHIQSPVAPPEPGKNTGDFVLVYMGSRQATGDYWGVSRLR  2721
DB      1     SGVQLTRPDRDLADLAAYTALKFYLGQ--PEPEPGQTEDEFVMTYMGSRQATGDYWGVSRLR  58

QY      2722  NQKWHVYRLKGAGTTLSIDENTGEOPAAVSDRTLOFGHMSVTVKQWHEIKGDTVA  2781
DB      59     DKXWHVYQLGEAGPAVLSIDEDTGEOPAAVSLDRTLOFGHMSVTVBEROMIQETKGDTVA  118

QY      2782  PGSEGLLNLPDPDFVYVYGGVPSNFTPEPELRFPGYLGCIEMETLNBEVSYLYNFEOTFM  2841
DB      119    PGAEGLLNLRPDPDFVYVYGGVPSFTFPPLRFFPGYGCIEMDTLNBEVSYLYNFERTFQ  178

QY      2842  LDTAVDKPCARSKATGDPWLTDGSLYDGSGPARISPEKQPSNTRKPOEURLVSYNGIIF  2901
DB      179    LDTAVDRPCARSKSTGDPWLTDGSLYDGTGPARI SPDSQI-STTKRFQELRLVSYSGVLF  238

QY      2902  FLKQBSQFLCLAVQEGTLAVLFDVFGSLKKADPLQPPQALTAASKAQVFLLAGNRKVL  2961
DB      239    FLKQBSQFLCLAVQEGSLVLYLDFGGLKKAVLPLOPPPPITSASKALQVFLLGSRKVL  298

QY      2962  VRVERATVFSVDQNNMLEMADAYVLYGGVPPPEQLPLSLRQLPSPGSGVRCIKGKALGKY  3021
DB      299    VRVERATVYSVEQNDLELADAYVLYGGVPPDQLPPLSRWLFPPTGGSVRGCVKGIKALGKY  358

QY      3022  VDLKELNTTGISFCTADLLVGRMTWTHGCFLEALPDVAPITEVTVSGGFRGTODNN  3081
DB      359    VDLKRLNTTGISACTADLLVGRANTTHGGRFURLALSNVAPLTGNVYSGFGFHSAGDSA  418

QY      3082  LLYVRTSPDGPYQVSLREGHVTLRFMMNQEVETORVFADGAPHYVAFVSNVTGVMLVYDDQ  3141
DB      419    LLYVREASPDGLCQVSLQCGRVSLQLLATEVKTQAGFADGAPHYVAFVSNATGVWLYVDDQ  478

QY      3142  LQLVKSHERTPMLOLOPEBPSRLLLGGLPVSGTFHNFSGCISNVFQRLRGQRVPDLH  3201
DB      479    LQOKPKHRGPPPELOQPOEGEPRLLLGGLPESGTITNFGSCISNVFVQRLLGQRVPDLQ  538

QY      3202  QNMGGSNVVSGCTEPAQLIETS-----RATAOKVRRSRQPSQDLACTTTPWLPGTIDA  3254
DB      539    QNLGSNVNISTGCAPALQAOFTGLPGRLQATARKASRSRQPARHPACMLPPLHRTTRDS  598

QY      3255  YQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPAAASQGLLLSTAPMWSGRSPSLVLFNHG  3314
DB      599    YQFGGSLSSHLEFVIGILLARHNWPSLSMHVLP-RSRGILLFTARLPSPGSPSLVLFNSG  657

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QY 3315 HFVAQTEGPGPRLQVQSRQHSRAGQWHRVVRWGMQQTQLVVDGSSQWQKALHHRVPR 3374  
Db 658 HFVAQMEGUGTLRAQSRQSRSPGRWVKVSRWVKRILLVTDGARAWSGEGPHRQCGA 717  
QY 3375 ERFPQYTLVSVGLPASPSSYSSKLPVSVFSGGCKLKLQDLKQPLRTPQWGVTPCVSGPLE 3434  
Db 718 EHPQHTLVGGLPASPSSSKLPVTVFSGGCKRLRLHGRPLGAPTRWAGVTPCILGPLE 777  
QY 3435 DGLFFPGSGVUTLBPXKAMPYVSLELEMPALAAAGLPHLGGALATPYNMQLKVLTEOV 3494  
Db 778 AGLFFPGSGVUTLBPXKAMPYVSLELEMPALAAAGLPHLGGALATPYNMQLKVLTEOV 837  
QY 3495 LIQANDGAGEFSTWYTPK-LDGRWHRVAVIMGRDTRLRLVDTQSNHTTGRPLPESLAGS 3553  
Db 838 LLRADDGAGEFSTWYTPK-LDGRWHRVAVIMGRDTRLRLVDTQSNHTTGRPLPESLAGS 897  
QY 3554 PALLHLGSLPKSSTARBELPAYRGCLRLKLLINGAPVNVVATASVOIQAGVWRCPS 3608  
Db 898 PAPLYLGLPEPMVQFPPAPPCGCMRRRLAVNRSPVMTSRVSVHGAAGVAGGCPA 952

## RESULT 3

US-09-562-702A-12  
; Sequence 12, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 3084  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-12

Query Match 15.6%; Score 3096; DB 4; Length 3084;  
Best Local Similarity 24.1%; Pred. No. 5e-181;  
Matches 960; Conservative 470; Mismatches 1208; Indels 1350; Gaps 125;

QY 1 DLYCKLVGPGVAGDPNQTIOGVCDICTAANSN--KAHPVSNADIGTERWQSPPLSRG 58  
Db 38 EMYCKLVEHV-----PGQVVENPQCRICNQNSSNPYQRHPITNAIDGKNTWQSPGIKNG 92  
QY 59 LEYNEVNTLDLGOVHVAVYLKIFANSRPEDLWLERSTDFGHTYQPMQOFFASSKEDCL 118  
Db 93 VETHYVTTLDLQVQFQAYVIVVAANSRPNFNWILERSLD-DVEYKPMQYHATVTECL 151  
QY 119 ERFG--PRT-LERITQDDVCTTEYSRIVPLENGEIVWSLVNRPQALNFYSPLRDF 175  
Db 152 TLNIIYPRTPGPSYAKDDEVICTSYSKIPLNGEIHISLINGRPSA--DDPSPELLER 209  
QY 176 TKATNIRLRLRTNLLHLMGKALR-----DPTVTRYYSIKDISIGORCVCHGADV 230  
Db 210 TSARVIRLRFQIRTLNADLMFPAKHPREIDPIVTRYIYSKDISVGGNCICYGHARA 269  
QY 231 CDADKPLDFF--RLQACQHNCTCGSDRCCEFGNQFPKPAATDTSANECQSNCHGHAY 288  
Db 270 C-----PLDPATNKSRCCEHNTCGSDRCCEFGNQFPKPAATDTSANECQSNCHGHAY 325  
QY 289 DCYYDPEVDRNASQDNVYQGGGVCLDQCHHTTGINCERCULFGFRAPDQPLDSPHYC 348

Db 326 EGYDETIVASRLNLSINTHGKYIGGVGVCINHTAGINCETCVDGFRPKGVSNPRPC 385  
QY 349 RPDCESDFTDGTCELTGRCYCRPNFTGBLCAACA--EGYTDFFHCHYPLPSFPHNDTRE 406  
Db 386 QFCHCDP-----TGSLSVGVCKDEK----- 406  
QY 407 QVLPAQIIVNCDNAAGTQGNACRKPRLGRVCVCKPNFRGAHCELCAPEGPHG--PSCHPQ 465  
Db 407 -----AORGLKPGSCHCKTGTGGVNCDCRCVGRVGHGYPDCQPCN 444  
QY 466 CSSPGVANSLCDPESGGQCMRTGPEGDRCDHICALGYHFFPL-----COLGCCSPAGTLPE 520  
Db 445 CSGLGSTNE--DPCVGPSCCKENVEGEDCRCKSGRPNLQEDNQKGBECFCGSGVSNRCQ 502  
QY 521 G-----CDEAGRCQCPGPDGHCUR-----CLPGY----- 546  
Db 503 SSIYTYGNIQDMRWYLTDLGSRIRMAPQLNDPDSPOQISISNSEARKSLDDGYWYSAAPP 562  
QY 547 ----- 546  
Db 563 PYLGNRLPAVGGQLSFTISYDLBEEEDDEKLLQLMIPEGNDLRISTAYKEYLEPSEE 622  
QY 547 -----HG----- 548  
Db 623 HVEVSLKEBAFTTHGNLNPVTRKDFMIVUTNLGELIQTNYLGMDAIRLSSVNLSP 682  
QY 549 --YPDCHACADPRGALDQCGVGLCHCRPNTGATCQECSEF-----FYGFPSCI 598  
Db 683 VPYP-----TDRRIATDVE-----VCQPPGYSGSGSCETCWRHRRVNGTIFGGI--CE 729  
QY 599 PCHCSAGSLHTTCDPTTGOC--RCRPVTVGLHCDMVGAYNFPYCEAGSCHPAGLAPAN 657  
Db 730 PQCFNAHB---ACDDITGELCKCKHTGPGYCNELPGYGDG--TRGS----- 774  
QY 658 PALPETQAPCMCAHV-----EGPSCDRCKPGYWGSLAS 691  
Db 775 ---PEDCQPCACPLNIPSNFNPTCHLDRSLGLICBCEPIGYTGPCCERCAEYFGQPSV 831  
QY 692 NPECTRCSCDPRGTGLGVTECOG--NGQC--FCKAHVCGKTCACKDGFGLDYADYFGCR 749  
Db 832 PGSGCQPCQNDNLDSIPGSCDSLSGSLICKPGTTGRYCELCADGYFG--DAVTKNCQ 890  
QY 750 SCRCVGGALGQGCPEKTKGACRCRPNTPQPTCSEPAKDHVLPDLHMRLEBEAATPEGH 809  
Db 891 PCRDINGSFSEDCHTRTQCECRPNVQGRHCD----- 924  
QY 810 AVRFGFNPLEFENFWSRGAHMAIQPRIVARLNVTSPLDLFRLVPRVYVNRGTSVNGQIS 869  
Db 925 -----CKPTEFGL----- 932  
QY 870 VREBGLSSCTNCTEQSQPVAFPPSTEPAFVTVPGFGBEPFVLNPGI WALLVEAGVLL 929  
Db 933 ----- 932  
QY 930 DYVLLPSTYVEAALLQHRVTEACTYRPSALHSTENCLVVAHLPLDGFPSAAGTEALCRH 989  
Db 933 ----- 932  
QY 990 DNSLPRPCPTEQLSPSHPLPLATCFGSDVDIQLMAYVPGQVYLVVEYGEDSHQBMGYA 1049  
Db 933 ----- 932  
QY 1050 VHTQAPQVQVNLNHPYSSLCRSPARDTQHHLAI PHLDSEASIRLTAEQAHPFLHSV 1109  
Db 933 ----- 932  
QY 1110 TLVPVEEFSTFVEPRVFCVSSHGTNFPNSAACLASRFPKPPQPIKDCQVLPPLDLP 1169  
Db 933 ----- 932  
QY 1170 LTQSCSLPGAPPEGQPRPTAVDFAENBPTLLRHPGTVTVTTQVPTLGRYAFLLHGQV 1229

16	5018.5	25.2	3712	13	US-10-108-605-103	Sequence 103, Appl
17	5012.5	25.2	3712	12	US-10-037-417-51	Sequence 51, Appl
18	4831.5	24.3	3672	15	US-10-369-493-6146	Sequence 6146, Ap
19	3488.5	17.6	953	9	US-09-845-583-4	Sequence 4, Appli
20	3488.5	17.6	953	12	US-10-037-417-50	Sequence 50, Appl
21	3325	16.7	908	12	US-10-037-417-4	Sequence 4, Appli
22	2970	14.9	3070	10	US-09-961-403-7	Sequence 7, Appli
23	2792	14.0	3084	9	US-09-938-275-4	Sequence 4, Appli
24	2792	14.0	3084	14	US-10-263-670-2	Sequence 2, Appli
25	2729.5	13.7	3075	9	US-09-938-275-5	Sequence 5, Appli
26	2460	12.4	2823	15	US-10-369-493-5220	Sequence 5220, Ap
27	2460	12.4	2823	15	US-10-369-493-5221	Sequence 5221, Ap
28	2185	11.0	1823	12	US-10-363-618-457	Sequence 457, App
29	2184.5	11.0	1816	14	US-10-299-058-4	Sequence 4, Appli
30	2182.5	11.0	1816	14	US-10-299-058-2	Sequence 2, Appli
31	2171.5	10.9	1816	15	US-10-372-683-4	Sequence 4, Appli
32	2149.5	10.8	1693	15	US-10-603-725-4	Sequence 4, Appli
33	2149.5	10.8	1693	15	US-10-603-725-8	Sequence 8, Appli
34	2149.5	10.8	1713	14	US-10-171-311-113	Sequence 113, App
35	2149.5	10.8	1713	15	US-10-372-683-10	Sequence 10, Appl
36	2149.5	10.8	1713	15	US-10-603-725-6	Sequence 6, Appli
37	2149.5	10.8	1724	15	US-10-603-725-2	Sequence 2, Appli
38	2067	10.4	1694	15	US-10-603-725-12	Sequence 12, Appl
39	2067	10.4	1725	15	US-10-603-725-10	Sequence 10, Appl
40	1685	8.5	634	10	US-09-949-029-134	Sequence 134, App
41	1675	8.4	1798	9	US-09-938-275-9	Sequence 9, Appli
42	1672.5	8.4	1801	9	US-09-938-275-8	Sequence 8, Appli
43	1668.5	8.4	1799	9	US-09-845-583-6	Sequence 6, Appli
44	1605	8.1	1765	14	US-10-037-182-8	Sequence 8, Appli
45	1605	8.1	1786	9	US-09-873-676-113	Sequence 113, App

ALIGNMENTS

RESULT 1  
US-09-845-583-2  
; Sequence 2, Application US/098455583  
; Patent No. US20020142954A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champilaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-2

Query Match	100.0%	Score 19876;	DB 9;	Length 3635;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 3635;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	DLYCKLVGGPVAGGDPNQTTCGQYCDICTAANSKAHPVNAIDGTERWQSPPLSRGLE	60	
QY	61	YNEVNVTLDLQGVFHVAVLTKFANSRPDLVLERSTDFGHTYQPFQFASSKRDCLER	120	
Db	61	YNEVNVTLDLQGVFHVAVLTKFANSRPDLVLERSTDFGHTYQPFQFASSKRDCLER	120	
QY	121	FGPRTLERTITDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYPLLRFTKATN	180	
Db	121	FGPRTLERTITDDVICTTYSRIVPLENGEIVVSLVNGRPGALNFSYPLLRFTKATN	180	

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OM protein - protein search, using sw model

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Scoring table: BLOSUM62  
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  - 9: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*
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  - 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
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  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19876	100.0	3635	9	US-09-845-583-2
2	19876	100.0	3635	12	US-10-037-417-47
3	19876	100.0	3635	14	US-10-037-182-4 ✓
4	15842	79.7	3695	12	US-10-312-352-22
5	15839	79.7	3695	14	US-10-037-182-2
6	15830.5	79.6	3696	15	US-10-312-088-31
7	15819.5	79.6	3690	12	US-10-112-944-347
8	15815	79.6	3705	15	US-10-312-088-30
9	14771	74.3	3600	12	US-10-037-417-2
10	14706.5	74.0	3597	12	US-10-037-417-6
11	12354.5	62.2	2743	14	US-10-037-182-36
12	6110	30.7	1677	12	US-10-112-944-801
13	6092	30.7	1640	12	US-10-037-417-8
14	5495.5	27.6	1634	12	US-10-037-417-49
15	5018.5	25.2	3712	12	US-10-037-417-48

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Db 181 IRLFLRNTLLGLHMKALRDPVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 240  
QY 241 RLOCAOHNNTCGSCDRCCFQNOQPKPATTDSDANECOSCHGHADVCDYDPEVDRN 300  
Db 241 RLOCAOHNNTCGSCDRCCFQNOQPKPATTDSDANECOSCHGHADVCDYDPEVDRN 300  
QY 301 ASQNDNVYGGGVCLDCOHHHTTGINCERCLPFFFAAPDQPLDSPHVCRPCDCESDFTDG 360  
Db 301 ASQNDNVYGGGVCLDCOHHHTTGINCERCLPFFFAAPDQPLDSPHVCRPCDCESDFTDG 360  
QY 361 TCSDLTGRCYCRPNFTGELCAACAGYTDFFHCYPLPSPPHNDTREQVLPAGQIVNCDN 420  
Db 361 TCSDLTGRCYCRPNFTGELCAACAGYTDFFHCYPLPSPPHNDTREQVLPAGQIVNCDN 420  
QY 421 AAGTQVACRNDRLGRVCVKNFRGAHCELCAPFHGSPCHPCQCSPPGVANSLCDPES 480  
Db 421 AAGTQVACRNDRLGRVCVKNFRGAHCELCAPFHGSPCHPCQCSPPGVANSLCDPES 480  
QY 481 GQCMCRITGPEGDRCDHCALGYFHFPLCQJCGSPAGTLPPEGCDRAGRCQCRPGDGHCD 540  
Db 481 GQCMCRITGPEGDRCDHCALGYFHFPLCQJCGSPAGTLPPEGCDRAGRCQCRPGDGHCD 540  
QY 541 RCLPGHYGPDCHACADPRGALDQCGVGGJCHCRPGNTGATQECSPGYFPSPCIPC 600  
Db 541 RCLPGHYGPDCHACADPRGALDQCGVGGJCHCRPGNTGATQECSPGYFPSPCIPC 600  
QY 601 HCSADGSLHTTCDPTTGGCRPRVTGLHCDMVCAGYNYFYCEAGSCHPAGLAPANPAL 660  
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QY 661 PETQAPCMCAHVEGSDRCXPGYVGLSASNPBCTGCSDDPRGLTGGVTECGNGQCF 720  
Db 661 PETQAPCMCAHVEGSDRCXPGYVGLSASNPBCTGCSDDPRGLTGGVTECGNGQCF 720  
QY 721 CKAHVCGKCAACKDGFFGLDADYFGCRSDVGGALGOCBPKTGACRCRNTOGPT 780  
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QY 781 CSPAPKDHVLPDLHWRLEBAATPEGHAVRFGNPLEFENFWSRGAHMAIQPRIVA 840  
Db 781 CSPAPKDHVLPDLHWRLEBAATPEGHAVRFGNPLEFENFWSRGAHMAIQPRIVA 840  
QY 841 RLNVTSPLDLRLVFRVYVNGSTSVNGQISVREBGLSSCTNCTEQSQVAFPPSPTEPAFV 900  
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QY 1201 LLRHPOGTVFTTQVPTLGRVAFLLHGYQVHPGPPFVEVLINGRIWQHANASFCPHGY 1260  
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QY 1261 GCRTLVLCBGTMLDVTONELTVTVRVPEGRWMLDYLVIIVPEDAYSSSYLQEBPLDKSY 1320  
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QY 1921 HCERCAPFYGNALLPGNCTRCDCSPGTECTDPSQGRCLCKAGVTQORCDRCLEGYFGF 1980  
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RESULT 2

US-10-037-417-47  
; Sequence 47, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Leplev, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Scioire, Paul  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Stone, David J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Anderson, David W  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Miller, Charles E  
; APPLICANT: Eissen, Andrew J  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260,018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260,360  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/272,411  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/272,817  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/291,186  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/303,231  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/305,060  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/318,405  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/318,700  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 3635  
; TYPE: PRT

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QY 2761 GMSVTVSKQWHEIKGDTVAPGSEGLNLHPDDFVFVGGYPSNFTPEPLRPPGLGC 2820  
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QY 2881 FSNTRKFDQELRLVSYNGIIFFLKQESQFLCLAVOEGTLVLFYDFGSLKKADPLQPPQA 2940  
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QY 2941 LTAASKATQVLLAGNRKRLVVERATVFSVDQNMLEMDADAYVLGGVPPPEQLPLSLRQ 3000  
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Db 3001 LFPSSGSGVRCIKGKALKGVYDLKRLNTTGISFQCTADLLVGRMTPHGHGFLPLALPD 3060  
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QY 3301 SGRSPSLVFLNKGHFAVQTEGPRQLQVQSRQHSRAGQHWVSVRWGMQIQLVVDGSG 3360  
Db 3301 SGRSPSLVFLNKGHFAVQTEGPRQLQVQSRQHSRAGQHWVSVRWGMQIQLVVDGSG 3360  
QY 3361 TWSQKALHVRPRAERPPQYTLISVGLPASSYSKLPVSVGSGCLKKLQDKQLRTP 3420  
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QY 3421 QMVGVTCPVSGPLEDGLFFPGSEGVVTLLELPAKMPYVVSLEEMRPLAAAGLIPLHGOAL 3480



; ORGANISM: Mus musculus									
US-10-037-417-47									
Query Match 100.0%; Score 19876; DB 12; Length 3635;									
Best local Similarity 100.0%; Pred No. 0;									
Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	DLCKLVGGPVAGD	PNTTGGQYCDICTAANSKHAHPVSN	ADGTERWQSPPLSRGLE	60				
QY	61	YNEVNVTLDDGOV	FHVAYVLIKEANSRPLDWLERSTDFGHTYQ	PWQPFASKRDCLER	120				
Db	61	YNEVNVTLDDGOV	FHVAYVLIKEANSRPLDWLERSTDFGHTYQ	PWQPFASKRDCLER	120				
QY	121	FGPRTLERITDQDDV	ICTTEYSRIVPLENGEIVVSLVNGRPGALN	FSYSPLLRDTFKATN	180				
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QY	181	IRLRFRNTNLLGHL	MKALRDTVTRYVYSIKDISIGRCVCHGADV	CAKAPLDPF	240				
Db	181	IRLRFRNTNLLGHL	MKALRDTVTRYVYSIKDISIGRCVCHGADV	CAKAPLDPF	240				
QY	241	RLOCACQHNCTCGS	CDRCRCCFGNQPKPATTDSANECQSCNCH	GAYDYYDPEVDREN	300				
Db	241	RLOCACQHNCTCGS	CDRCRCCFGNQPKPATTDSANECQSCNCH	GAYDYYDPEVDREN	300				
QY	301	ASQNDNVYGGVCLD	QCHHTTGINCERCLPGFPAPDPLDSPHVC	RPCDCESFTDG	360				
Db	301	ASQNDNVYGGVCLD	QCHHTTGINCERCLPGFPAPDPLDSPHVC	RPCDCESFTDG	360				
QY	361	TCEDLTGRVCYCR	NFTGELCAACAGYTDPHCVPLSPFNHND	TRBQVLPAGQVINCDCN	420				
Db	361	TCEDLTGRVCYCR	NFTGELCAACAGYTDPHCVPLSPFNHND	TRBQVLPAGQVINCDCN	420				
QY	421	AAGTQGNACRDKP	RLGRVCYCKPNFRGAHCBELCAPGFHGP	SCHPCQSSPGVANSLCDPES	480				
Db	421	AAGTQGNACRDKP	RLGRVCYCKPNFRGAHCBELCAPGFHGP	SCHPCQSSPGVANSLCDPES	480				
QY	481	GQCMRTGFEGDR	CDHCHALGVHEPPLCQLCGSPAGTLP	PEGDEAGRCOCRPGFDGPHCD	540				
Db	481	GQCMRTGFEGDR	CDHCHALGVHEPPLCQLCGSPAGTLP	PEGDEAGRCOCRPGFDGPHCD	540				
QY	541	RCLPGYHGYDPD	CHACACDPRGALDQCGVGLCHCRPGNT	GATCQBCSPGYFPFSCIPC	600				
Db	541	RCLPGYHGYDPD	CHACACDPRGALDQCGVGLCHCRPGNT	GATCQBCSPGYFPFSCIPC	600				
QY	601	HCSADGSLHTT	CDTDTTQCRCPRTVGLHCDMCPGAYNE	FPYCEAGSCHPAGLAPANPAL	660				
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QY	661	PETQAPCMCAH	VEGSPCDRCCKPGYWGLSASNPEGCT	TRCSCDPRGTLGGVTECQGNQCF	720				
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QY	721	CKAHVCKTKA	CKDGFGLDYADYFCGRSCRDVGALQ	QGCEPKTGACRCRPNTOGPT	780				
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QY	781	CSEPAKHYPDL	HHMLELEEAATPEGHVRFGNFPLEFEN	FSWRGAYHMAIQPRIVA	840				
Db	781	CSEPAKHYPDL	HHMLELEEAATPEGHVRFGNFPLEFEN	FSWRGAYHMAIQPRIVA	840				
QY	841	RLNVTSPDLFL	VPYRYNRSSTVNGQISVREBGLSSCTN	CTEQSQOPVAFPPSTPAFV	900				
Db	841	RLNVTSPDLFL	VPYRYNRSSTVNGQISVREBGLSSCTN	CTEQSQOPVAFPPSTPAFV	900				
QY	901	TVPORGFGE	PVLPNGIIVALLVEAGVLLDVVLLPST	YEAALLQHRVTEACTYRPSAL	960				
Db	901	TVPORGFGE	PVLPNGIIVALLVEAGVLLDVVLLPST	YEAALLQHRVTEACTYRPSAL	960				
QY	961	HSTENCLVYAH	LPLDGFPSAAGTEALCRHNSLPRPC	TEQLSPSHPLATCFGSDVDIQ	1020				

Db	961	HSTENCLVYAH	LPLDGFPSAAGTEALCRHNSLPRPC	TEQLSPSHPLATCFGSDVDIQ	1020				
QY	1021	LEMAVPOFGQY	VLVVEYVEDSHQEMGVAVHTPQAPQ	QOQVNLHPCYPYSSLCKSPARDT	1080				
Db	1021	LEMAVPOFGQY	VLVVEYVEDSHQEMGVAVHTPQAPQ	QOQVNLHPCYPYSSLCKSPARDT	1080				
QY	1081	QHHLAIPLH	SEASIRLTAQAHPLHSVTLVPVEEST	EFVEPRVFCVSSHGTFNPSA	1140				
Db	1081	QHHLAIPLH	SEASIRLTAQAHPLHSVTLVPVEEST	EFVEPRVFCVSSHGTFNPSA	1140				
QY	1141	ACLASRFPKP	QPPQIILKDCQVLPPLPDLPLTQSO	ELSFGAPPEGPQPRPTAVDPNAEPT	1200				
Db	1141	ACLASRFPKP	QPPQIILKDCQVLPPLPDLPLTQSO	ELSFGAPPEGPQPRPTAVDPNAEPT	1200				
QY	1201	LLRHPOGT	VFTTQPTGLGRYAFLLHGYQVHRS	FPVEVLINGRIWQHANASFCPHGY	1260				
Db	1201	LLRHPOGT	VFTTQPTGLGRYAFLLHGYQVHRS	FPVEVLINGRIWQHANASFCPHGY	1260				
QY	1261	GCRTLVLCE	GTMLDVTDELTVTVRVEGRWLWDL	VILVPEDAYSSVLYQEBPLDKSY	1320				
Db	1261	GCRTLVLCE	GTMLDVTDELTVTVRVEGRWLWDL	VILVPEDAYSSVLYQEBPLDKSY	1320				
QY	1321	DFISHCATQ	GHISPSSSSPFCRNAATLSLSFYNG	ALPCGCHVGVASPTCEPFGGOC	1380				
Db	1321	DFISHCATQ	GHISPSSSSPFCRNAATLSLSFYNG	ALPCGCHVGVASPTCEPFGGOC	1380				
QY	1381	CRGHVIGR	DCSRCATGYWGFPCRCPCDGA	RLCDELGTQICPPRTVPPDC	1440				
Db	1381	CRGHVIGR	DCSRCATGYWGFPCRCPCDGA	RLCDELGTQICPPRTVPPDC	1440				
QY	1441	CHPLVGBE	CNCSGFGVQELTDTPTCDMD	SGQCRPNVAGRRCDTCA	1500				
Db	1441	CHPLVGBE	CNCSGFGVQELTDTPTCDMD	SGQCRPNVAGRRCDTCA	1500				
QY	1501	CHEAGTMA	SVCDPLTGTQCHCKENYQGR	CDQCRVGTFTSLDAANPKG	1560				
Db	1501	CHEAGTMA	SVCDPLTGTQCHCKENYQGR	CDQCRVGTFTSLDAANPKG	1560				
QY	1561	NSNLARH	EFVDMEGWVLLSSDRQVVP	HEHRPEIELLHADLR	SVADTTSLEYWQAPPSYLG	1620			
Db	1561	NSNLARH	EFVDMEGWVLLSSDRQVVP	HEHRPEIELLHADLR	SVADTTSLEYWQAPPSYLG	1620			
QY	1621	DRVS	YSGTTLHYELHSETQRGDI	FIPYESRDPVVLQGNQMS	IAFLELAYPPPGVHRGQL	1680			
Db	1621	DRVS	YSGTTLHYELHSETQRGDI	FIPYESRDPVVLQGNQMS	IAFLELAYPPPGVHRGQL	1680			
QY	1681	OLVEGNFR	HLTHNPVSREELMMVLAGLE	QIIRALFSQTS	SSVSLRRVLEVASEARG	1740			
Db	1681	OLVEGNFR	HLTHNPVSREELMMVLAGLE	QIIRALFSQTS	SSVSLRRVLEVASEARG	1740			
QY	1741	PPAS	NVELCMCPANVYGDSCQ	ECAPGYRDTKGLFLGR	CVPCQCHGSDRCLPGSGICVG	1800			
Db	1741	PPAS	NVELCMCPANVYGDSCQ	ECAPGYRDTKGLFLGR	CVPCQCHGSDRCLPGSGICVG	1800			
QY	1801	COHNT	EGQCCRCRCPGFVSSDP	SNPASPVCPCPLAVPS	NNFADGCVLRNGRTQCLCRP	1860			
Db	1801	COHNT	EGQCCRCRCPGFVSSDP	SNPASPVCPCPLAVPS	NNFADGCVLRNGRTQCLCRP	1860			
QY	1861	GYAG	ASCRCAPGFGNPLVLGSS	CQPCDSCGNGDPNMI	FSDCDPLTGACRGCLHTTGP	1920			
Db	1861	GYAG	ASCRCAPGFGNPLVLGSS	CQPCDSCGNGDPNMI	FSDCDPLTGACRGCLHTTGP	1920			
QY	1921	HCER	CAPGYGNALLPGNCT	RCDCSPCGTETCDPSGR	CLCKAGVTGQRCRCLGEGYGF	1980			
Db	1921	HCER	CAPGYGNALLPGNCT	RCDCSPCGTETCDPSGR	CLCKAGVTGQRCRCLGEGYGF	1980			
QY	1981	EQCQ	CRCPACAPAAKGECH	HPQSQCHQCPGTTGPQ	CLECAPGYWGLPEKGCRCQCP	2040			
Db	1981	EQCQ	CRCPACAPAAKGECH	HPQSQCHQCPGTTGPQ	CLECAPGYWGLPEKGCRCQCP	2040			
QY	2041	GHCD	SHTGCTCPGLSGER	CDTCSQHQVVPKPGH	GIGHCEVCDHCVVLLD	2100			
Db	2041	GHCD	SHTGCTCPGLSGER	CDTCSQHQVVPKPGH	GIGHCEVCDHCVVLLD	2100			

QY 2101 GALLPAIREQLOGINASSAAWRLHRLNASIADLOSRLRRPPGPRYQAAQLOTLQOOSI 2160  
DB 2101 GALLPAIREQLOGINASSAAWRLHRLNASIADLOSRLRRPPGPRYQAAQLOTLQOOSI 2160  
QY 2161 SLOQTERLGSQATGVQOAGQOLLDTTESTIGRAQKLLIESVRAGRALNELASRGQSP 2220  
DB 2161 SLOQTERLGSQATGVQOAGQOLLDTTESTIGRAQKLLIESVRAGRALNELASRGQSP 2220  
QY 2221 GDALVPSGEQLRWALAEVERLILWMDRTDLGAQGAVAEAEALAEAOQLMARVQEQLTFSWE 2280  
DB 2221 GDALVPSGEQLRWALAEVERLILWMDRTDLGAQGAVAEAEALAEAOQLMARVQEQLTFSWE 2280  
QY 2281 ENQSLATHIRDOLAQYESGLMDLRALNAQVNTTREAELNSRNOERKEALOWKQELSQ 2340  
DB 2281 ENQSLATHIRDOLAQYESGLMDLRALNAQVNTTREAELNSRNOERKEALOWKQELSQ 2340  
QY 2341 DNATLKATICAASLILGHVSELLQIGDQAKEDLEHLAASLDGAWTPLLKRMQAESPASSK 2400  
DB 2341 DNATLKATICAASLILGHVSELLQIGDQAKEDLEHLAASLDGAWTPLLKRMQAESPASSK 2400  
QY 2401 VDLVBAEAAHAKLNQALINLSGIIILGINQDRFIQRAVEASNAYSSIIQAVOAAEDAAGQ 2460  
DB 2401 VDLVBAEAAHAKLNQALINLSGIIILGINQDRFIQRAVEASNAYSSIIQAVOAAEDAAGQ 2460  
QY 2461 ALROASRTWEMVVRGLAAGAROLLANSALBETILGHQRLGLAQGRLOAAGIOLHNWV 2520  
DB 2461 ALROASRTWEMVVRGLAAGAROLLANSALBETILGHQRLGLAQGRLOAAGIOLHNWV 2520  
QY 2521 ARKNQLAQIOEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLOQGMKNVERWQ 2580  
DB 2521 ARKNQLAQIOEAQAMLAMDTSETSEKIAHAKAVAAEALSTATHVQSOLOQGMKNVERWQ 2580  
QY 2581 SOLGGLOGODLSQVERDASSYSTLEKTLPLLAKLSLENEGHNASIALSANGRYRK 2640  
DB 2581 SOLGGLOGODLSQVERDASSYSTLEKTLPLLAKLSLENEGHNASIALSANGRYRK 2640  
QY 2641 LTAQARSAAKVKVSKMFKNGRSGVRLRPDRLADLAAYTALKFHIQSPVPAPEPKNTGD 2700  
DB 2641 LTAQARSAAKVKVSKMFKNGRSGVRLRPDRLADLAAYTALKFHIQSPVPAPEPKNTGD 2700  
QY 2701 HFVLYNGSQAQTDYNGVSLRNQKHVYRLKAGPTTILSIDENTGEQFAAVISIDRTLOF 2760  
DB 2701 HFVLYNGSQAQTDYNGVSLRNQKHVYRLKAGPTTILSIDENTGEQFAAVISIDRTLOF 2760  
QY 2761 GHMSVTEKQWHEIKGDTVAPQSEGLNLNHPDDFVYVGGYPSNFTPEPLRFFGYLGC 2820  
DB 2761 GHMSVTEKQWHEIKGDTVAPQSEGLNLNHPDDFVYVGGYPSNFTPEPLRFFGYLGC 2820  
QY 2821 IEMETLNEEVSILYNPEQTFMLDTAVDKPCARSKATGDPWLTGSGYDGSFGARISFEKQ 2880  
DB 2821 IEMETLNEEVSILYNPEQTFMLDTAVDKPCARSKATGDPWLTGSGYDGSFGARISFEKQ 2880  
QY 2881 FSNTRKFDQELRLVSYNGIIFLKOESQFLCLAVQEGTLVLFYDFGSGIKKADPLQPPQA 2940  
DB 2881 FSNTRKFDQELRLVSYNGIIFLKOESQFLCLAVQEGTLVLFYDFGSGIKKADPLQPPQA 2940  
QY 2941 LTAASKAIQVFLLAGNKRVLVRVERATVFSVDQDNMLEMADAYILGGVPPQLPLSLRQ 3000  
DB 2941 LTAASKAIQVFLLAGNKRVLVRVERATVFSVDQDNMLEMADAYILGGVPPQLPLSLRQ 3000  
QY 3001 LPPSGSVGCGKIGKALGYDLKXLTNTGTSFGCTADLLVGRMTWGHGFLPLALPD 3060  
DB 3001 LPPSGSVGCGKIGKALGYDLKXLTNTGTSFGCTADLLVGRMTWGHGFLPLALPD 3060  
QY 3061 VAPITEVYSGFGFRGTQDNLLIYRTSPDGPYQVSLRGEHVTFLRFMNOQEVETQVFADG 3120  
DB 3061 VAPITEVYSGFGFRGTQDNLLIYRTSPDGPYQVSLRGEHVTFLRFMNOQEVETQVFADG 3120  
QY 3121 APHYAFYGNVTGVMVYDDQLOLVKSHERTTLMLOLQPEEPSRLILGGLPVSGTFHNF 3180  
DB 3121 APHYAFYGNVTGVMVYDDQLOLVKSHERTTLMLOLQPEEPSRLILGGLPVSGTFHNF 3180

QY 3181 GCISNVFQRLRQPVFQDLHQNMGSVNVSVGCTPAQLIETSRATAQKVRRSRQPSQDL 3240  
DB 3181 GCISNVFQRLRQPVFQDLHQNMGSVNVSVGCTPAQLIETSRATAQKVRRSRQPSQDL 3240  
QY 3241 ACTTPMLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3300  
DB 3241 ACTTPMLPGTIQDAYQFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHAAASQGLLLSTAPM 3300  
QY 3301 SGRSPSLVILFLNIGHFVQATGEGPRLQVQSRQHSRAGQWHRVSVZGWGQQIOLVVDGSG 3360  
DB 3301 SGRSPSLVILFLNIGHFVQATGEGPRLQVQSRQHSRAGQWHRVSVZGWGQQIOLVVDGSG 3360  
QY 3361 TWSQKALHHRVPAERPOPYTTLISVGGPLPASSYSKLPVSVGFGSGCLKLQDKQPLRTPT 3420  
DB 3361 TWSQKALHHRVPAERPOPYTTLISVGGPLPASSYSKLPVSVGFGSGCLKLQDKQPLRTPT 3420  
QY 3421 QMWGVTPCVSGPDLGGLFFPGSEGVTLPLKAKMPYVSLLEMRPLAAAGLIFHLGOAL 3480  
DB 3421 QMWGVTPCVSGPDLGGLFFPGSEGVTLPLKAKMPYVSLLEMRPLAAAGLIFHLGOAL 3480  
QY 3481 ATPYMQLVKTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTRLLEVDTQSN 3540  
DB 3481 ATPYMQLVKTEQVLLQANDGAGEFSTWVTYPKLCGRWHRVAVIMGRDTRLLEVDTQSN 3540  
QY 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLKLLINGAPVNVITASVQIOGA 3600  
DB 3541 HTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLKLLINGAPVNVITASVQIOGA 3600  
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DB 3601 VGMGCPSGTLLSKKQKALTQORHAKPSVSPLLWH 3635

RESULT 3  
US-10-037-182-4  
; Sequence 4, Application US/10037182  
; Publication No. US2003004899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Toyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-037-182-4

Query Match 100.0%; Score 19876; DB 14; Length 3635;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYCKLVGGPVAGGDPNQTIOGOYCDICTAANSKNAHPVSNADGTERMWQSPPLSRGLE 60  
DB 1 DLYCKLVGGPVAGGDPNQTIOGOYCDICTAANSKNAHPVSNADGTERMWQSPPLSRGLE 60  
QY 61 YNEVNVTLDGQVHFVAVYLIKFNANSPRDLVLERSTDFGHTYQWQFPASSKRDCLER 120  
DB 61 YNEVNVTLDGQVHFVAVYLIKFNANSPRDLVLERSTDFGHTYQWQFPASSKRDCLER 120  
QY 121 FGPRTLERITQDDDDVICTTEYSRIVPLENGEIVVSVNGRPGALNFSYSPLLRDFTKATN 180  
DB 121 FGPRTLERITQDDDDVICTTEYSRIVPLENGEIVVSVNGRPGALNFSYSPLLRDFTKATN 180

QY 181 IRLRFLRNTLLGHLMKALRDTVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 240  
Db 181 IRLRFLRNTLLGHLMKALRDTVTTRYYYSIKDISIGRCVCHGHADVCDKADPLDPF 240  
QY 241 RLOCACQHNTCGSCDRCCPGFNQPKPATTOSANECQSCNCHGHAYDCYDPEVDREN 300  
Db 241 RLOCACQHNTCGSCDRCCPGFNQPKPATTISANECQSCNCHGHAYDCYDPEVDREN 300  
QY 301 ASQNDNVYGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESFTDG 360  
Db 301 ASQNDNVYGGVCLDCQHTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESFTDG 360  
QY 361 TCEDLTGRYCRNFTGELCAACAEYTDPHCVPLSPSPHNDTRBOVLPAQGVNCDQN 420  
Db 361 TCEDLTGRYCRNFTGELCAACAEYTDPHCVPLSPSPHNDTRBOVLPAQGVNCDQN 420  
QY 421 AAGTQGNACRDPRLGRVCCKPNFRGAHCBLCAPGPHGSPCHPCQSSPGVANSLCDPES 480  
Db 421 AAGTQGNACRDPRLGRVCCKPNFRGAHCBLCAPGPHGSPCHPCQSSPGVANSLCDPES 480  
QY 481 GQCMRTGFGEDRCHALGYFHPPLCOLCGCPAGTLPGCDBAQRCCQCPGDFGPHCD 540  
Db 481 GQCMRTGFGEDRCHALGYFHPPLCOLCGCPAGTLPGCDBAQRCCQCPGDFGPHCD 540  
QY 541 RCLPGYHGYDCHACADPRGALDQCGVGGLCHCRFGNTGATCQBCSPGYFPPSCIPC 600  
Db 541 RCLPGYHGYDCHACADPRGALDQCGVGGLCHCRFGNTGATCQBCSPGYFPPSCIPC 600  
QY 601 HCSADGSLHTTCDTTCQCRCPRTVGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL 660  
Db 601 HCSADGSLHTTCDTTCQCRCPRTVGLHCDMCPVPGAYNFPYCEAGSCHPAGLAPANPAL 660  
QY 661 PETQAPCMRAHVGPSCDRCKPGYGLSASNPEGCTRCSCDPRGTILGGVTECGNGQCF 720  
Db 661 PETQAPCMRAHVGPSCDRCKPGYGLSASNPEGCTRCSCDPRGTILGGVTECGNGQCF 720  
QY 721 CKAHVCGKTCACXGDFGLDYADYFGRCRCDVGGALGGGCEPKTGACRCRPNQGT 780  
Db 721 CKAHVCGKTCACXGDFGLDYADYFGRCRCDVGGALGGGCEPKTGACRCRPNQGT 780  
QY 781 CSEPAKHLYLPDLHMLLELEBEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIVA 840  
Db 781 CSEPAKHLYLPDLHMLLELEBEAATPEGHAVRFGFNPLEFENFSWRGYAHMMAIQPRIVA 840  
QY 841 RLNVTSPLFLVRYVNRGTSVNGQISVREBEKLSCTNCTEQSQPVAFPPSTPAFV 900  
Db 841 RLNVTSPLFLVRYVNRGTSVNGQISVREBEKLSCTNCTEQSQPVAFPPSTPAFV 900  
QY 901 TVPQRGCEPFLVNPGLWALVBEAGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL 960  
Db 901 TVPQRGCEPFLVNPGLWALVBEAGVLLDYVLLPSTYEAALLQHRVTEACTYRPSAL 960  
QY 961 HSTENCLVYHLPLDGFPSAAGTEALCRHNSLPRCPTTEQLSPSHPPPLATCFGSVDIQ 1020  
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QY 1081 QHHLAIFHLDSIASIRLTAEQAHPFLHSVTLVPVEEFSTEFVEPRVFCVSSHGTFNPSSA 1140  
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QY 1201 LLRHPQGTVFTTQVPTLGRVAFLLHGYQPVHPSPFPVEVLINGGRIWQHANASFCPHGY 1260  
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QY 1261 GCRTLVLCGQTMLDVTDNELTTVRVPEGRWLWLDVLIIVPEDAYSSSYLQEBPLDKSY 1320

Db 1261 GCRTLVLCGQTMLDVTDNELTTVRVPEGRWLWLDVLIIVPEDAYSSSYLQEBPLDKSY 1320  
QY 1321 DF1SHCATQGYHI1SPSSSSPFCRNAATSLSYFNNGALPCQCHVGVAVSPCEPFGQCP 1380  
Db 1321 DF1SHCATQGYHI1SPSSSSPFCRNAATSLSYFNNGALPCQCHVGVAVSPCEPFGQCP 1380  
QY 1381 CRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLCLDELTGQCICPPTVPPDCVLVQPOSFG 1440  
Db 1381 CRGHVIGRDCSRCATGYWGFPCNCRPCDCGARLCLDELTGQCICPPTVPPDCVLVQPOSFG 1440  
QY 1441 CHPLVGCBECCNCSGPGVOELTDPCTCDMDSGQCRCPNVAGRRCDTCAPGFGYFSCRPDC 1500  
Db 1441 CHPLVGCBECCNCSGPGVOELTDPCTCDMDSGQCRCPNVAGRRCDTCAPGFGYFSCRPDC 1500  
QY 1501 CHEAGTMAVSCDPLTGQCHCKENVGSRCDQCRVGTFTSLDAANPKGCTRCFCGATERCG 1560  
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QY 1561 NSNLARHEFVDMEGWVLLSSDRQVVPVHEHRPEIELLHADLRVADTFSELVWQAPPSYLG 1620  
Db 1561 NSNLARHEFVDMEGWVLLSSDRQVVPVHEHRPEIELLHADLRVADTFSELVWQAPPSYLG 1620  
QY 1621 DRVSSYGGTILHYELHSETQRGDI1FIPYESRDPVVLQGNQMSIAFLELAYPPPGVHRQOL 1680  
Db 1621 DRVSSYGGTILHYELHSETQRGDI1FIPYESRDPVVLQGNQMSIAFLELAYPPPGVHRQOL 1680  
QY 1681 QLVENGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVLSRRVLEVASEAGR 1740  
Db 1681 QLVENGNFRHLETHNPVSREELMMVLAGLEQLQIRALFSQTSSSVLSRRVLEVASEAGR 1740  
QY 1741 PPASVVEI1CMCPANTRYGDSQCECAPYYRTKGLFLGRCPVQCHGSHDRCLPSSGICVG 1800  
Db 1741 PPASVVEI1CMCPANTRYGDSQCECAPYYRTKGLFLGRCPVQCHGSHDRCLPSSGICVG 1800  
QY 1801 COHNTGEOQCRERCPGFVSSDPSPASPASCVSCPFLAVPSNNFADGCVLRNGRTQCLCRP 1860  
Db 1801 COHNTGEOQCRERCPGFVSSDPSPASPASCVSCPFLAVPSNNFADGCVLRNGRTQCLCRP 1860  
QY 1861 GVAGASCRCAPGFPFNPLVJGSSCQPCDCSNGDGNMI1FSDCDPLTGACRGCLRHHTGP 1920  
Db 1861 GVAGASCRCAPGFPFNPLVJGSSCQPCDCSNGDGNMI1FSDCDPLTGACRGCLRHHTGP 1920  
QY 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCLEGYFGF 1980  
Db 1921 HCERCAPGFYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCLEGYFGF 1980  
QY 1981 EQCQCRPCACGPAAGKSECHPQSGQCHCQPGTTPGQCLCAPGYWGLPEKGCRCQCP 2040  
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QY 2041 GHCDPHTGHTCPCPGLSGERCDTCSQOHQVVPVPGKPGHGHICEVCDHCVLLDLDLERA 2100  
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QY 2101 GALLPAIRELOGINASSAAWALHRLNASTADLOSRLRRPPGPRYQAAQLOTLLEQOSI 2160  
Db 2101 GALLPAIRELOGINASSAAWALHRLNASTADLOSRLRRPPGPRYQAAQLOTLLEQOSI 2160  
QY 2161 SIQODTERLGSOATGVQOAGQLDITTESTLGRAQKLLSVRAVGRALNELASRMGQSP 2220  
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QY 2221 GDALVPSGQLRWALAEVERLLWMDRDLGQAGVAAEALBAQRLMARVQOELTSWE 2280  
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QY 2281 ENQSLATH1RDOLAQVESGLMDLREALQAVNTTEASELNSRNERVKEALQWQELSQ 2340  
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Db 2401 VDLVEAEEAQAQKLNOLAINSGIILGINODRFQRAVEASNAYSSTILOQVAAEDAAQ 2460  
Qy 2461 ALRQASRTWEMVQVQGLAAGARQLANSSALEETILGHQGRGLAQAQGLQLNHV 2520  
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Db 2521 ARKNOLAQIOEAQAMLANDTSETSEKIAHAKAVAAEALSTATHVSOLOQMQKNVERW 2580  
Qy 2581 SOLGLOQODLSQVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASLALSANIGVRK 2640  
Db 2581 SOLGLOQODLSQVERDASSVSTLEKTLPLLAKLSRLNENRGVHNASLALSANIGVRK 2640  
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Db 2641 LIAQARSAAKVKVSMKFNKSGVRLRPPRLADLAAYTALKPHIQSPVPAPEKNTGD 2700  
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Db 2701 HFVLYMGRQATGDMVGSYLRNKHVWYRLGKAGPTTSLSDENIGBQFAAVSIDRTLQF 2760  
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Db 2821 TEMETLNEVSVLYNFETQFMDLTAVDKPCARSATGDPWLTDCSYLDGSGFARISPEK 2880  
Qy 2881 PSNTRKFPQDELRLVSNGIIFPLKQESQFLCLAVOEGTLVLFYDFGSGGLKADPLQPQA 2940  
Db 2881 PSNTRKFPQDELRLVSNGIIFPLKQESQFLCLAVOEGTLVLFYDFGSGGLKADPLQPQA 2940  
Qy 2941 LTAASKATOVFLLAGNRKRVLRVERATVFSVDQNMLEMDADAYLGVVPEEQPLSLRQ 3000  
Db 2941 LTAASKATOVFLLAGNRKRVLRVERATVFSVDQNMLEMDADAYLGVVPEEQPLSLRQ 3000  
Qy 3001 LFPSSGSGVRGCIKIGALKGVYDLKRLNTGISFCGTADLLVGRMTFPHGHGFLPLALPD 3060  
Db 3001 LFPSSGSGVRGCIKIGALKGVYDLKRLNTGISFCGTADLLVGRMTFPHGHGFLPLALPD 3060  
Qy 3061 VAPITEVYVSGFGRGTQDNNLLYRTSPDGPYQVSLRREGHTVLRFWNQEVETQVRFADG 3120  
Db 3061 VAPITEVYVSGFGRGTQDNNLLYRTSPDGPYQVSLRREGHTVLRFWNQEVETQVRFADG 3120  
Qy 3121 APHYVAFYSNVTGVWLYYVDDQLQVKSHERITPMLQLOPEPSRLLGLLPVSGTFNFS 3180  
Db 3121 APHYVAFYSNVTGVWLYYVDDQLQVKSHERITPMLQLOPEPSRLLGLLPVSGTFNFS 3180  
Qy 3181 GCISNVFQRLRGPORVFDLHQNMGSVNVVSGCTPAQLIETSRATAQVSRSRQPSQDL 3240  
Db 3181 GCISNVFQRLRGPORVFDLHQNMGSVNVVSGCTPAQLIETSRATAQVSRSRQPSQDL 3240  
Qy 3241 ACTTTPWLTQDQYQFGSLPYSYQFVIGISPSHNRHLHSLVLRPHAAASQGLLSTAPM 3300  
Db 3241 ACTTTPWLTQDQYQFGSLPYSYQFVIGISPSHNRHLHSLVLRPHAAASQGLLSTAPM 3300  
Qy 3301 SGRSPSLVFLNHHGFVAQTGPGPRLOVQSRQHSRAGQWHRVSVRGMQOQIQLVWDGSG 3360  
Db 3301 SGRSPSLVFLNHHGFVAQTGPGPRLOVQSRQHSRAGQWHRVSVRGMQOQIQLVWDGSG 3360  
Qy 3361 TWSQKALHHRVPRAERPOPYTLVSGGLPASSYSKLPVSVGSGCLKKLQLDKQPLATPT 3420  
Db 3361 TWSQKALHHRVPRAERPOPYTLVSGGLPASSYSKLPVSVGSGCLKKLQLDKQPLATPT 3420  
Qy 3421 QMVGVTVCVSGPLEDGLFPFGSEGVVTLLEPKAKMPYVVSLEKRPVLAAGLIFHLQAL 3480  
Db 3421 QMVGVTVCVSGPLEDGLFPFGSEGVVTLLEPKAKMPYVVSLEKRPVLAAGLIFHLQAL 3480

Qy 3481 ATPYMLKYLTEQVLLQANDGAGEFSTWVTPKLCDSGRHVRVAVIMGRDITLLEVDVTQSN 3540  
Db 3481 ATPYMLKYLTEQVLLQANDGAGEFSTWVTPKLCDSGRHVRVAVIMGRDITLLEVDVTQSN 3540  
Qy 3541 HTTGRLPESLAGSPALLHIGSLPKSSTARPELPAYRGCLRKLLINGAPVNVVTASVQIOGA 3600  
Db 3541 HTTGRLPESLAGSPALLHIGSLPKSSTARPELPAYRGCLRKLLINGAPVNVVTASVQIOGA 3600  
Qy 3601 VGMRGCPSTLALSQKQKALTQORHAKPSVSPLLWH 3635  
Db 3601 VGMRGCPSTLALSQKQKALTQORHAKPSVSPLLWH 3635

RESULT 4  
US-10-312-352-22  
; Sequence 22, Application US/10312352  
; Publication No. US20040053824A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom  
; APPLICANT: YUE, Henry; AZIMZAI, Yaida  
; APPLICANT: HE, Ann; BATRA, Sajeev  
; APPLICANT: LO, Terence P.; NGUYEN, Damiel B.  
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameen R.  
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam  
; APPLICANT: BURFORD, Neil; YAO, Monique G.  
; APPLICANT: CHAWLA, Narinder K.; KHAN, Farran A.  
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farran A.  
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.  
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.  
; APPLICANT: LU, Yan; BOROWSKY, Mark L.  
; APPLICANT: LI, Dying Aina M.; RAMKUMAR, Javalaxmi  
; APPLICANT: YANG Junming; GURURAJAN, Rajagopal  
; APPLICANT: WARREN, Bridget A.; GIENZEN, Kimberly J.  
; APPLICANT: XU, Yuming; KALLICK, Deborah A.  
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha  
; APPLICANT: DELEGANE, Angelo M.; LEE, Sally  
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES  
; FILE REFERENCE: PF-0794 USN  
; CURRENT APPLICATION NUMBER: US/10/312,352  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: PCT/US01/21067  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215,454  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/219,462  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 60/240,111  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: US 60/240,106  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: US 60/244,021  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/248,887  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/249,570  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PERL Program  
; SEQ ID NO 22  
; LENGTH: 3695  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CDI  
US-10-312-352-22

Query Match 79.7%; Score 15842; DB 12; Length 3695;  
Best Local Similarity 79.4%; Pred. No. 0;  
Matches 2874; Conservative 278; Mismatches 451; Indels 18; Gaps 8;

QY 1 DLYCKLVGGFVAGDNPQITQGYCDICTAANSNKAHPVSNADIGTFRWQSPPLSRGLE 60  
Db 79 DLYCKLVGGFVAGDNPQITQGYCDICTAANSNKAHPASNAIDGTERWQSPPLSRGLE 138  
QY 61 YNEVNTLIDGOVHYAVYVLIKEANSRDLWLERSTDFGHTYQPMQFFASCKDCLER 120  
Db 139 YNEVNTLIDGOVHYAVYVLIKEANSRDLWLERSMDFGRTYQPMQFFASCKDCLER 198  
QY 121 FGPRTLERITQDDVDICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYPLLRDTFKATN 180  
Db 199 FGPRTLERITRDAACICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYPLLRDTFKATN 258  
QY 181 IRLRFLRTNLLHLMGKALRDFTVRRYYYSIKDISIGRCVCHGHADCAKADPLDPF 240  
Db 259 VRLRFLRTNLLHLMGKALRDFTVRRYYYSIKDISIGRCVCHGHADCAKADPTDPF 318  
QY 241 RLQCAQCHNTCGSCDRCCPGFNQPKWATTDANECQSCNCHGHAYDCCYDPEYDRN 300  
Db 319 RLQCTCHNTCGTCDRCCPGFNQPKWATANSANECQSCNCHGHATCCYDPEYDRR 378  
QY 301 ASQNDNVYGGVCLDCHHTTGINCERCLPGFPFRAPQDPLDSHVCRPCDCESDFTDG 360  
Db 379 ASQSLDGTQYGGVCLDCHHTTAGVNCERCLPGFYRSPNHPLDSHVCRRCNCESDFTDG 438  
QY 361 TCEDLTGRCYCRNFTGELCAACAEGYTDPHCYPLPSFPHNDTRBQVLPAGQIVNCDN 420  
Db 439 TCEDLTGRCYCRNFSGERCDVCAEGTGPSPCYPTPS-SSNDTRBQVLPAGQIVNCDCS 497  
QY 421 AAGTQGNACRDKPLRGVCVKPNFRGAHCBLCAPGFHGPSCPCQSCSPGVANSJCDPES 480  
Db 498 AAGTQGNACRDKPRVGRCLCKPNFQGTCHCBLCAPGFVGPQCQPCQSSPGVADDRCDPT 557  
QY 481 GQCMCRTFGEGDRCDHCLGYFHPFLCOLGCGSPAGTLPBGCDCAEGRCCRCRPGFDPHCD 540  
Db 558 GQCRVGFEGATCDRCAPGYFHPFLCOLGCGSPAGTLPBGCDCAEGRCLCQPEFAGPHCD 617  
QY 541 RCLPGHYGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQCSFGFYGFPSCIFC 600  
Db 618 RCRPGYHGFNCQACTCDPRGALDQCGAGLRCRCRPGYTGACQCSFGFHFPSCVPC 677  
QY 601 HCSADGSLHTCDPTTQCCRCRVRTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660  
Db 678 HCSAEGSLHAACDRSQSCRCRVRTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPAL 737  
QY 661 PETQAPCMCAHVEGSPCDCKPGYMGLSASNPEGCTRCSCDPRGTGLGVTECQ-GNGQC 719  
Db 738 PEAVQPCMAHVEGSPCDCKPGFWGLSPSNPEGCTRCSCDLRGLTGLGVABEQPTGQC 797  
QY 720 FCKAHVCGKTCACCKDFFGLDYADYFGCRSCRDVGGLGQCGCEPKTGTACRCRPNTOGP 779  
Db 798 FCKPHVCGQACASCKDFFGLDQADYFGCRSCRDIGGALGQSCPEPTGVCRCPNTOGP 857  
QY 780 TCSEPAKHLYLPDLHLMLELEEAATPEGHAVRFGFNPLEFENFSNRGYAHMAIOPRIV 839  
Db 858 TCSEPAKHLYLPDLHLMLELEEAATPEGHAVRFGFNPLEFENFSNRGYAQMAYQPRIV 917  
QY 840 ARLVNTSPDLFLRVFRYVNRGSTSVNGQISVREEGKLSSTNCTNCTQSQPVAFPPSTEPAF 899  
Db 918 ARLVNTSPDLFLRVFRYVNRGMSVSRVSVREGRSAACANCTAQSQPVAFPPSTEPAF 977  
QY 900 VTVQRGEGEFVLNPGIALLVEAEGVLDYVLLPSTVYEAALLOHRYVTEACTYRBSA 959  
Db 978 ITVPQRGEGEFVLNPGTALRVEAEGVLDYVLLPSTVYEAALLOHRYVTEACTYRPSA 1037  
QY 960 LHSSTENCILVYAHLPDGPSPSAAGTEALCRHDSNLPRECPTEQLSPSHPPIATCFGSDVDI 1019  
Db 1038 QOSGDNCLLYTHLPDGPSPSAGLEALCRQNSLPRPCPTQLSPSHPPIITCTGSDVDV 1097  
QY 1020 QLEMAVPOGQVLYVVEVGEDSQBMGVAVHTPQAPQOGLVNLHPCPSYSSLCRSPARD 1079  
Db 1098 QLOVAVPOGQVLYVVEVANEDARQEVAVHTPQAPQOGLVNLHPCPSYSSLCRGTARD 1157  
QY 1080 TQHLAIPLHLDSEASIRLTAEOAHFFLHSVTLVPVEBFSTEFVEPRVFCVSSHGTNPSS 1139

Db 1158 TQDLAVFHLDEASVELTAEQARFFLHGVTLVPIBEFSEFVEPRVSCSISSHGAQFNS 1217  
QY 1140 AACLASFPKPPQPIILKDCQVLPLPDLPLTQSQELSPGAPPEGQFRPPTAVDPNAEP 1199  
Db 1218 AACLPSEFPKPPQPIILRDCQVPLPLPGLPLTHAQDLTPATSPAGPRPRPTAVDPAEP 1277  
QY 1200 TLLRHPOGTVVFTTQVTLGRYAFLLHGYQVPHSPPEVEVLINGGRVMOGHANASFCPHG 1259  
Db 1278 TLLREPOATVVFTTQVTLGRYAFLLHGYQVPHSPPEVEVLINAGRVMQGHANASFCPHG 1337  
QY 1260 YGCRTLVLCGOTMLDVTNDELTVTVRVPGRWMLWLDYVILVPEDAYSSSYLOREPJDKS 1319  
Db 1338 YGCRTLVVCBQALLDVTTHSELTVTVRVPGRWMLWLDYVILVPEENVYSFGVREEPJDKS 1397  
QY 1320 YDFTSHCATQGYHISPSSSPFCNNAATSLSFVNNGALPCGCHVECAVSEPTCEPFGQC 1379  
Db 1398 YDFTSHCAQGYHISPSSSLFCNNAASLSLFYNNGARFCGCHVEGATOPTCEPFGQC 1457  
QY 1380 PCRGHVLRGDCSRCATGWGFPNCRPCDCGALRCDELGTGOCICPPRTVPPDCLVCQSQSF 1439  
Db 1458 PCHAVLVRGDCSRCATGWGFPNCRPCDCGALRCDELGTGOCICPPRTIPDCLVCQPTF 1517  
QY 1440 GCHPLVGCCECNCSPGVQVELTDPCTDMDSGQCRCPNVAGRRCDTCAPOFYGYPSRCP 1499  
Db 1518 GCHPLVGCCECNCSPGIGTDELTDPTCDTDSQCKCRPNVTGRRCDTCSPGFHYPRCRPC 1577  
QY 1500 DCHAGTMAVSYCDPLTGQCKENVOGSRCDQCHVGTFSLDAANPKGCTRCFCGATERC 1559  
Db 1578 DCHAGTAPGVCDDLPTGQCKENVOGPKCDQCSLGTFSLDAANPKGCTRCFCGATERC 1637  
QY 1560 GNSLRAHEFVDMEGWLLSDRQVVPHEHRPEIETELHADLR----SVADTFSELYWOAP 1615  
Db 1638 RSSVYTRQEFVDMEGWLLSTDRQVVPHEHRQPGTEMLRADLRHVEAVPEAFPELYWOAP 1697  
QY 1616 PSYLGDRVSSYGGTLHVELHSETORGDIPTPYERSPDVVLQGNQMSIAFLAYLPPPGQV 1675  
Db 1698 PSYLGDRVSSYGGTLRYVELHSETORGDFVPMESRDPVVLQGNQMSITFLEPATFPGHV 1757  
QY 1676 HRGQLQVNEGFRHLETHNPVSREELMMVLQALQIRALFQSTSSSVSLRVRVLEVAS 1735  
Db 1758 HRGQLQVNEGFRHTERTNTVSRREELMMVLQALQIRALFQSISSAVSLRRVALEVAS 1817  
QY 1736 BAGRPASNVLCVCPANYRGDSQCECAPGYRDTKGLFLGRVCVQCCHGHSRCLPGS 1795  
Db 1818 PAGQALASNVLCVCLCPASVYRGDSQCECAPGYRDKVGLFLGRVCVQCCHGHSRCLPGS 1877  
QY 1796 GICVGCQHTNTRGDQCRCPGVSSDPSNPASPCVSCPCLAVPSNNPADCVLRNGRTQ 1855  
Db 1878 GVCVDCQHTNTRGACRCAQAGFMS-RDDPSAPCVSCFCLSVPSNNFAEACVLRGGRTQ 1936  
QY 1856 CLCRPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNMTFSDCDPLTGACRCLR 1915  
Db 1937 CLCRPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDPNMTFSDCDPLTGACRCLR 1996  
QY 1916 HTTGPHCERCAPGVGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCDCLE 1975  
Db 1997 HTTGPRCICAPGVGNALLPGNCTRCDCPCGTEACDPHSGHCLCKAGVTGRCDCRQOE 2056  
QY 1976 GYFGEQCCQGRPCAPCAKGSBCHPOSQCHQCPGTGTPQCCECAPGYWGLBEKGCR 2035  
Db 2057 GHFGNGCGCRPCAPCAKGSBCHPOSQCHQCRPGTMGTPQCRECAPGYWGLBEQGR 2116  
QY 2036 CQCPGHCDPTGHTCTCPGLSBERCDTCOOHVVPVPGKPGHGHCEVCDHCVLLLD 2095  
Db 2117 CQCPGRCDPHTGRCNCPGLSBERCDTCOOHVVPVPGKPGHGHCEVCDHCVLLLD 2176  
QY 2096 DLERAGALLPATREQLQINASSAAWALHRLNASIADLOSKLRRPPGPRYQAAQQLQTL 2155  
Db 2177 DLERAGALLPATHEQLRGINASSMAWALHRLNASIADLOQLASPLGPRHETAQQL 2236  
QY 2156 BOOSISLOOPTHGSOATGVQGOGLDTESTIGRAQKLLSVRAGVGRALNELASRM 2215





QY	1380	PCRGHVGRIDCSRCA	TGYWGFNCRPCDCG	ARLACDEL	TGQCICBPRTVPP	PCILVCQPOSF	1439	
Db	1458	PCHAHVGRIDCSRCA	TGYWGFNCRPCDCG	ARLACDEL	TGQCICBPRTTTPP	PCILCQPOTF	1517	
QY	1440	GCHPLVGBECNCSPG	YQELTDP	TCMDWSGCRPNV	AGRRCDTCA	PGFVGYPCSRPC	1499	
Db	1518	GCHPLVGBECNCSPG	YQELTDP	TCDDTDSGQCKRPN	TGRCDDTCS	PGFHHGYPCRPC	1577	
QY	1500	DCHAEAGTWASVCD	PLTGTQCHCKENYQ	SGRCDQCRVGT	FSLDAANPKG	CTRCFCGATERC	1559	
Db	1578	DCHAEAGTAPGVCD	PLTGTQCYCKENYQ	SGKPCQCSLGT	FSLDAANPKG	CTRCFCGATERC	1637	
QY	1560	GNSNLARHBFVDM	EGWLLSSDRQVVP	PEHHP	PEIELLHADLR	---SVADTFSELYWOAP	1615	
Db	1638	RSSSYTRQBFVDM	EGWLLSSDRQVVP	HERPGTEMLRAD	LHRVPEAVEA	FPELWYQAP	1697	
QY	1616	PSYLGDRVSSYG	TTLHYELHSETQR	GDFIPYESRP	VDVLOGNQMSIA	FLAYLPPQOV	1675	
Db	1698	PSYLGDRVSSYG	TTLRYELHSETQR	GDFVPMESRP	VDVLOGNQMSIT	FLPAYETPGHV	1755	
QY	1676	HGQLOLVGEGNFR	HLTHNPFVSREEL	MMVLASLEQ	LQIRALPSOT	SSSVLSLRVLEVAS	1735	
Db	1758	HGQLOLVGEGNFR	HLTHNPFVSREEL	MMVLASLEQ	LQIRALFSQ	SSAVLSLRVALEVAS	1817	
QY	1736	EAGRGPPASNV	ELCWPANYRODS	COEAPGYROT	KGLFLGR	CVPCOCHGHSRCLGS	1795	
Db	1818	PAGQALASNV	ELCLCPASYRDS	COEAPGYRDK	GLFLGR	CVPCOCHGHSRCLGS	1877	
QY	1796	GLCVGCOHNT	EDQCEBRCPPG	SVSDPNPAPCV	SCPLAVP	SNPNFADGCVLNRGTQ	1855	
Db	1878	GVCVDCQHNT	EGAKCERCOAG	FWSS-RDP	SPAPCVSC	PLSPVSNNAEGCVLRGGRTQ	1936	
QY	1856	CLCRPGYAGAS	CERCAPGFGN	PLVLGSSCQ	PCDCSGNDP	NMTFSDCDEL	TGACEGCLR	1915
Db	1937	CLCKPYAGAS	CERCAPGFGN	PLVLGSSCQ	PCDCSGNDP	NLLFSDCDEL	PTGACRGCLR	1996
QY	1916	HTTGPCHCE	CAPFGYNALL	PGNCTRCDCS	PCGTETCD	PQSGRCLCKAGVT	QQRCDRLE	1975
Db	1997	HTTGPCHCE	CAPFGYNALL	PGNCTRCDC	TPCTPGTEACD	PHSGHCLCKAGVT	GRRCDRQOE	2056
QY	1976	GYVGFQCGO	GRPCACGPA	AKSGECH	POSGQCHC	OPGTTGPOCLE	BCAPGYWGLPKGGER	2035
Db	2057	GHEFGNGCG	GRPCACGPA	AKSGECH	POSGQCHC	PGTGMGPOCR	BCAPGYWGLPEQGR	2116
QY	2036	CQCPRGHCD	PHTGCTC	PPGLGGER	CDTCSQ	QHQVVPVPGKPG	HGHIHCEVCDHCVLLLD	2095
Db	2117	CQCPRGHCD	PHTGRCNC	PPGLGGER	CDTCSQ	QHQVVPVPGFVGH	SIHCEVCDHCVLLLD	2176
QY	2096	DLERAGALL	PAIRELOQ	GINASAAW	LRHUNASI	ADLQSKLR	PPPGRYQAAQOQLT	2155
Db	2177	DLERAGALL	PAIRELOQ	GINASSAAW	LRHUNASI	ADLQSKLR	SFLGPRHTAQOQLEVL	2236
QY	2156	BOOSISLOQ	TBELGSA	TGVQAGOL	DDTTESTIG	RAQKLLES	VRAVGRALNELASRM	2215
Db	2237	BOQSTSLGQ	ARRLGGQAV	GTDRDQAS	LLAGTEATL	GHAKTL	LAIRAVDRTLSELMST	2296
QY	2216	GQSGPGDAL	VPGEQLRW	ALAEVER	LLMDMT	TRDILGAQ	AVAEIAENORLMARVQEO	2275
Db	2297	GHLGLANAS	APSQEQLRTL	AEVERILL	MMWRARDIL	GAPQAAAE	AEIAAAQRLARVQEO	2356
QY	2276	TSFWENQ	SLATHIR	DOLAQ	SEGLMDL	REALNOAV	NTTREAELNSRNOERKEALQWK	2335
Db	2357	SSUWENQ	ALATQ	TRDLQ	ACHAGLMD	REALNRA	VDATREAEQLNSRNOERLEALQK	2416
QY	2336	QELSQDNAT	LKATLOAS	LILGHV	SELGQ	DOAKED	LEHLAASLDGAWTPLLKMQAFS	2395
Db	2417	QELSRDNAT	LQATLHA	ARDTLAS	VFRLLSH	LQAKEELER	LAASLDGARTPLLQMQTES	2476
QY	2396	PASSKVD	LVEAAHAK	NOLAIN	LSGIL	GINODR	FTQRAVEASNAVSSYLQAVQAAE	2455
Db	2477	PASSKURL	VEAAHAAQ	QLOAL	NUSSIL	LDVNO	DLTQRAIEASNAVSRILQAVQAAE	2536



Db 2537 DAAGALQADHTWATVVRQGLVDRQQLLANSTALEEAMQEQORLGLVWALQAGTQ 2596  
Qy 2516 LBNVARKNQLAAQIQEAQAMLAMDTSETSEKIAHAKAAVAABALSTATHVOSQLOQMKN 2575  
Db 2597 LADVRAKQDLAHIQAQAQAMLAMDTSETSKIAHAKAAVAABAOQTATRVOSQLOQMKN 2656  
Qy 2576 VERWOSQLOGLQODLSQVERDASSVSTLEKTLIOLLAKLSRLNRCVGNHNASLALSANI 2635  
Db 2657 VERWQOQYEGRLQODLQAVLDAGHSVSTLEKTLIOLLAKLSRLNRCVGNHNASLALSANI 2716  
Qy 2636 GVRKLIQAARSAASAKVKYSKMFNRSRGLRPRDLADLAAYTALKFHIQSPVPAPBPG 2695  
Db 2717 GVRRELIQAARSAASAKVKYSKMFNRSRGLRPRDLADLAAYTALKFHIQSPVPAPBPG 2774  
Qy 2696 KNTGDFVLYMGRQATGDMYVSLNQRKQVHYVRLKAGPTTILSDENIGBQFAVSD 2755  
Db 2775 QCTEDRFVYMGSRQATGDMYVSLNQRKQVHYVRLKAGPTTILSDENIGBQFAVSD 2834  
Qy 2756 RTLOFQGHMVSIVTEKQVHBIKGTVPAGSEGLNLNHPDDVFYVGGYPSNFTPPPLRFP 2815  
Db 2835 RTLOFQGHMVSIVTEKQVHBIKGTVPAGSEGLNLNHPDDVFYVGGYPSNFTPPPLRFP 2894  
Qy 2816 GYLGIEMETLNEEVVSLNFTQTMFLDTAVDKPCARSKATGDPMLTDGSLYDGSFARI 2875  
Db 2895 GYRGCIEMETLNEEVVSLNFTQTMFLDTAVDKPCARSKATGDPMLTDGSLYDGSFARI 2954  
Qy 2876 SPEKQFNTKRDQELRLVSYNGILFELKQESQFLAVQEGTLVLFYDFGSLKKAADPL 2935  
Db 2955 SPDSQISTTKRFEQEURLVSYNGILFELKQESQFLAVQEGTLVLFYDFGSLKKAADPL 3014  
Qy 2936 QPPQALTAASKATQVFLLAGNRKRLVVRERATVSVDDNNLEADAYLLGGVPEQLP 2995  
Db 3015 QPPPLTASAKAIOVFLLAGNRKRLVVRERATVSVDDNNLEADAYLLGGVPEQLP 3074  
Qy 2996 LSLRQILPSSGSRVGIKIGKALGVYDLKRLNTTGISFECTADLLVGRMTFFHGHGLP 3055  
Db 3075 PSLRWLFPPTGSGRVGKIGKALGVYDLKRLNTTGISFECTADLLVGRMTFFHGHGLP 3134  
Qy 3056 LALPDVAPTEVVYSGFGRGTQNNLLYRTSPDGFYVSLREHGVTLRFMNQEVETQR 3115  
Db 3135 LALSNVAPLTGNVYSGFGRHSADQSLLYRASPDGLQCVSLQCGRVSLQLLRTVKTQA 3194  
Qy 3116 VFADGAPHYVAFVSNVTVGWLVDYDQOLVKSHERTTLMQLOPEBPSLLIGGLPVSGT 3175  
Db 3195 GFADGAPHYVAFVSNVTVGWLVDYDQOLVKSHERTTLMQLOPEBPSLLIGGLPVSGT 3254  
Qy 3176 FHNFGSCISNVFVORLGRPORVFDLHONMGSVNVSVGCTPAOLIETS-----RATAOK 3228  
Db 3255 IYNFSGCISNVFVORLGRPORVFDLHONMGSVNVSVGCTPAOLIETS-----RATAOK 3314  
Qy 3229 VSRRSRQPSODLACTPMLPGITQDAYQFGGGLPVLQFVIGISPSHRNLHLMLVRPFA 3288  
Db 3315 ASRRSRQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGLARHNRNWPSSLMHVLPR- 3373  
Qy 3289 ASQGLLLSTAPMGRSPSLVLFNLHGHFVAQTEGPGFRLQVOSRQHSRAGQWHRYSVRWG 3348  
Db 3374 SSRGLLLFTARLPSPSLALFSLNGHFVAQTEGPGFRLQVOSRQHSRAGQWHRYSVRWG 3433  
Qy 3349 MQOILVDPGWSQVSAKALHHRVPRERPOPYTLVSGGLPSSYSSKLPVSVFGSGCLKK 3408  
Db 3434 KNRILLVTDGARAWSQEGPHRQGAHEHTQPHTLFVGGPLPASHSSKLPVTVFGSGCVKR 3493  
Qy 3409 LQDKOPLRPTOMGVTPCVSGPLEDLFFPGSEGVVTLPLPKAMPVVSLELEMRPLA 3468  
Db 3494 LRLHGPGLGAPTMAGVTPCILGFLBAGLFFPGSGGVITLIDLPGLTLPVGLVLEVRPLA 3553  
Qy 3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRHWRVAVING 3527  
Db 3554 VTGLIFHLGQARTPPYLQVTEKQVLLRADDGAGEFSTVTRPSVLCVCGQWHLRAVMKS 3613  
Qy 3528 RDTLRLEVDTOQSHHTGRPLPESLAGSPALLHLSLPKSTARPELPAYRGCLARKULLINGA 3587

Db 3614 GNVLRLEVDASQNHNTVGPILLAAAGAPAPLYLGLLPEPMAVQWPWPAYCOCMRRLAVNRS 3673  
Qy 3588 PVNVTASVOIQAGVGRGCPSS 3608  
Db 3674 PVANTRSEVHGAVGASGCPA 3694  
RESULT 6  
US-10-312-088-31  
; Sequence 31, Application US/10312088  
; Publication No. US20030219862A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Cogswell, John P.  
; APPLICANT: Kabnic, Karen S.  
; APPLICANT: Lai, Ying-Ta  
; APPLICANT: Martensen, Shelby A.  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Strum, Jay C.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Xie, Qing  
; APPLICANT: Rizni, Safia K.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GPO0029  
; CURRENT APPLICATION NUMBER: US/10/312,088  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/19929  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,161  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/213,156  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 3696  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-312-088-31  
Query Match 79.6%; Score 15830.5; DB 15; Length 3696;  
Best Local Similarity 79.3%; Pred. No. 0;  
Matches 2874; Conservative 279; Mismatches 450; Indels 19; Gaps 9;  
Qy 1 DLYCKLVGGPVAGGDPNQTTGGYCDICTAANSKHAHPVSNADIGTERWQSPPLSRGLE 60  
Db 79 DLYCKLVGGPVAGGDPNQTTGGYCDICTAANSKHAHPVSNADIGTERWQSPPLSRGLE 138  
Qy 61 YNEVNVTLDLQGVHVAVLIKPA NSPRPDLWLERSTDFGHTYQWPQFFASSKRDCLER 120  
Db 139 YNEVNVTLDLQGVHVAVLIKPA NSPRPDLWLERSTDFGHTYQWPQFFASSKRDCLER 198  
Qy 121 FGPRTLERTODDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSLRLRFTKATN 180  
Db 199 FGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSLRLRFTKATN 258  
Qy 181 IRLRFLRNTLLGLHMGKALRDPVTTRRYYSKIDISIGRCVCHGADVCDADPLDPF 240  
Db 259 VRLRFLRNTLLGLHMGKALRDPVTTRRYYSKIDISIGRCVCHGADVCDADPLDPF 318  
Qy 241 RLQCAQHTCGGSCDRCCPFNQPKPATTPDSANECSQCNCHGHAYDCYDEVDERN 300  
Db 319 RLQCTQHNTCGGTCDRCCPFNQPKPATTPDSANECSQCNCHGHAYDCYDEVDERN 378  
Qy 301 ASQNDNVYGGVCLDQHHHTGNCERCLPGFFRAPPDPLSDPSHYCRPCDCESDFTDG 360  
Db 379 ASQSLDGTGQGGVCIQDQHHHTGNCERCLPGFFRAPPDPLSDPSHYCRPCDCESDFTDG 438  
Qy 361 TCEDLTGRCYCRNFTGELCAACAGYTDFFHCYPLPSFFPHNDTREQVLPAQIVNCDN 420  
Db 439 TCEDLTGRCYCRNFTGELCAACAGYTDFFHCYPLPSFFPHNDTREQVLPAQIVNCDN 497

Db	1578	DCHEAGTAPGCDPLTGGCYCKENVQPKDCQCSLGTFSLDAAHPKGCCTRCFCGATERC	1637	
QY	1560	GNSNIARHEFYDMEGWLLSSDRQVPPHHRPEIELLHADUR----	SVADTFSELYMOAP	1615
Db	1638	RSSSYTROFEYFDMEGWLLSSDRQVPPHHRQGTETMLRADLHRVPEAVEAPPPELYMOAP	1697	
QY	1616	PSYLGDRVSSYGGTLHYELHSETQGDIFIVESRSPDVLOQNMWSIAFLSLAYPPPOQV	1675	
Db	1698	PSYLGDRVSSYGGTLHYELHSETQGDVFPWMSRPDVVLOQNMWSITFLSPAYPTPGHV	1757	
QY	1676	HRGQQLQVEGNFRHLFETHNPVSREELMMVLAGLBOLQIRALFQSTSSVSUSIRVVLVVAS	1735	
Db	1758	HRGQQLQVEGNFRHTTETNTVYSREELMMVLASLQQLTRALFQSTSSAVFVRRVALEVAS	1817	
QY	1736	EAGRGPPASNVELCMCPANYRGDSCQECAPGVYRDTKGLFLGRCPVPCOCHGHSRCLPES	1795	
Db	1818	PAGQALASNVVELCLCPASYRGDSCQECAPGFYRDVKGLFLGRCPVPCOCHGHSRCLPES	1877	
QY	1796	GIQVCGQHNTEGDCQECRCPGFVSGDSPSNPASCPCPIAVPSNNPADCGVLNNGTQ	1855	
Db	1878	GVYDCQHNTEGAHCERCQACQAFVSS-RDDPAPCVSCPCPIASVPSNNFAEGCVLGGRTQ	1936	
QY	1856	CLCRPGYAGASCERCAPGFNGPLVLGSSCOPDCSGNGDPMWIFSDCDPLTAGCRGCLR	1915	
Db	1937	CLCKPGYAGASCERCAPGFNGPLVLGSSCOPDCSGNGDPMWIFSDCDPLTAGCRGCLR	1996	
QY	1916	HTTGPHERCAPFFYGNALLPNCNTRCPCQGTETCDPQSGRCLCKAGVTGQRDCRLE	1975	
Db	1997	HTTGPCEICAPFFYGNALLPNCNTRCPCDCTPGTEACDPHSGHCLCKAGVTGRRDCRQE	2056	
QY	1976	GYTFPEQCGCRPCACGPAAGSECHPOSGQCHOPGTTGQCULECAPGYWGLPEKGCRR	2035	
Db	2057	GHFGDGGCGCRPCACGPAAGSECHPOSGQCHOPGTTGPMGQPCRECAEGYWGLPEQGCRR	2116	
QY	2036	CQCPRGHCDPHTGHCTCPPLGSGERCDCSCQOHQVPVPKPGCGHIGHEVCDHCYVLLLD	2095	
Db	2117	CQCPGRCDPHTGRCNCPPLGSGERCDCSCQOHQVPVPFGPVGHSHICEVCDHCYVLLLD	2176	
QY	2096	DLERAGALLPAIREOLOGINASSAWARHLRNASIALQSKLRPPGPRPVQAQOLOTL	2155	
Db	2177	DLERAGALLPAIREOLOGINASSAWARHLRNASIALQSKLSPGPRHTAQQLSVL	2236	
QY	2156	EQQSTSLQDTERLQSG-ATGVQAGQGLDTESTLGRAOKLLESVRAVGRALNELASR	2214	
Db	2237	EQQSTSLQDARRLGGQAVGTRDQASQLLACTEATLGHAKTLAAIRAVDRTLSELWSQ	2296	
QY	2215	MGQSGFDALVPSGQLRWALAEVERLLWDMTRDLGAGGVAEAEAEABOELMARVOEQ	2274	
Db	2297	TGHLGLANASPSGQLLTLAEVERLLWEMRARDLGAPQAAAEAEALAAQGLLARVOEQ	2356	
QY	2275	LTSFPEENQSLATHIRDQLOAVESGLMDLREALNOAVNTTAEELNSRNOBRVKEALQW	2334	
Db	2357	LSSELNEENQALATQTRDLQAQHEAGMDLREALNRVADTATRAQELNSRNOBRSEALQR	2416	
QY	2335	KQELSQDNATKLQAASLILGHVSEILQGIQDAKEDLEHAAASLDGAWPTLLKRMQAF	2394	
Db	2417	KQELSRDNATLQATLHAARDTTLASVFRLLHSJDQAKEBLERLAAASLDGARTPLLQRMOTF	2476	
QY	2395	SPASSKYDILVEAAEBAHAQKLNOLANLSGILGINODRFIOAPVASNAYSIILOQAOAA	2454	
Db	2477	SPAGSKLRLVEAAEBAHAQGLQGLANLSIILDVNQDLRTQPAIBASNAYSIRILOAQVAA	2536	
QY	2455	EDAAGQALRQASRTWEMVQVQGLAAGAROLLANSBALBETTLGHQGRGLGAQGRLOAGI	2514	
Db	2537	EDAAGQALQADHTWATVVRQGLVDRQAQLLANSTALEEAMLEQOQRLGLVWAAQLQART	2596	
QY	2515	QLHNWARKQOLAQIOEAQAMLMDTSETSEKIAHAKAVAAEALSTATHVOSQLOGMQK	2574	
Db	2597	QLRDVRAKQDQLEAHIQAQANLWMDTSETSKIAHAKAVAAEADQATATRVOSQLOAMQE	2656	
QY	2575	NYERWOSQGLGQGDLSQVEDASSYSTLEKTLPLQLLAKLSRLNREGVHNASLANSAN	2634	



Db 439 TCBDLTGRCYCRPNFGSERCNDVCAEGFTGFFSCYTPPS--SSNDTREQVLPAGQVNCDCS 497  
QY 421 AAGTQGNACKRDLRGLRCVCKNFRGAHCELCAFGPHGSPCHPCQSSPGVANSCLDPES 480  
Db 498 AAGTQGNACKRDLRGLRCVCKNFRGAHCELCAFGPHGSPCHPCQSSPGVANSCLDPES 557  
QY 481 GQCKRTGFGGDRCDHICALGYFHPPJLQICGCSFAGTLPBEGDEAGRCOCRFPGDPGPHCD 540  
Db 558 GQCKRTGFGGDRCDHICALGYFHPPJLQICGCSFAGTLPBEGDEAGRCOCRFPGDPGPHCD 617  
QY 541 RCLPGYHGYPDCHACADPRGALDQOCGVGLCHCRPGNTGATQCSCSPGFYGFSCIPC 600  
Db 618 RCPYHGFNFQACTCDPRGALDQOCGVGLCHCRPGNTGATQCSCSPGFYGFSCIPC 677  
QY 601 HCSADGSLHTTCDPTTGGQCRPRVTGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660  
Db 678 HCSAEGSLHAACDPRSCQSCRCRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPANPAL 737  
QY 661 PETQAPCMCAHVEGSCDCKGKGYGLSASNEGTCRSCDPRGLTGVTGTCQ--GNQOC 719  
Db 738 PEQAQVPCMAHVEGSPSCDCKGKGYGLSASNEGTCRSCDPRGLTGVTGTCQ--GNQOC 797  
QY 720 FCKAHVCGKTCAACKDGFGLDYADYFGCRSCRDVGGALGQCEBPKTGACRCRPNTOGP 779  
Db 798 FCKPHVCGQACASCKDGFGLDQADYFGCRSCRDVGGALGQCEBPKTGACRCRPNTOGP 857  
QY 780 TCSEPAKHVLPDLHNRHLELEAAPEGHAVRFGFNPLEFENFNRGVAHMAIOPRIV 839  
Db 858 TCSEPAKHVLPDLHNRHLELEAAPEGHAVRFGFNPLEFENFNRGVAHMAIOPRIV 917  
QY 840 ARNLNTPDLFLVFRVYNRGTSVNGQISVREBGLSKSCTNCTECSQVAPPPPTPEAF 999  
Db 918 ARNLNTPDLFLVFRVYNRGTSVNGQISVREBGLSKSCTNCTECSQVAPPPPTPEAF 977  
QY 900 VTVPORGFGFPVNLPGIALLVEAGVLDYVLLPSTVYEAALQHRVTEACTVPSA 959  
Db 978 ITVPORGFGFPVNLPGIALLVEAGVLDYVLLPSTVYEAALQHRVTEACTVPSA 1037  
QY 960 LHSNENCLVTAHPLDGFPSAAGTEALCRHNSLPRCPTEQLSPSPHPLATFCGSDVDI 1019  
Db 1038 QOSGDNCLLTHLPDGFPSAAGTEALCRHNSLPRCPTEQLSPSPHPLATFCGSDVDI 1097  
QY 1020 QLEMAVPOQOYLVVYVEDSHOENGVAHVHPQAPQOVLNHPCHPSSILCRSPARD 1079  
Db 1098 QLVAVPQGRYALVWEYANEDARQEVAVHTPQAPQOGLSLHPLCYLTLCRGTARD 1157  
QY 1080 TOHHLAIFHLDSIASIRLTABOAHFLLHSVTLVPVEEFSTFVPRVFCVSSHGTNPS 1139  
Db 1158 TODHLAVFHLDSIASIRLTABOAHFLLHSVTLVPVEEFSTFVPRVFCVSSHGTNPS 1217  
QY 1140 AACLASRFPKPPQPIILKDCQVLPPLPDLPLTOSQELSPGAPPEGQOPRPTTAVDNABP 1199  
Db 1218 AACLPSPRFPKPPQPIILKDCQVLPPLPDLPLTOSQELSPGAPPEGQOPRPTTAVDNABP 1277  
QY 1200 TLLSHPOGTVFTTQVPTLGRYAEALLHGXOPVHPSFPVEVLINGRIWQHGANASCPHG 1259  
Db 1278 TLLSEPOATVFTTHVPTLGRYAEALLHGXOPVHPSFPVEVLINGRIWQHGANASCPHG 1337  
QY 1260 YGCRTLVCEGQMLDVTDBELTIVRVPEGRMLWLDYLVLPEDAYSSSYLOEPLDKS 1319  
Db 1338 YGCRTLVCEGQMLDVTDBELTIVRVPEGRMLWLDYLVLPEDAYSSSYLOEPLDKS 1397  
QY 1320 YDFTSHCATQYHISPSSSSPFCNAATSLIFVNGALPCGCHVEGAVPTCEPFGQC 1379  
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Db 1458 PCRHVIGRDCSRCATGWGPNCRPCDCCARLDCDELTCGICPPRTVPPDCLVCPQSF 1517  
QY 1440 GCHPLVCEBNCSCGPGVQELTDTPTCDMSQCRPNVAGRCDDTCAPGYGPRCPC 1499

Db 1518 GCHPLVCEBNCSCGPGVQELTDTPTCDMSQCRPNVAGRCDDTCAPGYGPRCPC 1577  
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QY 1560 GNSNLARHEFVDMEGWLLSSDROVWPHHRPEIELLHADLR-----SVADTFSELYWQAP 1615  
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Db 1698 PSYLGDRVSSYGGTLYELHSETGORDIFIPYSRPRDVLQGNQMSIATLELAYPPPGQV 1757  
QY 1676 HRGOLQVVEGNFRHLETHNPVSRRELMVLAGLBOLOIRALFSOTSSSVSLRRVVLEVAS 1735  
Db 1758 HRGOLQVVEGNFRHLETHNPVSRRELMVLAGLBOLOIRALFSOTSSSVSLRRVVLEVAS 1817  
QY 1736 EAGGPPASNVVELCMCPANYRGDSQCBAPGYRYKDTKGLFLGRVCPQCCHGSHDRCLPGS 1795  
Db 1818 PAGQALASNVVELCLCPASVYRGDSQCBAPGYRYKDTKGLFLGRVCPQCCHGSHDRCLPGS 1877  
QY 1796 GICVGCQHTNEGDCRCRCPGVSSDPSNPASPCVPCPLAVPNNFADQCVLRNRTQ 1855  
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QY 1856 CLCRPGYAGASCERCAPFGFNGNPLVLGSSCQPCDCSGNGDPNMTFSDCDPLTGACRCGLR 1915  
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QY 1916 HTTGPHCERCAPGVGNALLPGNCTRCDCSCPGTETDCPOSGRCLKAGVGTGQRCDCLE 1975  
Db 1997 HTTGPHCERCAPGVGNALLPGNCTRCDCSCPGTETDCPOSGRCLKAGVGTGQRCDCLE 2056  
QY 1976 GYFPEQCGQRCPCACGPAKGSCHPQSGQCHQCPGTTPQCLECAPGYWGLPEKQCR 2035  
Db 2057 GYFPEQCGQRCPCACGPAKGSCHPQSGQCHQCPGTTPQCLECAPGYWGLPEKQCR 2116  
QY 2036 CQCPRGHCDPTHTGCTCPPLSGRCDTCSQOQVVPVPGKPGHIGCEVCDHCVLLLD 2095  
Db 2117 CQCPRGHCDPTHTGCTCPPLSGRCDTCSQOQVVPVPGKPGHIGCEVCDHCVLLLD 2176  
QY 2096 DLERAGALLPAIREQLOGINASSAAWALHRLNLSIADLOSLRSLPLGPRHETAQOQLEVL 2236  
Db 2177 DLERAGALLPAIREQLOGINASSAAWALHRLNLSIADLOSLRSLPLGPRHETAQOQLEVL 2296  
QY 2156 EQQSISLOQDTERLGSQATVQOQAGQLLDTTESTLGRAQKLESVRAVGRALNELASRM 2215  
Db 2237 EQQSISLOQDTERLGSQATVQOQAGQLLDTTESTLGRAQKLESVRAVGRALNELASRM 2296  
QY 2216 GOGSPGDALVPSGEOLRWALAEVERLLWDMRTRDLGAQCAVAEAELAAQRLMARVQEQ 2275  
Db 2297 GOGSPGDALVPSGEOLRWALAEVERLLWDMRTRDLGAQCAVAEAELAAQRLMARVQEQ 2356  
QY 2276 TSFWEENOSLATHIRDOQAQYESGLMDREALNOAVNTTREAELNSRNQSRVKEALQWK 2335  
Db 2357 TSFWEENOSLATHIRDOQAQYESGLMDREALNOAVNTTREAELNSRNQSRVKEALQWK 2416  
QY 2336 QELSODNATLKATLOAASLIIGHVSELLQDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2395  
Db 2417 QELSODNATLKATLOAASLIIGHVSELLQDQAKEDLEHLAASLDGAWTPLLKRMQAFS 2476  
QY 2396 PASSKVDLVEAAEAHAQKINQALNLSGIIILGINQDPTFOBAVEASNAYSILQAVQAAE 2455  
Db 2477 PASSKVDLVEAAEAHAQKINQALNLSGIIILGINQDPTFOBAVEASNAYSILQAVQAAE 2536  
QY 2456 DAAGQALQOQADHTWATVVRQGLVDRQAQALLANLSIIILDVNQDRLTORAIEASNAYSILQAVQAAE 2515  
Db 2537 DAAGQALQOQADHTWATVVRQGLVDRQAQALLANLSIIILDVNQDRLTORAIEASNAYSILQAVQAAE 2596  
QY 2516 LHNWARKNQALQOQADHTWATVVRQGLVDRQAQALLANLSIIILDVNQDRLTORAIEASNAYSILQAVQAAE 2575  
Db 2597 LHNWARKNQALQOQADHTWATVVRQGLVDRQAQALLANLSIIILDVNQDRLTORAIEASNAYSILQAVQAAE 2656

2576 VERWQQLGLOGLDLSQVERDASSVSTLEKTLPLLAKLRLNENRGNVHNASLALSANI 2635  
2657 VERWQQLGLOGLDLSQVERDASSVSTLEKTLPLLAKLRLNENRGNVHNASLALSANI 2716  
2636 GRVRLKIAQARSAAKVKVSMKENGSGVRLRPRDLADLAAYTALKFHIQSPVAPPEG 2695  
2717 GRVRLKIAQARSAAKVKVSMKENGSGVRLRPRDLADLAAYTALKFHIQSPVAPPEG 2774  
2696 KNTGDFHVLVYMSGRQATGDMVYSLRNQKWHYRLGKAGPTTSLIDENIGBQFAVSD 2755  
2775 QGTEDRFVYMSGRQATGDMVYSLRNQKWHYRLGKAGPTTSLIDENIGBQFAVSD 2834  
2756 RTLOFGHMSVTVKQWHEIKGTVPAGSEGLNLHPDDFVYVGGYPSNFTPEPLRPP 2815  
2835 RTLOFGHMSVTVKQWHEIKGTVPAGSEGLNLHPDDFVYVGGYPSNFTPEPLRPP 2894  
2816 GYLGCITEMETNEVYSLNFEOTFMDTAVDKPCARSKATGDPMLTDCSYLDSGSGFARI 2875  
2895 GYGCITEMETNEVYSLNFEOTFMDTAVDKPCARSKATGDPMLTDCSYLDSGSGFARI 2954  
2876 SPFKQPSNTRKFOEHLRLVSYNGIIFLQKBSOFLCLAVOEGTLYLFFYFGSGLKKADEL 2935  
2955 SPFKQPSNTRKFOEHLRLVSYNGIIFLQKBSOFLCLAVOEGTLYLFFYFGSGLKKADEL 3014  
2936 QPQALTAASKATQVLLAGNRKRVLRVERATVSVDDNMLEMADAYVLGGVPEQLP 2995  
3015 QPQALTAASKATQVLLAGNRKRVLRVERATVSVDDNMLEMADAYVLGGVPEQLP 3074  
2996 LSLRQLPPSGSGVRCIKGKALGVYDLKRLNTTGISFCTADLLVGRMTFPHGHGFLP 3055  
3075 LSLRQLPPSGSGVRCIKGKALGVYDLKRLNTTGISFCTADLLVGRMTFPHGHGFLP 3134  
3056 LALPDVAPITEVYSGFEGTODNLLVYRTSPDGPYOVSLREGHVTLRPNQVETOR 3115  
3135 LALPDVAPITEVYSGFEGTODNLLVYRTSPDGPYOVSLREGHVTLRPNQVETOR 3194  
3116 VFADGAPHYVAFVSNATGVLVYDDQLQVKSHERITPMLQLQEPBPSSLLGLPVSQT 3175  
3195 VFADGAPHYVAFVSNATGVLVYDDQLQVKSHERITPMLQLQEPBPSSLLGLPVSQT 3254  
3176 FHPFSGISNVFVORLGRQVDFLQNGMSVNVSVGCTPAQLIETSRATAQ--KVSRSS 3233  
3255 FHPFSGISNVFVORLGRQVDFLQNGMSVNVSVGCTPAQLIETSRATAQ--KVSRSS 3314  
3234 RQPSQDLACTPMLPGTIQDAYOFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHASOGL 3293  
3315 RQPSQDLACTPMLPGTIQDAYOFGGPLPSYLOFVGISPSHRNRLHLSMLVRPHASOGL 3373  
3294 LLSTAPMSGRSPSLVFLNHHGVFAOTEGPBLQVOSQHSRAGQWHRVSVRWGMQQTQ 3353  
3374 LLSTAPMSGRSPSLVFLNHHGVFAOTEGPBLQVOSQHSRAGQWHRVSVRWGMQQTQ 3433  
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3434 LVVDGQSTWQKALHHRVPAERPPQVTLVSGGLPASSYSSKLPVSGFSGCLKQLDOK 3493  
3414 QPLRTPTQMVGVTPCVSGPLEDGLFPFGSGGVVTLBLPKAKMPYVSLLEMRPLAAGLI 3473  
3494 QPLRTPTQMVGVTPCVSGPLEDGLFPFGSGGVVTLBLPKAKMPYVSLLEMRPLAAGLI 3553  
3474 FHLGOALATPMOLVTEOVLLQANDGAGEFSTWVTPK-LCDGRHVAIVMIGMDTLR 3532  
3554 FHLGOALATPMOLVTEOVLLQANDGAGEFSTWVTPK-LCDGRHVAIVMIGMDTLR 3613  
3533 LEVDTSNHTTGRLPESLAGSPALLHLSLPKSSSTARPELPAYRGCLRLKLLINGAPVNT 3592  
3614 LEVDTSNHTTGRLPESLAGSPALLHLSLPKSSSTARPELPAYRGCLRLKLLINGAPVNT 3673  
3593 ASVQIQAGVNRGCGPS 3608  
3674 RSVEVHGAVGASGCPA 3699

RESULT 8  
US-10-312-088-30  
; Sequence 30, Application US/10312088  
; Publication No. US20030219862A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Cogswell, John P.  
; APPLICANT: Kabnic, Karen S.  
; APPLICANT: Lai, Ying-Ta  
; APPLICANT: Martensen, Shelby A.  
; APPLICANT: Murodock, Paul R.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Strum, Jay C.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Xie, Qing  
; APPLICANT: Rizni, Safia K.  
; FILE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50029  
; CURRENT APPLICATION NUMBER: US/10/312,088  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/19929  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,161  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/213,156  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 3705  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-312-088-30

Query Match 79.6%; Score 15815; DB 15; Length 3705;  
Best Local Similarity 79.1%; Pred. No. 0;  
Matches 2873; Conservative 279; Mismatches 451; Indels 28; Gaps 9;  
QY 1 DLYCKLVGGPVAGDPNQTIQGYCDICTAANSNAKHPVSNADIGTERWQSPPLSRGLE 60  
DB 79 DLYCKLVGGPVAGDPNQTIQGYCDICTAANSNAKHPVSNADIGTERWQSPPLSRGLE 138  
QY 61 YNEVNTLQGVHAYVLIKFNAPRDLVWLERSTDFHTYQWQFPAKSKDCLE 120  
DB 139 YNEVNTLQGVHAYVLIKFNAPRDLVWLERSTDFHTYQWQFPAKSKDCLE 198  
QY 121 PGPRLERITQDDVICCTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDFTKATN 180  
DB 199 PGPRLERITQDDVICCTEYSRIVPLENGEIVVSLVNGRPGALNFYSPLLRDFTKATN 258  
QY 181 IRLRFLRNTLLHLMGKALRDPVTTRYYYSIKDISIGRCVCHGADVCADKDPDP 240  
DB 259 VLRFLRNTLLHLMGKALRDPVTTRYYYSIKDISIGRCVCHGADVCADKDPDP 318  
QY 241 RLQACAOHNTCCGSCDRCCPGFNQPKPATTDSANCSQCNCHGHAYDCYDPEVDRN 300  
DB 319 RLQCTCQHNTCCGSCDRCCPGFNQPKPATTDSANCSQCNCHGHAYDCYDPEVDRN 378  
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DB 379 ASQSLDGYQGGVCLDQHHHTTGINCERCLPGFFRAPDQPLDSPHYCRPCDCSDFTDG 438  
QY 361 TCEDLTGRCYCRNFTGELCAACAGYTDPEHCYPLSPFPHNDTREOVLPAGIUNCDN 420  
DB 439 TCEDLTGRCYCRNFTGELCAACAGYTDPEHCYPLSPFPHNDTREOVLPAGIUNCDN 497  
QY 421 AAGTQGNACRDXPRIGRCVCKPNFRGAHCELCAPGFHGPSCHPCCQSSPGVANSCLDPES 480  
DB 498 AAGTQGNACRDXPRIGRCVCKPNFRGAHCELCAPGFHGPSCHPCCQSSPGVANSCLDPES 557  
QY 481 GQCMCRTOFEGDRCDHCHALGYFHFPLQLCCSCSAGTLPBGCDEAGRCQCPGPDGHCD 540

Db 558 GQCRVGVFGATCDRCAPGYFHFPLCQLCGCSGAGTLPEGDEAGRCCLQBPFAHPHCD 617  
Qy 541 RCLPGYHGYPDCHACADPRGALDQCGVGGLCHCRPGNTGATCQBCSPGFYFPPSCIPC 600  
Db 618 RCRPGYHGFNCQACTCDPRGALDQCGAGGLCRCPGYTGACQBCSPGFHGFPPSCVPC 677  
Qy 601 HCSADGSLHTTCDPTTQCRPRVTLGLHCDMCPGAYNFPYCEAGSCHPAGLAPANPAL 660  
Db 678 HCSAEGSLHAACDPRSCQCRPRVTGLRCDTVPAGYNFPYCEAGSCHPAGLAPVDPAL 737  
Qy 661 PETQAPCMCAHVEGPGCDCKGKGYWGLSASNEGCTRCSCDPRGTLGGVTECQ-GNGQC 719  
Db 738 PEAQVPCMAHVEGPGCDCKGKGFWSNPNEGCTRCSCDLRGLTGLGVABEQPGTGQC 797  
Qy 720 FCZAHVCGKCAACKDGFGLDVADYFGCRSCRDVGGLGQCEBPKTGACRCRPNTOGP 779  
Db 798 FCKPHVCGQACSKDGFGLDQADYFGCRSCRDIGGALGQCEBPKTGACRCRPNTOGP 857  
Qy 780 TCSEPAKDHVLPDLJHMLLELEAATPEGHAVFNGFNFLEFENFMRGVAHMAIOPRIV 839  
Db 858 TCSEPAKDHVLPDLJHMLLELEAATPEGHAVFNGFNFLEFENFMRGVAHMAIOPRIV 917  
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Qy 900 VTYPORGFGBPVLPNGIMWALLVEAGVLLDYVLLPSTVYEALLCHRVTEACTYRPSA 959  
Db 978 ITVPORGFGFVLPNGITWALRVEAGVLLDYVLLPSTVYEALLCHRVTEACTYRPSA 1037  
Qy 960 LHSFENCLVLAHLPLDGFPSAAAGTEALCRHNSLPRCPTEQLSPSHPPLATCFGSDVDI 1019  
Db 1038 QCSGDNCLLYLHLPLDGFPSAAAGLEALCRQNSLPRCPTEQLSPSHPPLITCTGSDVDV 1097  
Qy 1020 QLEMAVPOPGQYVJVEYVEDSHQENGVAHVHPORAPQOGLNLHPCVSSLCRSPARD 1079  
Db 1098 QLOVAVPQGRYALVWBYANEDAEQVGVAVHPORAPQOGLNLHPCVSSLCRGTARD 1157  
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Db 1158 TQDLAVFLHLDSEASVRLTAEQARFFLHSLTVLVEEFTFVEPRVFCVSSHGTFNPS 1217  
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Qy 1200 TLLRHQPGTVFTTQVPTLGRYAFLLHGYOPVHPSPVEVLINGRIWQGHANASFCPHG 1259  
Db 1278 TLLRPOATVFTTHVPTLGRYAFLLHGYOPVHPSPVEVLINAGRWQGHANASFCPHG 1337  
Qy 1260 YGCRTLVLCGQTMLDVTDNELTVTVRVPBGRMLWLDYLVIPEDAYSSYLQEEPLDKS 1319  
Db 1338 YGCRTLVVCQALLDVTHSBLTVTVRVPKGRMLWLDYLVIPENYVSFGYLRREEPLDKS 1397  
Qy 1320 YDFISHCATQGYHISPSSSSPFCRNAATSLSFYNNGALPCGCHEVGAVSPTCEPFGQC 1379  
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Db 1458 PCHAVHGRDCSRCATGYWGPNNPCDCCGARLDELGTGQICPPRTIPDCLVCPQTF 1517  
Qy 1440 GCHPLVGBECNCSGPGVQELTDTCDMDSQCECRNVAGRCADTCAGFYGVPSCRPC 1499  
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Qy 1500 DCHAGTMAVSCDPLTGQCHCKENVQSRCDQCRVGTFSLDAANPKGCTRCFCFGATERC 1559  
Db 1578 DCHAGTAPGCDPLTGQCYCKENVQPKCDQCSLGTFSLDAANPKGCTRCFCFGATERC 1637  
Qy 1560 GNSNLARHEFVDMEGWLLSSDRQVPHHPEPELHLDLR-----SVADTFPELYWQAP 1615  
Db 1638 RSSSYTROEFVDMEGWLLSSDRQVPHHPEPELHLDLR-----SVADTFPELYWQAP 1697

Qy 1616 PSYLGDRVSSYGGTLHYELHSETQGRDIFITYESRDPVVLQGNQMSAFLELAPPPGOV 1675  
Db 1698 PSYLGDRVSSYGGTLRYELHSETQGRDVFVPMESRDPVVLQGNQMSITFLEPAYTPGHV 1757  
Qy 1676 HRGQLQVLEGVFRHLETHNPVSREELMMVLAGLOLQIRALFSOTSSTSSVSRVVLEVAS 1735  
Db 1758 HRGQLQVLEGVFRHLETHNPVSREELMMVLASLQLOQIRALFSQISSAVFRRVALEVAS 1817  
Qy 1736 EAGRPPASNYVELCVPANYRGDSQCECAPGYXRTKGLFLGRVCPQCCHGSHSRCLPGS 1795  
Db 1818 PAGQALASNYVELCLCPASVYRGDSQCECAPGYRDKGLFLGRVCPQCCHGSHSRCLPGS 1877  
Qy 1796 GICVGCQNTGDCQCECRPGFVSDFSNPASPCVSCPLAVPSNNFADGCVLRNGRTQ 1855  
Db 1878 GVCVDCQNTGDCQCECRPGFVSFVS-RDPSPAPCVSCPLAVPSNNFADGCVLRNGRTQ 1936  
Qy 1856 CLCRPGYAGASCERCAPGFFGNPLVLGSSQCPDCSGNGDPNMFIPDCLPTGTACRCGLR 1915  
Db 1937 CLCRPGYAGASCERCAPGFFGNPLVLGSSQCPDCSGNGDPNMFIPDCLPTGTACRCGLR 1996  
Qy 1916 HTTGPHCRCAPGVGNALLPGNCTRCDCSCPGTETCDPQSGRCLCKAGVGTGRRCDRQE 1975  
Db 1997 HTTGPHCRCAPGVGNALLPGNCTRCDCSCPGTETCDPQSGRCLCKAGVGTGRRCDRQE 2056  
Qy 1976 GYFQPEQCGCRPCACGPAKXGSECHPGQSGOCHQCPGTTGPQCCECAPGYMGLPEKGR 2035  
Db 2057 GHFGDGGCGCRPCACGPAKXGSECHPGQSGOCHQCPGTTGPQCCECAPGYMGLPEKGR 2116  
Qy 2036 CQCPHCHDPTGHTCTCPPLGSGERCDCSQOHOVPPGKPGHIGCEVCDHCVWLLLD 2095  
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Db 2177 DLERAGALLPAIREQLOGINASSAAWALHRLNASIADLQSKLRPPGPRYQAAQQLQTL 2236  
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Db 2237 EQQSISLQODTERLGSQATVGQ-----QAGQLLDTTESTLGRAQKLLSVAVG 2296  
Qy 2206 RALNELASRMGQSGDVALVPSGEOLWALAEVRLMLDMTRDLGACGAVAEAELEAAQ 2265  
Db 2297 RALNELASRMGQSGDVALVPSGEOLWALAEVRLMLDMTRDLGACGAVAEAELEAAQ 2356  
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Db 2417 ERVKEALQWKELOSDNATLQAAASLILGHVSELLQGIQDQAKEDLHAAASLDGAWT 2476  
Qy 2386 PLLKRMQAFSPASSKVDLVEAAEAHAQKLNQALINLSGIIILGINQDRFIQRAVNASAYS 2445  
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Qy 2446 SILQAVQAAEDAAQALPQASRTWMTVQVQGLAAGAPOLLANSALBETILGHQGRIGLA 2505  
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Qy 2566 QSQLOQMKNVBERWQSGGLGQDLSQVERDASSVSTLEKTLPOLLAKLSELRNGVH 2625  
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Db 2717 NASLALSANIGVRKLIQAARSAASKVVKMFNGRSGVRLRPPDLADLAAYTALKPHI 2776

2686 QSPVPAPEGKNTGDHFLVYMGSRQATGDMGVSLRNQKVVYRLGKAGPTTSLIDENI 2745  
2777 QG--PEPEGQGTEDRFVYMGSRQATGDMGVSLRNQKVVYRLGKAGPAVLSDIDENI 2834  
2746 GQFAVSTDRITLOFCHMSVTVYKQMVHEIKGDTVAPSGSEGLNLHPDDFVYVGGYPSN 2805  
2835 GQFAVSTDRITLOFCHMSVTVYKQMVHEIKGDTVAPSGSEGLNLHPDDFVYVGGYPSN 2894  
2806 FTPEPLRPPGVLGCIEMETLNEEVSVLNFEQTFMLDTAVDKPCARSKATGDPMLTDCS 2865  
2895 FTPEPLRPPGVLGCIEMETLNEEVSVLNFEQTFMLDTAVDKPCARSKATGDPMLTDCS 2954  
2866 YLDGSGFARISPEKQFSNTRKDOELRLVSYNGIIFELKQESQFCLAVQEGTLLVYDF 2925  
2955 YLDGTFARISDSQISTTKRFEQELRLVSYSGVFFLQKQSQFCLAVQEGTLLVYDF 3014  
2926 GSKLKADQLPQPQALTAASKAIQVFLLAGNRKRLVVRVERATVFSVDQNNLEMDAYY 2985  
3015 GAGLKAQVLPQPPLTASAKAIQVFLLAGNRKRLVVRVERATVFSVDQNNLEMDAYY 3074  
2986 LGQVPEQLPLSLRQLPFGSGVRCIKGKALGKVKYDLKRLNTTGISFGCTADLLVGR 3045  
3075 LGQVPPDQLPPLSLRQLPFGSGVRCIKGKALGKVKYDLKRLNTTGVSGAGCTADLLVGR 3134  
3046 MTFHGHGFLPLALPDVAPITEVYVSGFPRGTQDNNLLYRTSPDGPVQVSLREGHVTLR 3105  
3135 MTFHGHGFLRLALSNAVPIITGVYSGFPHSQAQDSALLYRASPDGLCQVSLQGRVSLQ 3194  
3106 FMNQEVETQRFADGAPHYVAVSYNVTVGLVYDQQLVKSHERITPMLQPEPRL 3165  
3195 LLRTVKTQAGFADGAPHYVAVSYNVTVGLVYDQQLVKSHERITPMLQPEPRL 3254  
3166 LLGLPVSTGFNFSCISNVFQRLRQVDFDLHONMGVNVSGTCTPAQLRTS--- 3222  
3255 LLGLPESTGTYNFSCISNVFQRLRQVDFDLHONMGVNVSGTCTPAQLRTS--- 3314  
3223 ----RATAQVRRSRQPSQDLACTTTPMLPGTIQDAYQFGLPSPYLOFVGSPSHRNL 3278  
3315 PRGLQATARKASRRSQAPHPACMLPPLHRTTRDSYQFGSLSHLEFVGLARHNP 3374  
3279 HLSMLVPHAAQGLLSTAPMSGRSPSLVPLNHGHFVAQTEGPGPQLOVQSRHNSAG 3338  
3375 SUSMHVLPF--SRGGLLFTFARLPPGSPSLALFLSNHGFVAQMEGLGTRLRASQRORSPG 3433  
3339 QHWRVVRVGMQOQLVVDGOSTWQKALHVRPRAERPPQYTLVSGGLPASYSKSLPV 3398  
3434 RWHKYSVRVEKNRILLVTDGARAWSGEGPHRQHQGAEPHQPHTLPVGGLPASSHSSKLPV 3493  
3399 SVGFSCCLKQLDKQPLTPTQMVGTTCVSGPLEDGLFFPGSGGVVTLLELPKAKMPYV 3458  
3494 TVGFSGCVKRLHGRPLGAPTEAGVTECIIILGPLEAGLFFPGSGGVITLDLPFATLPDV 3553  
3459 SLELEMRPLAAAGLIFHLGALATPYMOLKVLTEQVLLQANDGAGEFSTWVTPK-LCDG 3517  
3554 GLELEVRPLAVTGLIFHLGQARTPPVLOLVTEKQVLLRADDDGAGEFSTVTRPSVLCDG 3613  
3518 RHRVAVIMGRDTRLREVDTSQNHHTGRPLPESLAGSPALLHLGSLPKSSTARPELPAYRG 3577  
3614 QWERLAVMKSQNVRLVDAQSNHTVGPPLAAAGAPAPLYLGLFEPMAVQVWPFPAYCG 3673  
3578 CLARKLLINGAPVNTVATASVOIQAGVNRGCP 3608  
3674 CMRLAVNRSPVMTSRVSVZVHGAAGSGCPA 3704

RESULT 9

US-10-037-417-2  
; Sequence 2, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-235  
CURRENT APPLICATION NUMBER: US/10/037,417  
CURRENT FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: 60/260,018  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 60/260,360  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: 60/272,411  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: 60/272,817  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/291,186  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: 60/303,231  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 60/305,060  
PRIOR FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: 60/318,405  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 60/318,700  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 227  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 3600  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-037-417-2

Query Match 74.3%; Score 14771; DB 12; Length 3600;  
Best Local Similarity 74.8%; Pred. No. 0;  
Matches 2739; Conservative 275; Mismatches 472; Indels 178; Gaps 26;

QY 1 DLYCKLVGGPVAGDPNQTIGQYCDICTAANSKNAHPVSNADGTERWQSPPLSGLE 60  
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QY 61 YNEVNTLDDGVHFVAYVLIKEANSRPRDLWLERSTDPGHTYQKQPEASSKRCCLER 120  
DB 118 YNEVNTLDDGVHFVAYVLIKEANSRPRDLWLERSTDPGHTYQKQPEASSKRCCLER 177  
QY 121 FGPRTLERITQDDDDVICTTEYSRIVLENGEIVVSLVNGRPGALNFSYSPLLRDTTKATN 180  
DB 178 FGPOTLERITRDDAAICTTEYSRIVLENGEIVVSLVNGRPGALNFSYSPLLRDTTKATN 237  
QY 181 IRLRFLRTNLLGLHMGKALRDEFTVTRYYYSIKDISIGRCYCHGHADVCDKADPLDPF 240  
DB 238 VRLRFLRTNLLGLHMGKALRDEFTVTRYYYSIKDISIGRCYCHGHADVCDKADPLDPF 297



Qy 241 RLOCAOHNTCGSCDRCCBGFNQPKWKPATTSANECSCNCHGHAYDCYDPEVDREN 300  
Db 298 RLQCTCQHNTCGGTCRCCBGFNQPKWKPATANSANECO-CECYGHATDCYDPEVDREN 356  
Qy 301 ASQNOENVGGVCLDCQCHHTTGNCERCLPGFFRAPOPLDSPHVCRPCDCESDFTDG 360  
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Qy 421 AAGTQGNACRDKPRLGRCVCKPNFRGAHCBELCAPGHPGCHPCQCSS---PGVANSLOD 477  
Db 476 AAGTQGNACRDKPRLGRCVCKPNFRGAHCBELCAPGHPGCHPCQCSS---PGVANSLOD 534  
Qy 478 PEGGQCMCRGT-----FEGDRCDHCAFGVHFPL-CQJCGGSPAGTLPPEGCDGAG 526  
Db 535 ASAGAENASRGPHVIAVPPATFTSLSASH-----PLRSAYCGGSPAGTLPPEGCDGAG 586  
Qy 527 RCQCRPGFDPHCDRCLPGVGHVDPDHACADPRGALDQCGVGGIACHCRPGNTGATCOE 586  
Db 587 RCLQCPGAFAGHCDRCPGPHGHPNCACTCDPRGALDQCGAGGICRCPGVTGTACOE 546  
Qy 587 CSPGFGYPPSPICPCHCSADGSLHTTC-----DPTTGQCRCP-RVTGL-H-CDMCPFGAYN 639  
Db 647 CSPGFGHFPSS-----CPATALLKAPCTQPTPGVGSAAAGPVRGCGVTHVCPVPTTSPTA 701  
Qy 640 PPYCEASCHPAGLAPANPALPETQACMCAHVEGSPDCRCPGKMGWLSASNPEGCTRC 699  
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Qy 700 SCDPRGTGLGVTECOQNGQCFCKAHVCGKTCAACKDGFGLDYADYFGCRSCRDVGGAL 759  
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Qy 1120 EFVPRPFCVSSHGTENPSSAACLASRPPKPPQPIILKDCQVLPLPPDLPLTSQBELSPG 1179  
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Qy 1240 LINGRIWQHGHANASFCPHGIGCTLVLCGOTMLDVTDNELTVTVRVPGRMLWLDYVL 1299  
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Qy 1300 ITPEDAYSSSYLQEBPLDKSYDFTSHCATQGYHISPSSSSPFCRNNATSLSLFYNNGALP 1359

Db 1362 VVPENVISFGYLRSEPLDKSYDFTSHCAAQGYHISPSSSSLFCRNNATSLSLFYNNGAR 1421  
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Db 1422 CGCHEVGATGPTCBPFGQCPGRGHVIGRDCSRCATGYWGPFPNCRACDCGARLCEDETGG 1481  
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Qy 1480 GRRCDTCAPGYGYPSRCPDCHBAGTNVAVCDPLTGCHCKENVQSRCDQCRVGFPSL 1539  
Db 1542 GRRCDTCSGPHGYPRCPDCHBAGTNVAVCDPLTGCHCKENVQSRCDQCRVGFPSL 1601  
Qy 1540 DAAMPKGTCTCFGATERCGNSLARHFVDMGWLSSDROVPHHEPTELHAD 1599  
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Qy 1600 LR-----SVADTFSELYWQAPPSYLGDRVSSYGGTLHYELHSETQGRDIFIPYERPDVVL 1655  
Db 1662 LRHYPEAVPEAPPELYMQAPPSYLGDRVSSYGGTLHYELHSETQGRDIFIPYERPDVVL 1721  
Qy 1656 QGNQMSIAFLAYLPPGQVHRGQLOLVGEGFRHLETHNPVSRBELMMVLAGLEQLQIRA 1715  
Db 1722 QGNQMSITFLPAYPTPGHVRGQLOLVGEGFRHLETHNPVSRBELMMVLASLQQLQIRA 1781  
Qy 1716 LFSOTSSSVSRVVRVLEVAEAGRGPPASNVVELCMCPANYRGDSCQECAPGYRDTKGLF 1775  
Db 1782 LFSQISSAVFLRRVALEVASPAGQALASNVVELCLCPASVAGDSCQECAPGYRDTKGLF 1841  
Qy 1776 LGRVPCQCHGHSRCLPBGSGICVGCQHNTEGDCRCRPGFVSSDSPNPNASPCVSCPCP 1835  
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Qy 1836 LAVPNNFADGCVLRNGRTQCLRPGVAGASCRCAPGFCNPLVLGSSSCQPCDCSNGD 1895  
Db 1900 LSVPSN-----RCAPGFCNPLVLGSSSCQPCDCSNGD 1932  
Qy 1896 PMIPSDCDPLTGACRCGLRHTTGPHERCAPPGYGNALLPGNCTRCDCSCGTETCDPQ 1955  
Db 1933 ENLLPSDCDPLTGACRCGLRHTTGPHERCAPPGYGNALLPGNCTRCDCSCGTETCDPQ 1992  
Qy 1956 SGRCLCKAGVTGQRCDRCLEGVFGECQCGRPCACGPAAGSECHPOSGGCHQCPGTTG 2015  
Db 1993 SHCLCKAGVTGQRCDRCLEGVFGECQCGRPCACGPAAGSECHPOSGGCHQCPGTTG 2052  
Qy 2016 PQCLECAPGYWGLPEKGRCCQCPRGHCDPHTGHTCTCPPLGSGERCDCSCQHQVVPVGK 2075  
Db 2053 PQCRECAPGYWGLPEKGRCCQCPRGHCDPHTGHTCTCPPLGSGERCDCSCQHQVVPVGK 2112  
Qy 2076 PGHGIHCEVCDHCVVLLDDLERAGALLPAIREOLOGINASSAAWALHRLNASIADL- 2134  
Db 2113 PVGHSIHCEVCDHCVVLLDDLERAGALLPAIREOLOGINASSAAWALHRLNASIADLQ 2172  
Qy 2135 -----QSKLRPPGPRYQAAQLOTLQEQSISLQOQTLERLSQ 2172  
Db 2173 VLVLAFPPQPGPVQAFTRLPQSLRSPFLGRHETAQQLVLEQQSTSLP-----PQ 2225  
Qy 2173 ATVGQAGQLDTESTILGRAQKLLSVRAVGRALNELASRMGGSPGDALVPSGEOLR 2232  
Db 2226 AVGTEDQASQLAGTEATLGHAKTLAAIRAVDRTLSELMSQTHLGLANASAPSGEOLL 2285  
Qy 2233 WALAEVERLLMDRTRDLGAQAAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 2292  
Db 2286 RLAEVERLLMEMARDLGAQAAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 2345  
Qy 2293 LAQYSSGMLDREALNQAVENTREBELNSRQBRVKEALQWKQELSODNATLKATLOAA 2352  
Db 2346 LAQHEAGMLDREALNRAVDATREAEQLNSRQBRLEALQKQELSODNATLKATLOAA 2405  
Qy 2353 SLILGHVSELQIGDOAK-EDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVEAAEAH 2411

2406 RDTLASVFRLLGSLPLKFELESLERLAASLDGARTFLLQRMOTFFSPAGSKLRLEVAEEAHA 2465  
2412 QKLNQALNLSGIIILGINDRITQRAVEASNAYSSTILOAVAAEDAAAGALQRAQKRWEM 2471  
2466 QQLGQALNLS-IILDVNDRLTQRAIEASNAYSRILOAVAAEDAAAGALQRAQKRWEM 2524  
2472 VVQSGAAGAROLLANSALTEIIGHQGRGLAQ-----GRQAGQIHNWARKNQL 2526  
2525 VVRQGLVDRQAQLLANSTALEAMLEOQRLGLGECWAPGALRPAQTQLRDVRAKQDL 2584  
2527 AQIQEAOAWLMDTSETSEKTAHAKAVAAEALSTATHVQSOLQGMKNVVERWQSLGGL 2586  
2585 EAHQIAQAWLMDTGETSKTAHAKAVAAEADQDTRVQSOLQGMKNVVERWQSQYEGGL 2644  
2587 QGQDLSQVERDASSYSTLEKTLQALLAKSLRLENGVHNASLALSANTGRVKLIAQAR 2646  
2645 RGQDLQAVLDAGSAVSTLEKTLQALLAKSLRLENGVHNASLALSANTGRVRELLIAQAR 2704  
2647 SAASK-VKYSMKENGSGVRLRPPRLDLAAYTALKFHIQSPVPAPBEGKNTGHEVLY 2705  
2705 GAASKVVKVPKPNRSGVQLRPPRLDLAAYTALKFYLOG--PEPEPGQTEDRFVNY 2762  
2706 MGSROATGDMGVSNLRQKVVHYYRLGKAGPTTSLIDENIGRQFAAVSIDRTLQFGHMSV 2765  
2763 MGSROATGDMGVSNLRQKVVHYYRLGKAGPAVLSIDEDIGRQFAAVSIDRTLQFGHMSV 2822  
2766 TVEKQWHEIKGDTVAPGSEGLNLHPDDFVFVVGYPNSFTPPRPPGVLGCIEMET 2825  
2823 TVERQMIQETKGTAVAPGSEGLNLHPDDFVFVVGYPNSFTPPRPPGVLGCIEMDT 2882  
2826 LNEEVSLYNFEOTFMDLTAVDKPCARSKATGDPMLTDCSYLDGSGFARISPEKQFSNTK 2885  
2883 LNEEVSLYNFEOTFMDLTAVDKPCARSKATGDPMLTDCSYLDGSGFARISPEKQFSNTK 2942  
2886 RFDQELRLVSYNGIIIFLQKESOFCLAVQEGTLVLFYDFGSLKADPQPPQALTAAS 2945  
2943 RFEQELRLVSYNGIIIFLQKESOFCLAVQEGTLVLFYDFGSLKADPQPPQALTAAS 3002  
2946 KATQVFLLAGNRKRLVRVERATVFSVDQDMLMADAYLGGVPPPEQLPLSLROLFPFG 3005  
3003 KATQVFLLAGNRKRLVRVERATVFSVDQDMLMADAYLGGVPPPEQLPLSLROLFPFG 3061  
3006 GSVRGCIKGIKALGVYDLKRLNTTGISFGCTADLLVGRMTFHHGFLPLALPDVAPIT 3065  
3062 GSVRGCVKGIKALGVYDLKRLNTTGISFGCTADLLVGRMTFHHGFLPLALPDVAPIT 3121  
3066 EVYISGFGPGTODNLLYYRTSPDGPYQVSLRSGHVLRFMNQVETQRFADGAPHV 3125  
3122 GNYISGFGPHSAQDSALLYRASVPRPHQVSLQGGVSIQLLRTVKTQAGFADGAPHV 3181  
3126 AFYSNVTGWLWYDDQLQLVKSHERTTPMLQLQPEPSPRLLGLPVSCTFFNFSGCISN 3185  
3182 AFYSNATGWLWYDDQLQLVKSHERTTPMLQLQPEPSPRLLGLPVSCTFFNFSGCISN 3241  
3186 VFQVRLGPGORVFDLHONMGSVNVSGCTPAQLIETSRATAKVSRSRQPSQDLACTTP 3245  
3242 VFQVRLGPGORVFDLHONMGSVNVSGCTPAQLIETSRATAKVSRSRQPSQDLACTTP 3301  
3246 WLPSTTQDAYQFGGPPSLYQFVIGISPSHNRHLHLSMLVRPHAAASQGLLLSTAPWSGRSP 3305  
3302 PHURTRDSYQFGGSLSHLEFVIGILARHN----- 3332  
3306 SLVFLFNHGHFVAQTEGPGPRLOVQSRQSRAGQWHRVSVRMGMQOIQLVDSQWTSQK 3365  
3333 -----VSVRWEKNRILLVTDGARAWSQE 3355  
3366 ALHHRVPRAEPOPYTLVSGGLPASSVSKLPVSVGFSGLKLDKQPLRTPQWGV 3425  
3356 GPHRQOGAEPHPHTLFGGLPASHSSKLPVTVGFSCKVRLUHGRLGAPTRMAOV 3415  
3426 TPCVSGPLEDGLFPFSGEVVTLELPKAKMPYVLSLEMRPLAAAGLIIFHLQALATPYM 3485  
3416 TPCILGPLEAGLFPFSGGGVITLGLPGATLPDVGLEVRPLAVTGLIIFHLQARTPPYL 3475

3486 QLKVLTSQVLLQANDGAGEFSTWVTPK-LCDGRWHRVAVIMGRDTRLRLVDTQSNHTTG 3544  
3476 QLVLPQVLLRADDGAGEFSTVTRPSPVLCDGQWHLAVKSGNVRLVDAQSNHTVG 3535  
3545 RLPESTAGSALLHLGSLPKSSTARPELPAYRGLCKRLKLLINGAPVNVVTSVQICQAYGMR 3604  
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3596 GCPA 3599

RESULT 10  
US-10-037-417-6  
; Sequence 6, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
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; FILE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260,018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260,360  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/272,411  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/272,817  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/291,186  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/303,231  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/305,060  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/318,405  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/318,700  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 3597  
; TYPE: PRT  
; ORGANISM: Homo sapiens

QY	1002	LSPSHPLATCFGSDVDIOLEMAVPOGQVYLVEYVGBEDSHQBMGVAVTTPQAPQGV	1061
DB	1061	LSPSHPLITGSDVDVQLQVAVPOGQRYALVVEYANEDARQEVGVAVTTPQAPQGL	1120
QY	1062	LNLHPCPVSSICRSPARDTQHILAIPLHLDSEASIRLTAEQAHFELHSHVTLVPEEFSTEF	1121
DB	1121	LSLHPCLYSTLCRTARDTQDLAVFLHLDSEASVRLTAEQAFLLHGVTLVPEEFSPF	1180
QY	1122	VEPRVFCVSSHGTFNPSAASCLASRFKPKPQPIILKCOVLPLPPDLPLTQSLSLGAP	1191
DB	1181	VEPRVSCISSHGAFGPNASACLPSRFKPKPQPIILRDCOVILPLPPGLFLTHAQDLTAMS	1240
QY	1182	PEGQOPRPTAVDNABPTLLRHPOGTVFTTQVPTLGRVAFLLHGYQFVHPSPPVEVLI	1241
DB	1241	PAGFAPRPTAVDPAEFTLLREPOATVFTTHVPTLGRVAFLLHGYQFPAHPTFPEVLI	1300
QY	1242	NGRHWQHMANASTCPHGYGCRITLVLCEGQMLDVTNELTTVTVRVEGRWLWDYVLIV	1301
DB	1301	NAGRVMQHMANASTCPHGYGCRITLWVCEGOALLDVTSELTVTVRVPKGRWLWDYVLW	1360
QY	1302	PEDAYSSVLOEELDKSYDFISHCATGQVHISFSSSSPPFCRNATATSLSLFYNNALPCG	1361
DB	1361	PENVTSFYLRKEEPLDKSYDFISHCAAGQVHISFSSSSLFCRNAAASLSLYNNARFCG	1420
QY	1362	CHEVGAVSPTCEPFGGQPCRGHVGIRDCSRCATGYMGFPNCRPCDCGARLDELGTQCI	1421
DB	1421	CHEVGATGPTCEPFGGQPCFCHAVIGRDCSRCATGYMGFPNCRACDCGARLDELGTQCI	1480
QY	1422	CPRTVPDDCLVQSPQSGCHPLVGCCECNCSGVQELTPTCTMDSPGQCRCPNVAGR	1481
DB	1481	CPRTTIPDCLLCPQTFGCHPLVGCCECNCSGPGIOELTPTCTDTSQGQCRCPNVTGR	1540
QY	1482	RCDTCAPOFYGPSRCPDCEAGTMAVCDPLTGQCHCKENQVQSRCDQCRCVGTFSLDA	1541
DB	1541	RCDTCSFGHGYPCRCPCDCEAGTAPGVCDPLTGQCYCKENVQPKDCQSLGTFSLDA	1600
QY	1542	ANPKGCTCPGFCGATERCNGNLAHBEFVMEGWILLSSDRQVPHERPHEIILLHADLR	1601
DB	1601	ANPKGCTCFGATERCRSSSYTRQEFVDMEGVILLSTDRQVPHERPQGTMLRADLR	1660
QY	1602	---SVADTFSELVWQAPPSYLGDRVSSYGGTTLVHLSHETQRGDIFTPYESSRDVVLQ	1657
DB	1661	HYPEAVPAFAFELYWQAPPSYLGDRVSSYGGTTLVHLSHETQRGDVFVPMESRPDVVLQ	1720
QY	1658	NQMSIAFLAYLAPPYQVHRGQLQVGNFRHLETHNPVSREELMMVLAGLEQLQIRALF	1717
DB	1721	NQMSITFLPAYPTPGHVRGQLQVGNFRHTTNTVTSREELMMVLASLEQLQIRALF	1780
QY	1718	SQTSVSLRVLVLEVASEAGRPASNVLCMPANVGRSDCOBAPGYVDTKGLFLG	1777
DB	1781	SOISSAVFLRRVLEVASPAGQALASNVLCPLCPASTYRGSDCOBAPGYVDTKGLFLG	1840
QY	1778	RCVPQCCHGSDRCLUPGSGICVGOHNTGEGQCRCPGFGVSSDPSPNASCVCSCPCPLA	1837
DB	1841	RCVPQCCHGSDRCLUPGSGVCV-CQHNTGAGHRCRCQAGFVSS-RDDPSAPCVSCFCPLS	1898
QY	1838	VPSNPFADGCVLRNGRTQCLCRPGVAGASCERCAPGFGNPLVLGSSQPCDCSNGGPN	1897
DB	1899	VPSN-----RCAPFGFNPLVLGSSQPCDCSNGGPN	1931
QY	1898	MFSDCDPLTGACRCLRHTTGPCHCERCAPGYGNALLPGNCTRCDSCPCGTETCDPSG	1957
DB	1932	LLFSDCDPLTGACRCLRHTTGPCHCERCAPGYGNALLPGNCTRCDCTPCGTETCDPSG	1991
QY	1958	RCLKAGVTGQCRDCLGEGYGFEGQCRCPACGPAKSGECHPQSCQCHCOPCTTGPQ	2017
DB	1992	HCLKAGVTGRCDCRGHFGDGGCRCPACGPAABGSECHPQSCQCHCOPCTTGPQ	2051
QY	2018	CLECAPGYWGLPEKCRRCQPRGHCDPHTGCTCPPLSGRCDTCSQQHGVVPVPGKG	2077
DB	2052	CRECAPGYWGLPEQCRRCQCEGGRCDPHTGCRNCPPLSGRCDTCSQQHGVVPVPGPV	2111

QY	1	DLVCKLVGGVAGDNDQTTQGOYCDICTAANKAHKHPVSNALDGTERRWQSPPLSRGLE	60
DB	58	DLVCKLVGGVAGDNDQTTQGOYCDICTAANKAHKHPVSNALDGTERRWQSPPLSRGLE	117
QY	61	YNEVNVTLDGQVPHVAVVLIKEANSRPRDLWLERSTDPGHTYQVQWQFASGRKDCLE	120
DB	118	YNEVNVTLDGQVPHVAVVLIKEANSRPRDLWLERSMDPGRYQVQWQFASGRKDCLE	177
QY	121	FGPRTLERITODDDVICTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPPLSRKATN	180
DB	178	FGPRTLERITODDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPPLSRKATN	237
QY	181	IRLRFLETNTLLGHLMKALRDPVTRRYYSIKDISIGRCVCHGHADVCAKADPLDFF	240
DB	238	VRLRFLETNTLLGHLMKALRDPVTRRYYSIKDISIGRCVCHGHADACADKADPTDFF	297
QY	241	RLOCAOHNCTGSCDRCPCFPNQPKPATTSANECOSCNCHGHAYDCYDPEVDRRN	300
DB	298	RLOCTQHNTCGGTCRCCFPNQPKPATANSANECQ-CECYGHATDCYDPEVDRRR	356
QY	301	ASQNDNVYGGGVCLDCQHTTGINCERCLPGFERAPDPLDSHVCRPCDCESDPTDG	360
DB	357	ASQSLDGTQGGVCLDCQHTTGVNCRCLPGFYSRPNPLDSHVCRGCNCESDPTDG	416
QY	361	TCEDLTGRCYCRNFTGELCAACAEYTDFFPHCYPLSPFPNDTREQVLPAGQIVNCDN	420
DB	417	TCEDLTGRCYCRNPFNSGERCDVCAEGTGFPSY-REHLPGNDTREQVLPAGQIVSCDGS	475
QY	421	AAGTQGNACRKPRLGRVCKPNPRGAHCLCARGHGPSCHPCQSS-----PGVANSICD	477
DB	476	AAGTQGNACRKPVRGRCLCKPNFQGTCHCLCAPGYFGPGC-PASVPALEWPNMTAVTLTQ	534
QY	478	PESGOCMCRG-----FEGDRCDHCAFGYFHPPL-CQLCGSPAGTLPPEGGDEAG	526
DB	535	ASAGAENASRGPHVIAVPPATFTLSASH-----PLASAVCGSPAGTLPPEGGDEAG	586
QY	527	RCQCRPFGDGHCDRCLPGVHYGPDCHACACDRPRGALDQCGGVGLCHCRPGMTGATQOE	586
DB	587	RCLQCPFAGPHCDRCPGYHGFNPNCACTCDPRGALDQLCGAGGLCRPGYGTGACOE	646
QY	587	CSPGFGYFPSCIPCHCSADGSLHTTC-----DPTTGQCRCPRTVTLGHCDMCPGAYNFPY	642
DB	647	CSPGFGHGFPS-----CFATALLKAPCTQVTPVGVSSAAGP-VRGCGVTRVCVPTTSPT	700
QY	643	CEAGSCHPAGLAPANPALPETQAPCMCRHVEGSPCDRCRPGYWGLSASNPEGCTRCSD	702
DB	701	AKLALATLPVWPVDPALPEAQVFCMCRHVEGSPCDRCRPGFWGLSPSNPEGCTRCSD	760
QY	703	PRGLTGGVTECO-GNGQCFCKAHVCGKTCACKDGFGLDYADYFGCRSCRDVGGLGQ	761
DB	761	LRGLTGGVABEQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRDIGGALGQ	820
QY	762	GCEPKTAGCRCPNTQGTCTSEPAKHVLPDLHMRLELEBEAATPEGHAVRFGNPLEPE	821
DB	821	SCBPTGVCRCPNTQGTCTSEPAKHVLPDLHMRLELEBEAATPEGHAVRFGNPLEPE	880
QY	822	NFSWRGYAHMAIOPRIVARLVNTSPDLFRLVFYVARGSTSVNGQISVREBKLSCTN	881
DB	881	NFSWRGYAQAAPVOPRIVARLVNTSPDLFRLVFYVNRGAMSVSGRVSVREBGRSAACAN	940
QY	882	CTEQSQVAFPPSTEPAPVTPQGFGEPPVFLNPGIIVALLVEAGVLLDYVLLPSTYE	941
DB	941	CTAQSQVAFPPSTEPAFITVQGFGEPPVFLNPGIIVALLVEAGVLLDYVLLPSTYE	1000
QY	942	AALQHRVTEACTYRPSALHSTENCLVYAHVPLDGPFSAGTEALCHRDNSLRPRCPTEQ	1001
DB	1001	AALQLRVTEACTYRPSAQPPSCLLYTHPLDGPFSAGLEALCRQDNSLRPRCPTEQ	1060

QY	1002	LSPSHPLATCFGSDVDIOLEMAVPOGQVYLVEYVGBEDSHQBMGVAVTTPQAPQGV	1061
DB	1061	LSPSHPLITGSDVDVQLQVAVPOGQRYALVVEYANEDARQEVGVAVTTPQAPQGL	1120
QY	1062	LNLHPCPVSSICRSPARDTQHILAIPLHLDSEASIRLTAEQAHFELHSHVTLVPEEFSTEF	1121
DB	1121	LSLHPCLYSTLCRTARDTQDLAVFLHLDSEASVRLTAEQAFLLHGVTLVPEEFSPF	1180
QY	1122	VEPRVFCVSSHGTFNPSAASCLASRFKPKPQPIILKCOVLPLPPDLPLTQSLSLGAP	1191
DB	1181	VEPRVSCISSHGAFGPNASACLPSRFKPKPQPIILRDCOVILPLPPGLFLTHAQDLTAMS	1240
QY	1182	PEGQOPRPTAVDNABPTLLRHPOGTVFTTQVPTLGRVAFLLHGYQFVHPSPPVEVLI	1241
DB	1241	PAGFAPRPTAVDPAEFTLLREPOATVFTTHVPTLGRVAFLLHGYQFPAHPTFPEVLI	1300
QY	1242	NGRHWQHMANASTCPHGYGCRITLVLCEGQMLDVTNELTTVTVRVEGRWLWDYVLIV	1301
DB	1301	NAGRVMQHMANASTCPHGYGCRITLWVCEGOALLDVTSELTVTVRVPKGRWLWDYVLW	1360
QY	1302	PEDAYSSVLOEELDKSYDFISHCATGQVHISFSSSSPPFCRNATATSLSLFYNNALPCG	1361
DB	1361	PENVTSFYLRKEEPLDKSYDFISHCAAGQVHISFSSSSLFCRNAAASLSLYNNARFCG	1420
QY	1362	CHEVGAVSPTCEPFGGQPCRGHVGIRDCSRCATGYMGFPNCRPCDCGARLDELGTQCI	1421
DB	1421	CHEVGATGPTCEPFGGQPCFCHAVIGRDCSRCATGYMGFPNCRACDCGARLDELGTQCI	1480
QY	1422	CPRTVPDDCLVQSPQSGCHPLVGCCECNCSGVQELTPTCTMDSPGQCRCPNVAGR	1481
DB	1481	CPRTTIPDCLLCPQTFGCHPLVGCCECNCSGPGIOELTPTCTDTSQGQCRCPNVTGR	1540
QY	1482	RCDTCAPOFYGPSRCPDCEAGTMAVCDPLTGQCHCKENQVQSRCDQCRCVGTFSLDA	1541
DB	1541	RCDTCSFGHGYPCRCPCDCEAGTAPGVCDPLTGQCYCKENVQPKDCQSLGTFSLDA	1600
QY	1542	ANPKGCTCPGFCGATERCNGNLAHBEFVMEGWILLSSDRQVPHERPHEIILLHADLR	1601
DB	1601	ANPKGCTCFGATERCRSSSYTRQEFVDMEGVILLSTDRQVPHERPQGTMLRADLR	1660
QY	1602	---SVADTFSELVWQAPPSYLGDRVSSYGGTTLVHLSHETQRGDIFTPYESSRDVVLQ	1657
DB	1661	HYPEAVPAFAFELYWQAPPSYLGDRVSSYGGTTLVHLSHETQRGDVFVPMESRPDVVLQ	1720
QY	1658	NQMSIAFLAYLAPPYQVHRGQLQVGNFRHLETHNPVSREELMMVLAGLEQLQIRALF	1717
DB	1721	NQMSITFLPAYPTPGHVRGQLQVGNFRHTTNTVTSREELMMVLASLEQLQIRALF	1780
QY	1718	SQTSVSLRVLVLEVASEAGRPASNVLCMPANVGRSDCOBAPGYVDTKGLFLG	1777
DB	1781	SOISSAVFLRRVLEVASPAGQALASNVLCPLCPASTYRGSDCOBAPGYVDTKGLFLG	1840
QY	1778	RCVPQCCHGSDRCLUPGSGICVGOHNTGEGQCRCPGFGVSSDPSPNASCVCSCPCPLA	1837
DB	1841	RCVPQCCHGSDRCLUPGSGVCV-CQHNTGAGHRCRCQAGFVSS-RDDPSAPCVSCFCPLS	1898
QY	1838	VPSNPFADGCVLRNGRTQCLCRPGVAGASCERCAPGFGNPLVLGSSQPCDCSNGGPN	1897
DB	1899	VPSN-----RCAPFGFNPLVLGSSQPCDCSNGGPN	1931
QY	1898	MFSDCDPLTGACRCLRHTTGPCHCERCAPGYGNALLPGNCTRCDSCPCGTETCDPSG	1957
DB	1932	LLFSDCDPLTGACRCLRHTTGPCHCERCAPGYGNALLPGNCTRCDCTPCGTETCDPSG	1991
QY	1958	RCLKAGVTGQCRDCLGEGYGFEGQCRCPACGPAKSGECHPQSCQCHCOPCTTGPQ	2017
DB	1992	HCLKAGVTGRCDCRGHFGDGGCRCPACGPAABGSECHPQSCQCHCOPCTTGPQ	2051
QY	2018	CLECAPGYWGLPEKCRRCQPRGHCDPHTGCTCPPLSGRCDTCSQQHGVVPVPGKG	2077
DB	2052	CRECAPGYWGLPEQCRRCQCEGGRCDPHTGCRNCPPLSGRCDTCSQQHGVVPVPGPV	2111

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2135 -----QSKLRPPGPRYQAAQQLTLEQQSISLQODTERLGSQAT 2174  
2172 SVLAPPPGPGVQAFTRFLPQSOLASPLGPRHETAQQLVLEQQSTSLP-----PQAV 2224  
2175 GVQGAQQLDTESTLGRAQKLESVRAVGRALNELASRGQSPGDALVPSGEOLRWA 2234  
2225 GTRDQASQLLACTEATLGHAKTLAAIRAVDRTLSELMSOTGHGLANASPSGQLLRT 2284  
2235 LAEVERLLWDMTRDLGAQCAVAEAEAEAOQLMARVQEQLTSEFWEENQSLATHIRDOLA 2294  
2295 LAEVERLLWEMARLDLGAPOAAEAEAEAAQVRLARVQEQLSLSEENQALATQTRDLA 2344  
2295 QYESGLMDLREALNQAQVNTREAEELNGRNQBRVKEALQWQKELSQDNATLKATLQAAASL 2354  
2345 QHEAGLMDLREALNRAVDATREAEELNGRNQBRVKEALQWQKELSQDNATLKATLHAARD 2404  
2355 ILGHVSELLOGTDOAK-EDLEHLAASLDGAWTPLLKRWQAFSPASSKVDLVEAAEAHAQK 2413  
2405 TLASVRLLEGUSPLKFKQELERLAASLDGARTPLLRQWQTSFAGSKLRLVERAAEAHAQK 2464  
2414 LNQLALNLSGIIIGINQDRFIQRAVEASNAYSIIQAVQAAEDAAQALRQASRTWVMV 2473  
2465 LQQLALNLS-IILDVNDRLTCRAEASNAYSRIILQAVQAAEDAAQALQQAADHTWQTV 2523  
2474 QRLAAGAROLLANSALBETTLHGQRLGLAQ-----GELQAGIOLHNYWARKNOLAA 2528  
2524 RQGLVRAQQLLANSTALBEMQLQEQRLGLGECWAPGALRPAGTQJRDVRAKQQLQEA 2583  
2529 QIQEAQAMLAMDTSETSEKIAHAKAAVAEALSTATHVQSQLOQMKNVEMWQSLGGLQG 2588  
2584 HQQAQAMLAMDTGETSKIAHAKAAVAEAOQTATRVQSQLOQMKNVEMWQSGVEGLRG 2643  
2589 QILSQVERDASSVSTLEKTLPLAKLRLNENRGVHNASLALSANIGRVKRLIAQARSA 2648  
2644 QDLGQAVLDAGSAVSTLEKTLPLAKLRLNENRGVHNASLALSANIGRVKRLIAQARSA 2703  
2649 ASK-VKVMKNGRSVRRLPRDLADLAAYTALAFHIQSPVPAPEPGKNTGDHVLVYMG 2707  
2704 ASKVVKVPKMFNGRSVQVRLPRDLADLAAYTALAFHIQSPVPAPEPGKNTGDHVLVYMG 2761  
2708 SRQATGDYMGVSLRNQKHWVYRLGKAGPTTISIDENTIGEQAFAVSDRTLQFGHMSVTV 2767  
2762 SRQATGDYMGVSLRNQKHWVYRLGKAGPTTISIDENTIGEQAFAVSDRTLQFGHMSVTV 2821  
2768 EKQWHEIKGDTVAPQSEGLNLHDPDFVYVYGGYPSNFTPEPLRFPYGLGCIEMETLN 2827  
2822 ERQMIQETKGDVAPQSEGLNLHDPDFVYVYGGYPSNFTPEPLRFPYGLGCIEMETLN 2881  
2828 EEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSFGARISFEKQFSNTKRF 2887  
2882 EEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSLDGSFGARISFEKQFSNTKRF 2941  
2888 DBELRLVSYNGIIFFLKQSOPLCLAVQBGITVLVDFGSGGLKXKADPLQPPALTAASKA 2947  
2942 EQELRLVSYNGIIFFLKQSOPLCLAVQBGITVLVDFGSGGLKXKADPLQPPALTAASKA 3001  
2948 IQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGGVPPRQLPLSLRQLFPFSGS 3007  
3002 IQVFLLAGNRKRVLRVERATVFSVDQDNMLEMADAYILGGVPPRQLPLSLRQLFPFSGS 3060  
3008 VRGCIKGIKALGKYVDLKLNTTGTISFGCTADLLVGRMTTFHGHLPLALPDVAPITEV 3067  
3061 VRGCIKGIKALGKYVDLKLNTTGTISFGCTADLLVGRMTTFHGHLPLALPDVAPITEV 3120  
3068 VYSGFGRGTQDNMLLYRTSPDGQVSLRSGHVTLEFMNQEVTQRFVADGAPHYVAF 3127  
3121 VYSGFGRGTQDNMLLYRTSPDGQVSLRSGHVTLEFMNQEVTQRFVADGAPHYVAF 3180  
3128 YSNVTGVWLVDDQLQVKSHERTPMLQLQPEEPESRLLLGGLPVSGTFHNFSGCISNVF 3187

3181 YSNATGVWLVDDQLQVKSHERTPMLQLQPEEPESRLLLGGLPVSGTTFHNFSGCISNVF 3240  
3188 VQRLRGPORVFDLHONMGSVNVTGCTPAQLIETSBATAQKYSRRSRQPSQDLACTTBMW 3247  
3241 VQRLRGPORVFDLHONMGSVNVTGCTPAQLIETSBATAQKYSRRSRQPSQDLACTTBMW 3300  
3248 PGTIQDAYQGGGGLPVSLQFVGISPSGRNRLHLSMLVRPHAAASQGLLLSTAPMGRSPSL 3307  
3301 LRTRUSYQFGGSLSSHLFEVGLIARHN----- 3329  
3308 VLFNLHGHFVAQTEGPGPRLQVOSRQAGQWHRVSVRWGMQOIQLVVDGQSTWQKAL 3367  
3330 -----VSVWEKNRILLVTDGARANQEGP 3354  
3368 HRVPAERAPQPYTLVSGGLPASSYSKLPVSVYGFSGCLKLQLDKQPLRTPTQMVGVTP 3427  
3355 HRQGAHHPQHTLVFGGLPASSHASKLPVTVYGFSGCVKRLHGRPLGAPTRMAGVTP 3414  
3428 CVSGPLEDGLFFPFGSGGVVTLPLKAMPYVSVLELEVRPLAAAGLFIHGLQALATPYMQL 3487  
3415 CILGPLEAGLFFPFGSGGVITLGLPGATLPDVGLEVRPLAVTGLFIHGLQARTPPVYLQ 3474  
3488 KYLTEQVLLQANDGAGEFSTWVTPK-LCDGRHVRVAVIMGRDTLRLVDTQSNHTTGR 3546  
3475 QVLPQVLLREADDGAGEFSTVTRPSVLCQDQWRLAVKMGVNLVLEVDQSNHTVGLP 3534  
3547 PESLAGSPALLHGLGSPKSTARPPELPAYRGCLRLKLLINGAPVNVTAISOAGVMGRG 3606  
3535 LAAAGAPAPLYLGLPEPMAVQPMPPAYCGCMRRLAVNRSPVAMTRSVVEHGAASGC 3594  
3607 PS 3608  
3595 PA 3596

## RESULT 11

US-10-037-182-36  
; Sequence 36, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggevason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 2743  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-36

Query Match 62.2%; Score 12354.5; DB 14; Length 2743;  
Best Local Similarity 82.4%; Pred. No. 0;  
Matches 2198; Conservative 172; Mismatches 290; Indels 7; Gaps 4;

Qy 1 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSKKAHPVSNADGTERWQSPPLSRGLE 60  
Db 79 DLYCKLVGGPVAGGDPNQTIGQYCDICTAANSKKAHPVSNADGTERWQSPPLSRGLE 138  
Qy 61 YNEVNTLDLQGVHFVAYVLIKFANSRPDLWYLERSTDFGHTYQPWQFASKRDCLER 120  
Db 139 YNEVNTLDLQGVHFVAYVLIKFANSRPDLWYLERSTDFGHTYQPWQFASKRDCLER 198  
Qy 121 FGPTLERITQDDDDVICTTEYSRIVPLENGEIVVSVLVNCRPGALNFSYSLLRDFTKATN 180

Db	199	FGPOTLERITRDAACITTEYSRIVPLENGEIVVLSVNGRFGAMNFSYSPLLREFTKATN	258
Qy	181	IRLRFLENTLTLGHLMKALRDPVTRRYYSIKDISIGRCVCHGHADVCDKADPLDPF	240
Db	259	VLRLFLNTLTLGHLMKALRDPVTRRYYSIKDISIGRCVCHGHADVCDKADPLDPF	318
Qy	241	RLQACAHNTGGSCDRCCPFNFQOPKPAATTSANECQSCNCHGHAYDCYYPEDVDRN	300
Db	319	RLQCTQHNTCGGTCDRCCPFNFQOPKPAATTSANECQSCNCHGHAYDCYYPEDVDRR	378
Qy	301	ASQNDNVYGGVCLDCOHHTTGINCERCLPGFPRAPDOPLSPHVCRPCDCESDFTDG	360
Db	379	ASQSLDGTGOGGVCIIDCOHHTAGNCRCLPGFIRFNHPLPSPHVCRRCNCESDFTDG	438
Qy	361	TCEDLTGRYCRPNFTGELCAACAEYTDFFHCYPLPSFPFNDTRQVLPAGQIVNCDN	420
Db	439	TCEDLTGRYCRPNFSGERCDVCAEGTGFPPSCYPTPS-SSNDTRQVLPAGQIVNCDGS	497
Qy	421	AAGTQGNACRKPRLGRVCKPNFRGAHCELCAPGFHGPSPCHPCOCSSPGVANSLCDPES	480
Db	498	AAGTQGNACRKPRLGRVCKPNFRGAHCELCAPGFHGPSPCHPCOCSSPGVANSLCDPDT	557
Qy	481	QOCRCRTGFEGRCDHCGALGYFHFPLQOLCGCSFAGTLPBGCDGAGRCQCRPGDFPHCD	540
Db	558	QOCRCRVGFEATCDRCAPGYFHFPLQOLCGCSFAGTLPBGCDGAGRCQCRPGDFPHCD	617
Qy	541	RCLPGYHGYPCHACADPRGALQOQGVGLCHCRGNTGATCOECSPGFYGFPCIPC	600
Db	618	RCRPGYHGFPCOACTCDPRGALQOQGVGLCHCRGNTGATCOECSPGFYGFPCIPC	677
Qy	601	HCSADGSLHTTCDPTTGCRCPRTVGLHCDMCPVGFAYNFPYCBAGSCHPAGLAPANPAL	660
Db	678	HCSAEGSLHAACDRSGQCSRPVTLGRCDTCVFGAYNFPYCBAGSCHPAGLAPVDPAL	737
Qy	661	PETAQCMCRHAHVGPSCDRCCKPGWGLSASNPGCTRCSCDPRGTLGGVTECO-GNGQC	719
Db	738	PEAQVPCMCRAHVEGPSCDRCCKPGWGLSASNPGCTRCSCDPRGTLGGVTECOGTQC	797
Qy	720	FKCAHVCKTCAACXGDFGLDYADYFCRCRCRDVGALGQCGEPTGTGACRCRPNTOGP	779
Db	798	FKCHVCCQACASCKDFGLDQADYFCRCRCRDVGALGQCGEPTGTGACRCRPNTOGP	857
Qy	780	TCSEPAKDHLPDLHMLLELEAATPEGHAVRFGFNPLFENFSPWGYAHMAIOPRIIV	839
Db	858	TCSEPAKDHLPDLHMLLELEAATPEGHAVRFGFNPLFENFSPWGYAHMAIOPRIIV	917
Qy	840	ARLNTVSPDLPLVPRYNRGTSVNGQISVREBGLSSCTNCTEQSQPVAFPPSTEPAF	899
Db	918	ARLNTVSPDLPLVPRYNRGTSVNGQISVREBGLSSCTNCTEQSQPVAFPPSTEPAF	977
Qy	900	VTVPORGFGEFVLPNGIWAIVAEGLLDYVLLPSTYYEALLQHRVTEACTYRPSA	959
Db	978	ITVPORGFGEFVLPNGIWAIVAEGLLDYVLLPSTYYEALLQHRVTEACTYRPSA	1037
Qy	960	LHSTENCLVIAHLPLDGFPSAAGTEALCRHNSLPRCPTEQLSPSHPLATCFGSVDVI	1019
Db	1038	QOSGDNCLLYLTHPLDGFPSAAGTEALCRHNSLPRCPTEQLSPSHPLATCFGSVDVI	1097
Qy	1020	QLEMAVPOPGQVLLVVEVVDSDSHQMGVAVHTTORAPOQGVNLHPCYSSLCRSPARD	1079
Db	1098	QQUAVPOPGQVLLVVEVVDSDSHQMGVAVHTTORAPOQGVNLHPCYSSLCRSTARD	1157
Qy	1080	TOHLIAFLHLDSEASIRLTAQAHFHLHSVTLVPVEBPSSTEFVPRVFCVSSHGTNPSS	1139
Db	1158	TQDHLAFLHLDSEASIRLTAQAHFHLHSVTLVPVEBPSSTEFVPRVFCVSSHGTNPSS	1217
Qy	1140	ACLASRPKPPQPIILKDCQVLPPLDPLTOSQELSPGAPPGPQPPPTAVDPNAEP	1199
Db	1218	ACLASRPKPPQPIILKDCQVLPPLDPLTOSQELSPGAPPGPQPPPTAVDPNAEP	1277
Qy	1200	TLLRHPOGTWFTQVPTLGRYAFLLHGYQVPHSPFVVEVLINGRIWQHANSFPCPHG	1259

Db	1278	TLLRHPOGTWFTQVPTLGRYAFLLHGYQVPHSPFVVEVLINGRIWQHANSFPCPHG	1337
Qy	1260	YGCRTLVLCGQTMLDVTDNBLTVTVRVEGRWLMWLYLVLPEDAYSSSSYQOEPLDKS	1319
Db	1338	YGCRTLVLCGQTMLDVTDNBLTVTVRVEGRWLMWLYLVLPEDAYSSSSYQOEPLDKS	1397
Qy	1320	YDFISHCATQVGHISPSSSSPSCNAATSLSFYNNGALPCGCHVEGVAVSPTCBPFGQC	1379
Db	1398	YDFISHCAQVGHISPSSSSPSCNAATSLSFYNNGALPCGCHVEGVAVSPTCBPFGQC	1457
Qy	1380	PCRGHVIGRDCSRCATGYWGFNCRPCDGCARLDELGTQICPCPRTVPPCLVCQPOSF	1439
Db	1458	PCRGHVIGRDCSRCATGYWGFNCRPCDGCARLDELGTQICPCPRTVPPCLVCQPOSF	1517
Qy	1440	GCHPLVGCBCNCSGPGVQELTDPTCDMDSGOCCRENVAGRRCDTCAFGVGVSPCRPC	1499
Db	1518	GCHPLVGCBCNCSGPGVQELTDPTCDMDSGOCCRENVAGRRCDTCAFGVGVSPCRPC	1577
Qy	1500	DCHZAGTMAVSCDPLTGQCHCKENYQSRQCRVGTFSLDAANPKGKTRCFCFGATERC	1559
Db	1578	DCHZAGTMAVSCDPLTGQCHCKENYQSRQCRVGTFSLDAANPKGKTRCFCFGATERC	1637
Qy	1560	GMSNLARHFVDMGMEWLLSSDRQVVPHEHREPELHADR- ---SYADTFSELYWAP	1615
Db	1638	RSSSYTROEFVDMGMEWLLSSDRQVVPHEHREPELHADR- ---SYADTFSELYWAP	1697
Qy	1616	PSYLGDRVSSYGGTLRVELHSETQRGDIPIYERSPDVVLQGNQMSIAFLAYPPPQV	1675
Db	1698	PSYLGDRVSSYGGTLRVELHSETQRGDIPIYERSPDVVLQGNQMSIAFLAYPPPQV	1757
Qy	1676	HRGQLQVVEGNPRHLETHNPSREELMMVLAGLEQLIRALFSQTSSSVSIRRVLEVAS	1735
Db	1758	HRGQLQVVEGNPRHLETHNPSREELMMVLAGLEQLIRALFSQTSSSVSIRRVLEVAS	1817
Qy	1736	EAGRGPASNVBLCMCPANYRGDSQCECAPGYRDTKGLFLGRVCVPCQCHGSDRCLPGS	1795
Db	1818	PAGQALASNVBLCLCPASYRGDSQCECAPGYRDTKGLFLGRVCVPCQCHGSDRCLPGS	1877
Qy	1796	GIYVCGQNTGDDQECRCRPFVSSDPNPAAPCVSCPCPLAVPSNNPADGCVLENGTQ	1855
Db	1878	GIYVCGQNTGDDQECRCRPFVSSDPNPAAPCVSCPCPLAVPSNNPADGCVLENGTQ	1936
Qy	1856	CLCRGYAGASERCAPGFFGNPLVLGSSCPCDSCGNDPNMIESDCDPLTGACRGCLR	1915
Db	1937	CLCRGYAGASERCAPGFFGNPLVLGSSCPCDSCGNDPNMIESDCDPLTGACRGCLR	1996
Qy	1916	HTTGPCHERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCRCL	1975
Db	1997	HTTGPCHERCAPGYGNALLPGNCTRCDCSPCGTETCDPQSGRCLCKAGVTGQRCRCL	2056
Qy	1976	GYFGTEQCGCRPCACGPAKSECHPOSQCHCQPGTTPCQCLCAPGYWGLPKGCR	2035
Db	2057	GYFGTEQCGCRPCACGPAKSECHPOSQCHCQPGTTPCQCLCAPGYWGLPKGCR	2116
Qy	2036	COCPRGHCDPHGTCHCTCPPGLSGERCDCSCQHQVFPVFKPGGHIHCEVCHVLLLD	2095
Db	2117	COCPRGHCDPHGTCHCTCPPGLSGERCDCSCQHQVFPVFKPGGHIHCEVCHVLLLD	2176
Qy	2096	DUERAGALLPATREOLQGINASSAWARHLRLNASIADLOSLRRPPGPRYQAAQLOTL	2155
Db	2177	DUERAGALLPATREOLQGINASSAWARHLRLNASIADLOSLRRPPGPRYQAAQLOTL	2236
Qy	2156	EQOSISLOQDTERLGSQATGVQAGQLDTESTLGRAQKLLSVAVRAGNALNELASRM	2215
Db	2237	EQOSISLOQDTERLGSQATGVQAGQLDTESTLGRAQKLLSVAVRAGNALNELASRM	2296
Qy	2216	GQSGPDALVPSGEQLRWALAEVERLLMDMTRDIQAQAVAEAEALAEQRLMARVQEQOL	2275
Db	2297	GHLGLANAPSQEQQLRLTAEVERLLMEMRARDIGAPQAAAEALAEQRLMARVQEQOL	2356
Qy	2276	TSPWENQSLATHIRDOLAQVSGELMDLREALNQAVNTTREAELNSRQERKEALQWK	2335
Db	2357	SLUWENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAQELNSRQERKEALQWK	2416

Best Local Similarity 72.0%; Pred. No. 0;  
Matches 1205; Conservative 159; Mismatches 295; Indels 14; Gaps 6;

QY	1970	CDRCLEGFYFPEQCGCRPCACGPAAGSECHSGOCHQCGTGTGQCCEGAYWGLP	2029
DB	1	CDRCOEGHFGNGCGGCRPCACGPAAGSECHSGOCHQCGTGTGQCCEGAYWGLP	60
QY	2030	EKGRRCCQPRGHCDPHTGCTCPGLSGERCDCSCQHQVPPVPGKPGHGHCEVDCDC	2089
DB	61	BOGRCQCPGCRDPTGRCNCPGLSGERCDCSCQHQVPPVPGKPGHGHCEVDCDC	120
QY	2090	VVLDDLERAGALLPAIRLOLGINASSAAWRLHRLNLSIADLQSKLRPPGPRVQAA	2149
DB	121	VVLDDLERAGALLPAIRHEQLGINASSAAWRLHRLNLSIADLQSKLRSPGPRHETA	180
QY	2150	QCLCTEQCSLSLODTERLGSOATGVQGOAGQLDTESTLGRAOKLLSVRAVGALN	2209
DB	181	QCLVTLQOSTLSQDARRLGQAVGTRDQASQLLACTEATLGHAKTLAAIRAVDTLS	240
QY	2210	ELASRMCGSPGDALVPSGQLRWALAEVRLMDWMTDLGAGGAVAEALAAQRLMA	2269
DB	241	ELMSOTGHLGLANASAPSGQLLRTLAVERLLWMEARDLGAQMAAEALAAQRLMA	300
QY	2270	RVOQLTSFWEENOSLATHIRDOLAQVESGLMDLREALNOAVNTTREAELNSRNQSRVK	2329
DB	301	RVOQLSSLWENQALATOTDRLAQHEAGLMDLREALNRVATREAOELNSRNQSRLE	360
QY	2330	EALQWKQELSDNATLKATLQAASLIILGHVSELLQGDQAKEDLEHLAASLDGAWTPLLK	2389
DB	361	EALQWKQELSRDNTATLQAASLIILGHVSELLQGDQAKEDLEHLAASLDGAWTPLLK	420
QY	2390	RMQAFSPASSKVDLVEAAEAHAKLNOLAINLSIILGINQDRFIQRAVEASNAYSILQ	2449
DB	421	RMQTFSPAGSKRLVEAAEAHAKLNOLAINLSIILGINQDRFIQRAVEASNAYSILQ	480
QY	2450	AVQAAEDAAQALQASRTWEMVQVGLAAGARQLLANSALBETILGHQRLGLAQRGL	2509
DB	481	AVQAAEDAAQALQADHTWATVVRQGLVDRAQQLANSTALEEAMLEQOORGLVMAAL	540
QY	2510	QAAGIQLHNWARKVQLAAQIOBAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSL	2569
DB	541	QAARTQLRDVRAKQQLAAQIOBAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSL	600
QY	2570	QGMOKNVERWQSLGGQGLDQSDVERDASSYSTLEKTLPLLAKLSRLNRGVHNASL	2629
DB	601	QAMQENVERWQGYEGLRGQDLQAVLDAGHSYSTLEKTLPLLAKLSRLNRGVHNASL	660
QY	2630	ALSANIQRVRLIAQARSAASKVKVSMKFNRSRGVRLRPPDLADLAAYTALKFHQSPV	2689
DB	661	ALSASIGRVELIAQARSAASKVKVPMKFNRSRGVQLRPRDLADLAAYTALKFYLQ--	718
QY	2690	PAPEPGKNTGDHFLVYNGSRQATGDYMGVSLRNQKVVHVVYRLGKAGPTTLLSIDENIGE	2749
DB	719	PEPEPGGNTEDRFVYNGSRQATGDYMGVSLRNQKVVHVVYRLGKAGPTTLLSIDENIGE	778
QY	2750	AAVSDRTLQFGHMSVTVERQVHEIKGDTVAPGSEGLLNLPDDEFVYVGGYPSNFTPP	2809
DB	779	AAVSLDRTLQFGHMSVTVERQVHEIKGDTVAPGSEGLLNLPDDEFVYVGGYPSNFTPP	838
QY	2810	EPLRFPGLGCIEMETINEEVSILYPEQTFMLDTAVDKFCARSKATGDPWLTDGSLDG	2869
DB	839	PLLRFPGLGCIEMETINEEVSILYPEQTFMLDTAVDKFCARSKATGDPWLTDGSLDG	898
QY	2870	SGFARISFEKQFNTRKFDQELVSYNGIIFELKQESQFLCLAVQEGTLVLFVDFGSGL	2929
DB	899	TGFARISFDQSISTTKFEQELVSYNGIIFELKQESQFLCLAVQEGTLVLFVDFGSGL	958
QY	2930	KKADPLQFPQALTAASKAIQVFLLAGNRKRLVVRERATVFSVDQDNMLMAAYILGGV	2989
DB	959	KKAVPLQFPPLPLTSASKAIQVFLLAGNRKRLVVRERATVFSVDQDNMLMAAYILGGV	1018
QY	2990	PPEOLPLSLRQLPSPGSGVRGCIKGIKALGKYVDLKLNTTSG:SFQCTADLLVGRMTTFH	3049

2336 QELSODNATLKATLQASLIILGHVSELLQGDQAKEDLEHLAASLDGAWTPLLKRWQAPS 2395  
2417 QELSRDNTATLQALHAARTLASVFLRLSLQAKEDLERLASLDGARTPLLQKQTFPS 2476  
2396 PASSKVDLVEAAEAHAKLNOLAINLSIILGINQDRFIQRAVEASNAYSILQAVQAAE 2455  
2477 PASKRLVEAAEAHAKLNOLAINLSIILGINQDRFIQRAVEASNAYSILQAVQAAE 2536  
2456 DAAGQALQASRTWEMVQVGLAAGARQLLANSALBETILGHQRLGLAQRGLQAGIQ 2515  
2537 DAAGQALQADHTWATVVRQGLVDRAQQLANSTALEEAMLEQOORGLVMAALQAGTQ 2596  
2516 LHNWARKVQLAAQIOBAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSLQOMQV 2575  
2597 LRDVRAKQDLQEAHIAQAAQAMLANDTSETSEKIAHAKAVAAEALSTATHVQSLQOMQV 2656  
2576 VERWQQLGGLQGLDQSDVERDASSYSTLEKTLPLLAKLSRLNRGVHNASLALSANI 2635  
2657 VERWQGYEGLRGQDLQAVLDAGHSYSTLEKTLPLLAKLSRLNRGVHNASLALSANI 2716  
2636 GRVRLIAQARSAASKVKVSMKFNRS 2662  
2717 GRVRELIAQARSAASKVKVPMKFNRS 2743

RESULT 12  
US-10-112-944-801  
; Sequence 801, Application US/10112944  
; Publication No. US20040048249A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Weng, Gezhi  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Zhiwei  
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and  
; TITLE OF INVENTION: Secreted Polypeptides  
; FILE REFERENCE: 805A  
; CURRENT APPLICATION NUMBER: US/10/112,944  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: US 09/515,126  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: US 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 09/552,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/577,408  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 924  
; SOFTWARE: pt\_FL\_genes Version 5.0  
; SEQ ID NO 801  
; LENGTH: 1677  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-112-944-801

Query Match 30.7%; Score 6110; DB 12; Length 1677;

Db 1019 PPQQLPSPRLRFPPTGGSVRGCVKGIKALGVKVDLKLRLNTTGVSAAGCTADLLVGRAMTFH 1078  
Qy 3050 GHGFLPLADVPAPITEVYSGFGRGTGDNLLYRTSPDGFYQVSLREGHVTLRFMNQ 3109  
Db 1079 GHGFLRLALSNVAPLGNVYSGFGRHSAQDSALLYRASPDGLCVSLQCGRVSLQLLRT 1138  
Qy 3110 EVETQVFEADGAPHYVAFVSNVTGWLVDYDQQLVKSHERTTLMQLQPEPSRLILGG 3169  
Db 1139 EVETQVFEADGAPHYVAFVSNVTGWLVDYDQQLVKSHERTTLMQLQPEPSRLILGG 1198  
Qy 3170 LPVSGTHNFGSGISNVFQVRURGPVDFLHNNMGVNVSVGCTTPAQLIETS----- 3222  
Db 1199 LPESGTIYNFSGISNVFQVRURGPVDFLHNNMGVNVSVGCTTPAQLIETS----- 1258  
Qy 3223 RATAQKVSRRSOPSODLACTPMLPGTIODAYQFGGLPSPVLOFVGPSPSHRNRLHLSM 3282  
Db 1259 QATARASRRSQPASHPACMLPPHLRTRDSYQFGGLSPSHLEFVGLARHNPWSLSM 1318  
Qy 3283 LVRPHAAOGLLSTAPMSGRSPSLVFLNHHGHFVAQTEGPPRLQVQSRQHSRAGQWHR 3342  
Db 1319 HVLPFR-SRGLLLFTARLRPGSPSLALFLSNHGHFVAQMEGLGLTLRAQSRQSRPRGWHK 1377  
Qy 3343 VSVRWCMQIQIIVVGSQWQSKALHHRVPRAPRPPYTLVSGGLPASSYSKSLPVSVGF 3402  
Db 1378 VSVRWKRLILVTDGARWSQEGPHRQHQGAHFPQHTLFVGGLPASSHSSKLPVTVGF 1437  
Qy 3403 SGCLKLQLDKOPRLTPTQMVGTFCVSGPLEBGLFFGSGVVTLELPKAMPYVLSLEL 3462  
Db 1438 SGCVKRLHGRPLGAPTRMAGVTPCILLGPLEBGLFFGSGVVTLELPKAMPYVLSLEL 1497  
Qy 3463 EMEPLAAGLILHGOALATPYMQLKVLTEQVLLQANDGAGEFSTWTYPK-LDGRWHR 3521  
Db 1498 EVRPLAVTGLIHLGQARTFPYQLQVTEKQVLLRADDGAGEFSTVTRPSVLCGQWHR 1557  
Qy 3522 VAVIMORDTLRLVEDTQSNHHTTGRPLPESLAGSPALLHLGLSPKSTARPELPAYRGCLRK 3581  
Db 1558 LAVKSGNVLRLVEDVAQSNHTVGPLLAAAAGAPAPLYLGLPEPMVQPMPPAYCGCWR 1617  
Qy 3582 LLIN-CAPVNVITASVQIQAGVWRCPCSTLA--LSKOGKALTQORHAKPSVSP 3631  
Db 1618 LAVNRPPVATRSVEVHGAVGASGCPSTRTPTPAPGQAPAAAASHRPLCSP 1670

RESULT 13  
US-10-037-417-8  
; Sequence 8, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Sciore, Paul  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Stone, David J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shency, Suresh G  
; APPLICANT: Anderson, David W  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260,018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260,360  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/272,411  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/272,817  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/291,186  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/303,231  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/305,060  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/318,405  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/318,700  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 1640  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-417-8

Query Match 30.7%; Score 6092; DB 12; Length 1640;  
Best Local Similarity 72.7%; Pred. No. 0;  
Matches 1197; Conservative 156; Mismatches 278; Indels 16; Gaps 5;

Qy 1970 CDRCLGVGFGEQCGGCPACGPAAGSGECPHSGCHQCPGTTGQCLECAPGVWGLP 2029  
Db 1 CDRCEGHFGNGCGGCPACGPAAGSGECPHSGCHQCPGTTGQCLECAPGVWGLP 60  
Qy 2030 EKGCRRCQCPHGHCDPHTGCTCPGLSGERCDTCSQOHQVPPVPGKEGGHGHCEVCDHC 2089  
Db 61 EKGCRRCQCPHGHCDPHTGCTCPGLSGERCDTCSQOHQVPPVPGKEGGHGHCEVCDHC 120  
Qy 2090 VVLLDDLLERAGALLPAIREOLQGINASSAAWALHRLNLSIADLQSKLRPPGPRYQAA 2149  
Db 121 VVLLDDLLERAGALLPAIREOLQGINASSAAWALHRLNLSIADLQSKLRPPGPRYQAA 180  
Qy 2150 QQLQTLQEQSISLQODTERIGSQATGVQGAQGLDTESTLGRAQKLSVAVGRALN 2209  
Db 181 QQLQTLQEQSISLQODTERIGSQATGVQGAQGLDTESTLGRAQKLSVAVGRALN 240  
Qy 2210 ELASRMGQSPGDALVPSGEOLRWALAEVERLLWDMETRLDQAGAVAEAEAEAEAEAEAE 2269  
Db 241 ELASRMGQSPGDALVPSGEOLRWALAEVERLLWDMETRLDQAGAVAEAEAEAEAEAEAE 300  
Qy 2270 RVQEQLTSTWENOSLATHIRDLAQYSGMLDLREALNOAVNTTREAELNSRNOERVK 2329  
Db 301 RVQEQLTSTWENOSLATHIRDLAQYSGMLDLREALNOAVNTTREAELNSRNOERVK 360  
Qy 2330 EALQWQELSDNATLKATLQAAASLIIGHVSELQGLDQAKEDLEHLAASLDGANTPLK 2389  
Db 361 EALQWQELSDNATLKATLQAAASLIIGHVSELQGLDQAKEDLEHLAASLDGANTPLK 420  
Qy 2390 RMQAFSPASSKVDLVEAAEAHAQKLNQALNLSIIGINQDRPTORAVASWAYSILQ 2449  
Db 421 RMQAFSPASSKVDLVEAAEAHAQKLNQALNLSIIGINQDRPTORAVASWAYSILQ 480  
Qy 2450 AVQAAEDAAAGALROASRTWEMVVOGRLAAGARQLLANSALBETILGHGRLGQAQRL 2509  
Db 481 AVQAAEDAAAGALROASRTWEMVVOGRLAAGARQLLANSALBETILGHGRLGQAQRL 540  
Qy 2510 QAAGIQLHNWVARKNQALQIAEQIAQAMLMDTSETSEKIAHAKAVAAEALSTATHVQSOL 2569



541 QCARLTQLRDVRAKDKQLBAHQAQAQMLAMWDTSTSKKIAHAKAVAAEAQDTATRVQSGL 600

2570 QQMKNVVERWQSLGGLODLSQVERDASSYSTLEKTLPLLAKLSRLNENGVNASL 2629

601 QAMQENVERWQVEGLRGQDLQAVLDAGHSVSTLEKTLPLLAKLSILENENGVNASL 660

2630 ALSANIGVRKLIQAARSAASAKVSKFKNGSRVLRPRDLADLAAYTALKFHIQSPV 2689

661 ALSASIGVRRELLIAQARSAASAKVSKFKNGSRVLRPRDLADLAAYTALKFHIQGG-- 718

2690 PAPEPGKNTGDFHVLNMGSRQATDYGVSILRNOKVHWYRLGKAGPTTSLIDENIGEOF 2749

719 PEPEPGQGTDRFVVMGMSRQATDYGVSILRNOKVHWYRLGKAGPTTSLIDENIGEOF 778

2750 AAVSDRLTLOFGHMSVTVKQWHEIKGDTVAPSGEGLNHLNPDVFFVYGGVPSNFTTP 2809

779 AAVSDRLTLOFGHMSVTVKQWHEIKGDTVAPSGEGLNHLNPDVFFVYGGVPSNFTTP 838

2810 BPLRPFGLGCIEMETLNEEVSYNFEQTPMLDTAVDKPCAKSKATGDPMLTDSYLDG 2869

839 PLLRPFGLGCIEMETLNEEVSYNFEQTPMLDTAVDKPCAKSKATGDPMLTDSYLDG 898

2870 SGFAISFEKQPSNTRKDFQELRLVSYNGIIFPKQESQFLCLAVQBGTTVLVYDFGSG 2929

899 TGFARISFDSQSTTRKFEQELRLVSYNGIIFPKQESQFLCLAVQBGTTVLVYDFGSG 958

2930 KKADPLOPPQALTAASKAIOVFLAAGNRKVLVVERATVFSVDODNMLEMADAYILGGV 2989

959 KCAVLPQPPPTTSKAKIOVFLGSSKRVLVVERATVFSVDODNMLEMADAYILGGV 1018

2990 PPEQLPLSLRQLPFGSGVRCIKIGKALGYVLDKRLNTGTSFGCTADLLVGRWTFH 3049

1019 PPDQLPPLSLRQLPFGSGVRCIKIGKALGYVLDKRLNTGTSFGCTADLLVGRWTFH 1078

3050 GGFPLPALPDVAPTEVYVSGFGRGQDNLLVYRTSPDPQVQVSLRGHTVTLFPMQ 3109

1079 GHGFURLALSNVAPITGVNYSGFHSQDSALLVYRASPDGLQVSLQGRVSLQLRT 1138

3110 EYETQRFADGADGAPHYVAFYVNTGVWLVYDQQLVKSHERTTTPMLQLOPEPSRLLGG 3169

1139 EVKTKAGFADGADGAPHYVAFYVNTGVWLVYDQQLVKSHERTTTPMLQLOPEPSRLLGG 1198

3170 LPVSGTFHNFSCISNVFVRLGRQRFVDLHONMGSVNTVSGCTPAQLIETS----- 3222

1199 LPESGTFHNFSCISNVFVRLGRQRFVDLHONMGSVNTVSGCTPAQLIETS----- 1258

3223 RATAQVSRSSQPSQDCLATPMLPGTIQDAYQFGGLPQSYLQFVGISPSHENRHLMS 3282

1259 QATKASRSRQPSRQPHACMLPHLRTTRDSYQFGGSLSHLEFFVGLARHNWLSM 1318

3283 LYRPHAAQGLLLSTAPMSGRSPSLVLFNGHFVAOTEGPPLQVQSRQHRAGQWHR 3342

1319 HVLPRL--SSRGLLFTARLPSPSLALFSLGHFVAQMEGLTFLRAQSRQRGRWHR 1377

3343 VSVRMGQOQLVVDGSSQTSOKALHHRVPAERPOVTLVSGGLPASSYSKLPVSVGF 3402

1378 VSVRMGQOQLVVDGSSQTSOKALHHRVPAERPOVTLVSGGLPASSYSKLPVSVGF 1437

3403 SGCLKQLQDKQPLRPTOMGVTPCVSGPLEDGLFFPGSEGVVTLBPKAKMPYVSL 3462

1438 SGCVKRLHGRPLGAPTRMAGVTPCILLGLEAGLFFPGSGGVITLPLGATLPDVGLEL 1497

3463 EMRPLAAGLIIFHLGALATPMOLKVTEOVLLQANDGAGESTWVTPK-LCDGRWHR 3521

1498 EVRPLAVTGLIFHLGALATPMOLKVTEOVLLQANDGAGESTWVTPK-LCDGRWHR 1552

3522 VAVIMGRDTRLREVDQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRCGLR 3581

1553 LAVMKSGNVRLVEDAQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRCGLR 1612

3582 LLINGAPVNTASVQIQAVMGRGCP 3608

1613 LAVNRSFVAMTSVEVHGAVGASGCP 1639

RESULT 14

US-10-037-417-49

Sequence 49, Application US/10037417

Publication No. US20040052806A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Alsobrook II, John P

APPLICANT: Tchernov, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Patturajan, Meera

APPLICANT: Grosse, William M

APPLICANT: Leplev, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malvankar, Uriel M

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APPLICANT: Stone, David J

APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia

APPLICANT: Shenoy, Suresh G

APPLICANT: Anderson, David W

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Miller, Charles E

APPLICANT: Eisen, Andrew J

FILE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-235

CURRENT APPLICATION NUMBER: US/10/037,417

PRIOR FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,018

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/272,411

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/272,817

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/291,186

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/303,231

PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/305,060

PRIOR FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 60/318,405

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/318,700

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 49

LENGTH: 1634

TYPE: PRT

ORGANISM: Homo sapiens

US-10-037-417-49

Query Match 27.6%; Score 5495.5; DB 12; Length 1634;

Best Local Similarity 70.3%; Pred. No. 0;

Matches 1107; Conservative 157; Mismatches 278; Indels 37; Gaps 6;

QY 2051 TCPEGLSGERCDCSQHQVPEKPGGHIHC-----AATPAASIRCLFQAGLWATASTVKVCDHCWVLLDDL 2097

DB 71 TAPRGSAGS-----AATPAASIRCLFQAGLWATASTVKVCDHCWVLLDDL 117

QY 2098 ERAGALLPATREILOGINASSAAWHLPLNLSIADLSKLRPPGPRVQAQOQLTLEQ 2157

Query Match	27.6%;	Score 5495.5;	DB 12;	Length 1634;
Best Local Similarity	70.1%;	Pred. No. 0;		
Matches 1107;	Conservative 157;	Mismatches 278;	Indels 37;	Gaps 6;
QY	2051	TCPPCLSGERCDCSQHQHVPVPGKPGHGHC-----	-----EYCDHCWVLLDDL	2097
Db	71	TAPRGSAGS-----	AATPAASSIRCLFQAGLWATASTVKYCDHCWVLLDDL	117
QY	2098	EPAGALLPAIRELOGINASSAAWHLRLINASTADLQSLKRRPPGPPYQAQOQLTLEQ	2157	

Db 118 ERAGALLIPATHEQURGINASSMAWARLHRNLNASTADIQSQRSLPGRPHETAQOQLEVBQ 177  
Qy 2158 QSILOQDTERLGSQATGVOGQAGQLDTESTIGRAQKILLESVAVGRALNELASRMGQ 2217  
Db 178 QSTSLGQDARLGGQAVGTDRDQASQALLAGTEATLGHAKTLLAAIRA VDRVTLSELMSQTH 237  
Qy 2218 GSPGDAIVPSGEOLRWALAEVERILWYRVEDIGACAVAEAEALAEORLMARVQSCITS 2277  
Db 238 LGLANASAPSGEQLRLTAEVERILWYRVEDIGACAVAEAEALAEORLMARVQSCITS 237  
Qy 2278 FWEENQSLATHIRDLQAYSGMLDREALNQAQVNTTREAELNQRNQRVKEALQWQKE 2337  
Db 298 LWEENQALATOTDRBLAQHEAGLMDREALNRAVDATREAELNQRNQRVKEALQWQKE 357  
Qy 2338 LSONATILKATLOASILGHVSELLOGIDQAKEDIEHLAASLDGAWTPLLKMQAFSPA 2397  
Db 358 LSRDNATLOATHAARDTLASVFLHLSLDQAEELERLASLDGARTPLLRMQTFSPA 417  
Qy 2398 SSKYDLVEABAHQAKLNALNLSGIIILGINODRFORAVEASNAVSSILQVQAEDA 2457  
Db 418 GSKLVEABAHQAKLNALNLSIIIDVNDRLTORALEASNAVSRILQVQAEDA 477  
Qy 2458 AGQALQASRTWVWVQGLAAGAROLLANSALLEETILGHQGRGLAQORLQAGIQLH 2517  
Db 478 AGQALQADHTWATVVRQGLVDRACQLLANSTALEEAMLOEQORGLGLVWAALQAGTQLR 537  
Qy 2518 NVMARKNOLAQIOBAQAMLMDTSETSEKTAHAKAVAAEALSTATHVQSOLOQMOKNVE 2577  
Db 538 DVRAKQDQLEHIIQAQAMLMDTSETSEKTAHAKAVAAEALSTATHVQSOLOQMOKNVE 597  
Qy 2578 RWQSLGLOQODLSQVERDASSVSTLEKTLPLLAKLRLNENRGVHNASLALSANIGR 2637  
Db 598 RWQSLGLOQODLSQVERDASSVSTLEKTLPLLAKLRLNENRGVHNASLALSANIGR 657  
Qy 2638 VRKLIQAARSASVKVSMKENGSRVLRPPRLADLAAYTALKFHIQSPVAPERGVN 2697  
Db 658 VRELIQAARGAASKVKVSMKENGSRVLRPPRLADLAAYTALKFHIQSPVAPERGVN 715  
Qy 2698 TGDHFLVYMGSRQATGDMYVSLRNQKVHYYRLGKAGPTTSLSIDENIGQFAAVSIDRT 2757  
Db 716 TGDHFLVYMGSRQATGDMYVSLRNQKVHYYRLGKAGPTTSLSIDENIGQFAAVSIDRT 775  
Qy 2758 LQGHMSVTVKQVHETKGTVPAGSEGLNLHPDDFVFGVGGYPSNTPPEPLFPFGY 2817  
Db 776 LQGHMSVTVKQVHETKGTVPAGSEGLNLHPDDFVFGVGGYPSNTPPEPLFPFGY 835  
Qy 2818 LGCIEMETLNEEVSILNFEOTFMDTAVDKPCARSKATGDPMLTDSYLDGSGFARISF 2877  
Db 836 RGCLEMDTNEEVSILNFEOTFMDTAVDKPCARSKATGDPMLTDSYLDGSGFARISF 895  
Qy 2878 EKQFSNTKRFPOELRLVSYNGIIIFLQBSQFCLAVQEGTLVLYFDGSGGLKADPLQ 2937  
Db 896 DSQISTTKRFBQELRLVSYNGIIIFLQBSQFCLAVQEGTLVLYFDGSGGLKADPLQ 955  
Qy 2938 PQALTAASKAIOVFLLAGNRKRLVVRERATVFSVDQDNMLEADAYVYLGVPPEQLPLS 2997  
Db 956 PPPLTSASKAIOVFLLAGNRKRLVVRERATVFSVDQDNMLEADAYVYLGVPPEQLPLS 1015  
Qy 2998 LRQLPSPGSGVRGCIKGKALGKYVDLKLNTTGISFGCTADLLVGRMTFHHGGLPLA 3057  
Db 1016 LRQLPSPGSGVRGCIKGKALGKYVDLKLNTTGISFGCTADLLVGRMTFHHGGLPLA 1075  
Qy 3058 LPDYAPITEVYSGFGRGTQDNLLYYRTSPDGPYVSLREGHVTLREWNQVETORVF 3117  
Db 1076 LSNVAPLFGNYSFGFGRGTQDNLLYYRTSPDGPYVSLREGHVTLREWNQVETORVF 1135  
Qy 3118 ADGAPHYVAFYVNTVYVWVYDQQLVYKSHERTTTPMLQLQPEPSPRLLGLGVSGTFH 3177  
Db 1136 ADGAPHYVAFYVNTVYVWVYDQQLVYKSHERTTTPMLQLQPEPSPRLLGLGVSGTFH 1195  
Qy 3178 NFSGCISNVFQRLGPRVFDLHONMGSVNVVSGCTPAQLIETS-----RATAQKVS 3230  
Db 1196 NFSGCISNVFQRLGPRVFDLHONMGSVNVVSGCTPAQLIETS-----RATAQKVS 1255

## RESULT 15

US-10-037-417-48

; Sequence 48, Application US/10037417

; Publication No. US20040052806A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Alsobrook II, John P

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Patturajan, Meera

; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

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; APPLICANT: Li, Li

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; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Anderson, David W

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/272,817

; PRIOR FILING DATE: 2001-03-02

QY 1 DLYCKLVGPFVAGDDN-OTIOGOVCDICTAANSKAPVSNALDGTERRWQSPPLSRGL 59  
Db 51 ELYCKLVGANTBHDHIDYVIGQVQCDYCDPTVPERNHPPENAI DGTBAWQSPPLSRGM 110  
QY 60 EYNEVNVLDLGOVHVAVYLIKAFNSPRPDLWVLRSTDFGHTYQPOFFPASSKRDCL 119  
Db 111 KNEVNLTFNQEFHVAFLFIRMGNSPRPG:WTLKSTDYKWTWPHQFSDTADCE 170  
QY 120 RGPRTLEITODDDVICTEYSRIVPLNGEIVSVLVNRPALNFYSPLLRDFTXAT 179  
Db 171 YFGKDYKTRDDDDVICTEYSKIVPELNGEIPVYMLNERPSSNYFNSTVLOQWTRAT 230  
QY 180 NLRLERLNTLLHLMGKALDPTVTRSYYSIKDISIGRCVCHGADVCDKADPLDP 239  
Db 231 NVRIRLRLNTLLHLMGKALDPTVTRSYYSIKDISIGRCVCHGADVCDKADPLDP 290  
QY 240 FR-LOCAQHNCTGSCDRCCFPNQPKWATTDSANEQSCNCHGAYDCYDPEYDR 298  
Db 291 VRILACRQHTCGIQNCECFQKQWQNTNARPNCEPCNCHGSHNECKYDEEVR 350  
QY 299 RNASQNDNVYGGVCLDQHTTGINCERCLPGFFRAPDPLDSPHVCRPCDESFT 358  
Db 351 KGLSLDIHGYDGGVQCNQHTNGINCKNPKYIRPKGHMNETVDCSPQCDYFYS 410  
QY 359 DGTCEDLTCRCYCRNFTGELCAACAEYTDPPHYPLSPFPHNDTRQVLPAGQIVNCD 418  
Db 411 TGHCEETGNCRAAFQPPSCDCAVGYGYPNC-----RE-----CE 449  
QY 419 CHAAGTQGNACRDKPRLGRVCNKPFRGAHCELCAPGPHG-PSCHPCQCSFPGVANSLCD 477  
Db 450 CNLNGTNGYHCEAESG-QQCPCKINFAGAYCKQCAEGYYPPECKACBCKNIGSITND 508  
QY 478 PESGQCMRTGFEGRDCHCALGYHFFPLCQCGSPAGTLPEGCD-BAGRCQCRPGFDG 536  
Db 509 VTIGCKCLTNFGDNCERCKEYFNYPCTSYCDNDQGTSEICNKGSGQICREGGG 568  
QY 537 PHCDRLPGYHYPCHACADPRGALDQCGVGLCHCRPNTGATCOESPGYGPFS 596  
Db 569 PRCDQCLPGYNYPCPKPCNCSSTGSSAITCDNTCKCNLNFAGKQCTLCTAGYSYDP 628  
QY 597 CIPCHSADSLHTTCDPTTGQCRPRVTGLHCDMCPVGAFFNYPCBAGSCHPAGLAP- 655  
Db 629 CLPCHDSHSGQVSN-SDGQCLQPNFDGQCDCKEYFNFPSCBDCNDPAGVIDX 687  
QY 656 -ANPALPETQAPCMCRAHYEGSCDRCKPGYWGLSASNPBGTCTRCSDPRGTLOGVTEC 714  
Db 688 FAGCGSVPGELCKCKERVTGRICNECKPLYWNLINSTECEICDCWTDGTISALDPT 747  
QY 715 G-NGOCFCKAHVCGKTCACKDPFGLDYADYFGCRSCRCVGNALGOCBPKTGACBR 773  
Db 748 SKSGQCPKPHQTGRRCQECRGTGTFDLSASLFGCKDCSDVGGSQVSCDKISGQCKCH 807

QY 774 PNTQGTCSBPAXDHYLPDLHHRLELEAANTPEGHAVRFGFNPLBENFESWEGYAHMMA 833  
Db 808 FRITGLACTQPLTTHFPFTLHQFYQYEDGSLPSGTQVRYDYDEAAAPPGSSGYYVVFNA 867  
QY 834 IQPRIVARLANVTSPLDFRLVFRYVNRGSIIVREBEGKLSCTNCTCTEQSQPVAFFP 893  
Db 868 IQNDRNEVNVFKSSLYRIVLVNPNNAENVATISVSDNPLE-----VDQHVKKVLLQ 922  
QY 894 STEPAPFVV--PORGEGEPFVLPNGIALLVEA-EGVLLDYVLLSTTYEALLQHRVT 950  
Db 923 TSEPFQFVTVAGPLGVPSAIVLDPGRYVFTTKANKNMVLDYFVLLPAAAYEAGILTRHS 982  
QY 951 EACTYRPSALHSTENCIVLAHLPLDGPSPSAAAGTEALCRHDSNLPSPCPTQLSPSH--- 1006  
Db 983 NPC-----ELGNMELCRHYKVASVEFSPAATFVI--GENSKPTNPVEITYTDEHLQIV 1035  
QY 1007 -----PPLATCFGSDVDIOLEMAVPOQYVLVVEYVGE-----DSHQENGVAVHTPQRA 1056  
Db 1036 SHVGDIPLVS---GSONELHYIVDVFRSGRYIFVIDYISDRNPPDSYV---INLKLKDN 1089  
QY 1057 PQQGVNLHPCPYSSLCRSPARTQHHLATFHLDS--ASIRLTA---BOAHFHLSTVL 1111  
Db 1090 DSETSVLLYPCLYSTICRTSVNEDGMEKS--FYINKEDLPVLIISADIEDGSRFPILSVTA 1148  
QY 1112 VPVEEFSTEVPRVFCVSSHGTENPSSAACLASRFPKPPQPIILKDCOVLPPLPDLPLT 1171  
Db 1149 IPVDQMSIDVINSPCVI-----HDQCATPKFERSVP-----DSKIEPETD--- 1191  
QY 1172 QSELSGAPPEGPQRPPTAVDPNAEPTLL--RHQGTVVFTTQV-----PTLGRYAFILH 1226  
Db 1192 HEDRIATNKPPY-----ASLDERVKLVHLDQNEATIVESKVDATKPNL--FVLVK 1242  
QY 1227 GYOPVHPSFVEVLINGGR-IMQGHANASCPHGYGCRITLVLCGQTMLDVTDNEILTV 1285  
Db 1243 YQPSHPKYQVYTLTAGKNQYDGEDIQHCPSSSSCGRGVIRPAGESSEI--DDEKFTI 1301  
QY 1286 RVPEGRWLMDYVLIIVPEDAYSSYIOEPDLKSYDFISHCATQGVHISPPSSSPFCRNA 1345  
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QY 1346 ATSLSPYNNGALPCGCHVEGAVSPCEPFGGQPCRGHVIGRDCSRCATGYWGFNCRP 1405  
Db 1361 VFSUTADYNSGALPCNDYAGSTSFCHPFGGQCKPNVIERTCGRCSRYVGFDDCKP 1420  
QY 1406 CDC-GARLDBELTGQCICPPRTVPPCLVQCPQSFGCHPLVGCCECNCSGFGVQELTDP 1464  
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Db 1540 VGRDCQCDVGTYNLQESNPDGCTTCFCGKTSRCDSAVLRYVNVSLKHVSITTFEHE 1599  
QY 1572 MEGWLLSSDRQVVPHEHREIEL-----LHAD--LRVADTFSELYWQAPPSVILG----- 1620  
Db 1600 ES-----IKFDMWVFPAD-----EILLNETTKADFTLEVND-----ERPAYFGVLDL 1644  
QY 1621 ----DRVSSYGGTLYHELHSETQRGIFIPYBSRPDVLQGNOMSTAFLELAYPPGQVH 1676  
Db 1645 LNQNWHISAYGGDLATLHFTSGFDCKYI---VAPDVILFSEHNAHVHVSIEQPSRNEFF 1701  
QY 1677 RGQQLVGNFRHLETHNPVSRBELMMVLAGELOLQIRALFQSTSSSVSLRRVLEVAS 1736  
Db 1702 TNRVNIVESNFQTI-SGKFPVSADFMVLRDLKVFIRANYMEQTLVUTVTHLSVYLTAD 1760  
QY 1737 AGSGPPASN---VELCMWCPANYRGDSQCAPGYRDTKGLFGRVCVPCQCHGSDRCLP 1793  
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QY 60 EYNEVNVLDLGOVHVAVYLIKAFNSPRPDLWVLRSTDFGHTYQPOFFPASSKRDCL 119  
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QY 120 RGPRTLEITODDDVICTEYSRIVPLNGEIVSVLVNRPALNFYSPLLRDFTXAT 179  
Db 171 YFGKDYKTRDDDDVICTEYSKIVPELNGEIPVYMLNERPSSNYFNSTVLOQWTRAT 230  
QY 180 NLRLERLNTLLHLMGKALDPTVTRSYYSIKDISIGRCVCHGADVCDKADPLDP 239  
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PRIOR APPLICATION NUMBER: 60/291,186  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: 60/303,231  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 60/305,060  
PRIOR FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: 60/318,405  
PRIOR FILING DATE: 2001-09-10  
PRIOR APPLICATION NUMBER: 60/318,700  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 227  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 48  
LENGTH: 3712  
TYPE: PPT  
ORGANISM: Drosophila melanogaster  
US-10-037-417-48  
Query Match 25.2%; Score 5018.5; DB 12; Length 3712;  
Best Local Similarity 31.3%; Pred. No. 7.9e-305;  
Matches 1227; Conservative 595; Mismatches 1527; Indels 569; Gaps 122;

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1912 QY GCLRHHTGPHCERCAPGFYGNALLPGNCTRCDSPCGTETCDPOSGBCLCKAGVTGQRCD 1971  
1940 Db RCLNNTFGAACNLCAPOFGYDAIKNQCSCDDDLGTQCDPFGVCTCHENVIGDRCD 1999  
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2317 Db HLEDLFNMS--EASQAKSADVERNVANQAFDNKSFDTVSEQKLOAKENIKDANGFLING 2375  
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Job time : 129.478 secs

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2911 QY CLAVEGGLVLVFDYDFGSLKKXADPLQPPQALTAASKAIQVFLLAGNRKRV-----LVRV 2964  
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3472 Db VELPIYILGVNKFLESEVKNLTDFTKEVEY---FNGCLKNHIFDAMDLETPEEFVGVPC 3528  
3429 QY VSGPLEDGLFFPGSGGVVTLPLPKAMPVSVSLEMRPLAAAGLIF--HLGQALA----- 3481  
3529 Db -SEQVERGLFFNNQKAFVKIFDHFVGTGEMKISPDFRDPDNGLLFSVHGKNSYALIELV 3587  
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3537 QY -TOSNHTTGRLPESLAGSPALLHLGS-----LPKSSSTARPELPAYRGCLRKLLINGAPV 3589  
3638 Db FISSNPGVNGESVITTRNRPFLGCHVAFQAPGKITKK-----SPKGCISKVEVNM 3693  
3590 QY NVTASVQIOGAVMRGCP 3607  
3694 Db NITPNM-VVGDWQGYCP 3710

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
QM protein - protein search, using sw model  
Run on: May 18, 2004, 14:56:24 ; Search time 94.0041 Seconds  
(without alignments)  
10937.572 Million cell updates/sec  
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Perfect score: 20118  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1145568 seqs, 278261457 residues  
Total number of hits satisfying chosen parameters: 1145568  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20104	99.9	3695	12	US-10-312-352-22
3	20060.5	99.7	3696	15	US-10-312-088-31
4	20035.5	99.6	3690	12	US-10-112-944-347
5	20030	99.6	3705	15	US-10-312-088-30
6	18254.5	90.7	3600	12	US-10-037-417-2
7	18231	90.6	3597	12	US-10-037-417-6
8	15839	78.7	3635	9	US-09-845-583-2
9	15839	78.7	3635	12	US-10-037-417-47
10	15839	78.7	3635	14	US-10-037-182-4
11	15120	75.2	2743	14	US-10-037-182-36
12	8504.5	42.3	1677	12	US-10-112-944-801
13	8499.5	42.8	1640	12	US-10-037-417-8
14	7804.5	38.8	1634	12	US-10-037-417-49
15	5097	25.3	3712	12	US-10-037-417-48

16	5097	25.3	3712	13	US-10-108-605-103	Sequence 103, Appl
17	5093	25.3	3712	12	US-10-037-417-51	Sequence 51, Appl
18	5002	24.9	953	9	US-09-845-583-4	Sequence 4, Appl
19	5002	24.9	953	12	US-10-037-417-50	Sequence 50, Appl
20	4974	24.7	3672	15	US-10-369-493-6146	Sequence 6146, Ap
21	4756.5	23.6	908	12	US-10-037-417-4	Sequence 4, Appl
22	3069.5	15.3	3070	10	US-09-961-403-7	Sequence 7, Appl
23	2933	14.6	3084	9	US-09-938-275-4	Sequence 4, Appl
24	2933	14.6	3084	14	US-10-262-670-2	Sequence 2, Appl
25	2854	14.2	3075	9	US-09-938-275-5	Sequence 5, Appl
26	2514	12.5	2823	15	US-10-369-493-5220	Sequence 5220, Ap
27	2514	12.5	2823	15	US-10-369-493-5221	Sequence 5221, Ap
28	2260.5	11.2	1693	15	US-10-603-725-4	Sequence 4, Appl
29	2260.5	11.2	1693	15	US-10-603-725-8	Sequence 8, Appl
30	2260.5	11.2	1713	14	US-10-171-311-113	Sequence 113, App
31	2260.5	11.2	1713	15	US-10-372-683-10	Sequence 10, Appl
32	2260.5	11.2	1713	15	US-10-603-725-6	Sequence 6, Appl
33	2260.5	11.2	1724	15	US-10-603-725-2	Sequence 2, Appl
34	2249	11.2	1694	15	US-10-603-725-12	Sequence 12, Appl
35	2249	11.2	1725	15	US-10-603-725-10	Sequence 10, Appl
36	2153.5	10.7	1816	14	US-10-299-058-4	Sequence 4, Appl
37	2149	10.7	1823	12	US-10-363-616-457	Sequence 457, App
38	2147.5	10.7	1816	14	US-10-239-058-2	Sequence 2, Appl
39	2136.5	10.6	1816	15	US-10-372-683-4	Sequence 4, Appl
40	1995	9.9	463	15	US-10-264-049-3039	Sequence 3039, Ap
41	1729	8.6	634	10	US-09-949-029-134	Sequence 134, App
42	1667	8.3	342	15	US-10-264-049-3068	Sequence 3068, Ap
43	1633	8.1	365	9	US-09-925-299-1007	Sequence 1007, Ap
44	1633	8.1	365	10	US-09-925-299-1007	Sequence 1007, Ap
45	1618.5	8.0	483	15	US-10-108-260A-3715	Sequence 3715, Ap

ALIGNMENTS

RESULT 1  
US-10-037-182-2  
; Sequence 2, Application US/10037182 -  
; Publication No. US2003004899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Tnybolli, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10  
; FILE REFERENCE: 99-274-F  
; CURRENT APPLICATION NUMBER: US/10/037,182  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2008-12-21  
; PRIOR APPLICATION NUMBER: 60/257,449  
; PRIOR APPLICATION NUMBER: 60/279,282  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 3695  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-182-2

Query Match	100.0%	Score	20118	DB	14	Length	3695
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Qy 421 DSPHYCRRCNESDPTDGTCEBTLTGRCYCRNPFSGERCDCVCAEGFTGPPSPYTPSSND 480  
Db 421 DSPHYCRRCNESDPTDGTCEBTLTGRCYCRNPFSGERCDCVCAEGFTGPPSPYTPSSND 480  
Qy 481 TREOVLPAQIIVNDCSAGTOGNACRDXPRVGRCLCKPNFGTHCELCAFGFYGPCQP 540  
Db 481 TREOVLPAQIIVNDCSAGTOGNACRDXPRVGRCLCKPNFGTHCELCAFGFYGPCQP 540  
Qy 541 CQCSFPGVADDCDEDTGQCRVGFEGATCDRCAPGYFHPFLQOLGCSAGTLPBSCD 600  
Db 541 CQCSFPGVADDCDEDTGQCRVGFEGATCDRCAPGYFHPFLQOLGCSAGTLPBSCD 600  
Qy 601 EAGRLCQEFAGPHCDRCRPGYHGFNQCQACTDPRGALDOLCGAGLCCRCGYGTGTA 660  
Db 601 EAGRLCQEFAGPHCDRCRPGYHGFNQCQACTDPRGALDOLCGAGLCCRCGYGTGTA 660  
Qy 661 CQCSFPGHGFSCVPCCHCSAGSLHAACDPRSGQSCRCRPRVTGLRCDTVPGAYNPPYC 720  
Db 661 CQCSFPGHGFSCVPCCHCSAGSLHAACDPRSGQSCRCRPRVTGLRCDTVPGAYNPPYC 720  
Qy 721 EAGSCHPAGLAVDPALPAQVPCMCRAHVEGSDCRCKPGFWGLSPNPGCTRCSCDL 780  
Db 721 EAGSCHPAGLAVDPALPAQVPCMCRAHVEGSDCRCKPGFWGLSPNPGCTRCSCDL 780  
Qy 781 RGTGLGVASQCGTGQCFKPHVCGOACASCKDGFGLDQADYFCRCRCRDIGGALQOS 840  
Db 781 RGTGLGVASQCGTGQCFKPHVCGOACASCKDGFGLDQADYFCRCRCRDIGGALQOS 840  
Qy 841 CEPRTGVCRCRNTQGTCEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFN 900  
Db 841 CEPRTGVCRCRNTQGTCEPARDHYLPDLHLRLLELEEAATPEGHAVRFGFNPLEFN 900  
Qy 901 FSNRGYAQAPQPRIVARILNTSPDLFWLVRYVNRGAMSVGRVSVREGRSAACANC 960  
Db 901 FSNRGYAQAPQPRIVARILNTSPDLFWLVRYVNRGAMSVGRVSVREGRSAACANC 960  
Qy 961 TAQSQVAPPPSTEPAFITVPQGFGEPPVLNPGTWALRVEABGVLLDYVLLPSAYYEA 1020  
Db 961 TAQSQVAPPPSTEPAFITVPQGFGEPPVLNPGTWALRVEABGVLLDYVLLPSAYYEA 1020  
Qy 1021 ALLQILRVTEACTYRPAQSGDNCLLYTHLPDGGPSAAGLEALCQDNLSPRCPTEQL 1080  
Db 1021 ALLQILRVTEACTYRPAQSGDNCLLYTHLPDGGPSAAGLEALCQDNLSPRCPTEQL 1080  
Qy 1081 SPSPHPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140  
Db 1081 SPSPHPLITCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140  
Qy 1141 SLHPCLYSTLCRGTAQDQHLAVFHLDSASVRLTAEQARFHLGVTLVPIEESPEFV 1200  
Db 1141 SLHPCLYSTLCRGTAQDQHLAVFHLDSASVRLTAEQARFHLGVTLVPIEESPEFV 1200  
Qy 1201 EPRVSCISSHGATGPNSAACLPSPFPKPPQPIITLRDCQVILPPLPGPLTHAQDLTPATSP 1260  
Db 1201 EPRVSCISSHGATGPNSAACLPSPFPKPPQPIITLRDCQVILPPLPGPLTHAQDLTPATSP 1260

Qy 1261 AGPRPRPPTAVDPDAEPTLLREPOATVVTFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320  
Db 1261 AGPRPRPPTAVDPDAEPTLLREPOATVVTFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320  
Qy 1321 AGRVQGHANASFCPHGCGCRTLVCEGALLDVTHSELVTVRVPEGRWLDVVLVVP 1380  
Db 1321 AGRVQGHANASFCPHGCGCRTLVCEGALLDVTHSELVTVRVPEGRWLDVVLVVP 1380  
Qy 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASLSLFYNNGARPCGC 1440  
Db 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSSLFCRNAAASLSLFYNNGARPCGC 1440  
Qy 1441 HEVGATGPTCEBFGGQCPCHAHVIGRDCSRCATGWGPNPNCRPCDCGARLDELTCGOCIC 1500  
Db 1441 HEVGATGPTCEBFGGQCPCHAHVIGRDCSRCATGWGPNPNCRPCDCGARLDELTCGOCIC 1500  
Qy 1501 PRPTTPDCLLQCPQTFGCHPLVGCCECNCSGPGI:QELTDPTCDTDSGCKCRPNVTGR 1560  
Db 1501 PRPTTPDCLLQCPQTFGCHPLVGCCECNCSGPGI:QELTDPTCDTDSGCKCRPNVTGR 1560  
Qy 1561 CDTCSFPGHYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCOSLGTSFLDAA 1620  
Db 1561 CDTCSFPGHYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCOSLGTSFLDAA 1620  
Qy 1621 NPKGCTRCFCGATERCRSSSYTROBFVDMEGWLLSTDRQVVPHERQPGTEMLRADLRH 1680  
Db 1621 NPKGCTRCFCGATERCRSSSYTROBFVDMEGWLLSTDRQVVPHERQPGTEMLRADLRH 1680  
Qy 1681 VPEAVPEAPPELWQAPPYSLGDRVSSYGGTLRLYLHSETQSGDVVFMESRDPVVLQGN 1740  
Db 1681 VPEAVPEAPPELWQAPPYSLGDRVSSYGGTLRLYLHSETQSGDVVFMESRDPVVLQGN 1740  
Qy 1741 QMSITILEPAYPTPGHVHGGQLQVEGNFRHTETNTVSREELMMVLASLEQLQIRALFS 1800  
Db 1741 QMSITILEPAYPTPGHVHGGQLQVEGNFRHTETNTVSREELMMVLASLEQLQIRALFS 1800  
Qy 1801 QISSAVSLRRVALLEVASPAGQAGALASNVLCICPASYRGDSQCBAPGYRVDVKGFLGR 1860  
Db 1801 QISSAVSLRRVALLEVASPAGQAGALASNVLCICPASYRGDSQCBAPGYRVDVKGFLGR 1860  
Qy 1861 CVPCQCHGSHDRCLPGSGVCTVCOHNTGACRQAGFMSRRDDPSAPCVSCPCPLSV 1920  
Db 1861 CVPCQCHGSHDRCLPGSGVCTVCOHNTGACRQAGFMSRRDDPSAPCVSCPCPLSV 1920  
Qy 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSNGDPNLL 1980  
Db 1921 SNNFAEGCVLRGGRTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSNGDPNLL 1980  
Qy 1981 FSDCDPLTGACRCGLRHTTGPCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPSHGC 2040  
Db 1981 FSDCDPLTGACRCGLRHTTGPCEICAPGYGNALLPGNCTRCDCCTPCGTEACDPSHGC 2040  
Qy 2041 LCKAGVTGRCDRCQEGHFGNGCGCRPCACGPAAGSECHPQSQCHCRPOTMGPOCR 2100  
Db 2041 LCKAGVTGRCDRCQEGHFGNGCGCRPCACGPAAGSECHPQSQCHCRPOTMGPOCR 2100  
Qy 2101 ECAPGYWGLPEQGRRCQCPGGRCDPHTRCNCPPGLSBERCDTCSQHQVVPVGGPVGH 2160  
Db 2101 ECAPGYWGLPEQGRRCQCPGGRCDPHTRCNCPPGLSBERCDTCSQHQVVPVGGPVGH 2160  
Qy 2161 SIHCEVCHDCVWLLDLLEBAGALLPAIHEQLRGINASSMAWARLHRLNASIADLOSQR 2220  
Db 2161 SIHCEVCHDCVWLLDLLEBAGALLPAIHEQLRGINASSMAWARLHRLNASIADLOSQR 2220  
Qy 2221 SPLGPRHETAQOQLEVLBQQSTSLGQDARRLGQAVGTRDOASQLLAGTEATLGHAKTLA 2280  
Db 2221 SPLGPRHETAQOQLEVLBQQSTSLGQDARRLGQAVGTRDOASQLLAGTEATLGHAKTLA 2280  
Qy 2281 AIRAVDTLSELMSOTCHILGLANASPSGQQLRTLAEBVRLLEWNRARDLGAPQAAEA 2340  
Db 2281 AIRAVDTLSELMSOTCHILGLANASPSGQQLRTLAEBVRLLEWNRARDLGAPQAAEA 2340

QY 2341 ELAAQRLLARVOEQSSILEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAOE 2400  
DB 2341 ELAAQRLLARVOEQSSILEENQALATQTRDLRAQHEAGLMDLREALNRAVDATREAOE 2400  
QY 2401 LNSRNOERLEALQKQELSRDNATLQATLHAARTLASVRLHSLDQAKBEELERLAAS 2460  
DB 2401 LNSRNOERLEALQKQELSRDNATLQATLHAARTLASVRLHSLDQAKBEELERLAAS 2460  
QY 2461 LDGARTPLLQRMQTFSPAGSKLRLVEAAEAAHQQLGQALANLSSIIILDNQDRLTQRAIE 2520  
DB 2461 LDGARTPLLQRMQTFSPAGSKLRLVEAAEAAHQQLGQALANLSSIIILDNQDRLTQRAIE 2520  
QY 2521 ASNAYSRILOAVQAAEDAAQALQADHTWATVVRQGLVDRQAQQLLANSTALEAMLOEQ 2580  
DB 2521 ASNAYSRILOAVQAAEDAAQALQADHTWATVVRQGLVDRQAQQLLANSTALEAMLOEQ 2580  
QY 2581 QRLGLVWALQCARQLDRVRAKQDLQEAHICAAQAMLANDTDETSKKIAHAKAVAAEAQ 2640  
DB 2581 QRLGLVWALQCARQLDRVRAKQDLQEAHICAAQAMLANDTDETSKKIAHAKAVAAEAQ 2640  
QY 2641 DTATRVQSQLOAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTLPOLLAKLISIL 2700  
DB 2641 DTATRVQSQLOAMQENVERWQOYEGRLRGQDLGOAVLDAGHSVSTLEKTLPOLLAKLISIL 2700  
QY 2701 ENRGVHNASIALSASIGRVERELIAQARGAASVKVPMKFNHSGVQLRTPRDLAALAYT 2760  
DB 2701 ENRGVHNASIALSASIGRVERELIAQARGAASVKVPMKFNHSGVQLRTPRDLAALAYT 2760  
QY 2761 ALKFYLGQPEPPGQGTEDRFVWYMGSRQATGDYMSLRDKKXVHWVYQLGEGAPVLSI 2820  
DB 2761 ALKFYLGQPEPPGQGTEDRFVWYMGSRQATGDYMSLRDKKXVHWVYQLGEGAPVLSI 2820  
QY 2821 DEDIGEQFAAASLDRTLOFQGHMSVTVVERQMIQETKGDVPAQAEGLNLRPDPFVYVGG 2880  
DB 2821 DEDIGEQFAAASLDRTLOFQGHMSVTVVERQMIQETKGDVPAQAEGLNLRPDPFVYVGG 2880  
QY 2881 YSTFTFPPLLPFPYRGCIEMDTLNEEVVSLYNFERTFQDVTADVRPCARSKSTGDPWL 2940  
DB 2881 YSTFTFPPLLPFPYRGCIEMDTLNEEVVSLYNFERTFQDVTADVRPCARSKSTGDPWL 2940  
QY 2941 TDGSLYLDGTGTFARISFDSQISTTKRPEQBLRVSVSGVLFFLKQOSQFCLAVQSGSLVL 3000  
DB 2941 TDGSLYLDGTGTFARISFDSQISTTKRPEQBLRVSVSGVLFFLKQOSQFCLAVQSGSLVL 3000  
QY 3001 LYDFGAGLKKAVLPQPPPLTSASKAIQVFLGSGSKRVLVVERATVSVSEQDNDLELA 3060  
DB 3001 LYDFGAGLKKAVLPQPPPLTSASKAIQVFLGSGSKRVLVVERATVSVSEQDNDLELA 3060  
QY 3061 DAYILGGVPPDQLPPSLRMLFPTGGSVRCVKGIKALGKYVDLKLNTTGVSACTADLL 3120  
DB 3061 DAYILGGVPPDQLPPSLRMLFPTGGSVRCVKGIKALGKYVDLKLNTTGVSACTADLL 3120  
QY 3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSNADSAALYYRASPDGLCOVSLQOGR 3180  
DB 3121 VGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSNADSAALYYRASPDGLCOVSLQOGR 3180  
QY 3181 VSIQLLRTVKTQAGPADGAPHVAFYSNATGWLYVDDQLQOMKPHRGPPPELPQPEG 3240  
DB 3181 VSIQLLRTVKTQAGPADGAPHVAFYSNATGWLYVDDQLQOMKPHRGPPPELPQPEG 3240  
QY 3241 PPRLLGLGPESGTTINFGSCISNVFQBLGSPQVDFDLOQNLGSVNVSTGCPALQOAT 3300  
DB 3241 PPRLLGLGPESGTTINFGSCISNVFQBLGSPQVDFDLOQNLGSVNVSTGCPALQOAT 3300  
QY 3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGLARH 3360  
DB 3301 PGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGLARH 3360  
QY 3361 RNWPSLSMHVLPSSRGLLIFTARLPSPGSLALFLSNGHFVAQMEGLGTRLRASQRORS 3420  
DB 3361 RNWPSLSMHVLPSSRGLLIFTARLPSPGSLALFLSNGHFVAQMEGLGTRLRASQRORS 3420  
QY 3421 RPRGWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAHEPQPHTLFVGGLPASSHSSK 3480

DB 3421 RPRGWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAHEPQPHTLFVGGLPASSHSSK 3480  
QY 3481 LPVTVGFSGCVKXRLRHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLTLDFCATL 3540  
DB 3481 LPVTVGFSGCVKXRLRHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLTLDFCATL 3540  
QY 3541 PDVGLLEVRPLAVTGLIFHLGOARTPPYLOLQVTEKQVLLRADDGAGSFSTSVTPSVL 3600  
DB 3541 PDVGLLEVRPLAVTGLIFHLGOARTPPYLOLQVTEKQVLLRADDGAGSFSTSVTPSVL 3600  
QY 3601 CDGQWHLAVMKSGNVLRLVDAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQWPWPPA 3660  
DB 3601 CDGQWHLAVMKSGNVLRLVDAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQWPWPPA 3660  
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DB 3661 YCGCMRLAVNRSPVAMTRSVVHGAVGASGCPAA 3695  
  
RESULT 2  
US-10-312-352-22  
; Sequence 22, Application US/10312352  
; Publication No. US20040053824A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom  
; APPLICANT: YUE, Henry; AZIMZAI, Yalda  
; APPLICANT: HE, Ann; BATRA, Sajeev  
; APPLICANT: LO, Terence P.; NGUYEN, Dannel B.  
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.  
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam  
; APPLICANT: BURFORD, Neil; YAO, Monique G.  
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.  
; APPLICANT: ARVIZO, Chandra S.; KHAN, Farrah A.  
; APPLICANT: BOUGHN, Mariah R.; HAFALIA, April, J.A.  
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.  
; APPLICANT: LU, Yan; BOROWSKY, Mark L.  
; APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi  
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal  
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.  
; APPLICANT: XU, Yuming; KALLICK, Deborah A.  
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha  
; APPLICANT: DELEGANE, Angelo M.; LEE, Sally  
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES  
; FILE REFERENCE: PF-0794 USN  
; CURRENT APPLICATION NUMBER: US/10/312,352  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: PCT/US01/21067  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215,454  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/219,462  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 60/240,111  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: US 60/240,106  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: US 60/244,021  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/248,887  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/249,570  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PERL Program  
; SEQ ID NO 22  
; LENGTH: 3695  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1



US-10-312-352-22

Query Match				99.9%; Score 20104; DB 12; Length 3695;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 3694; Conservative				0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MAKRLCAGSALCVRGPRGAPALLVGLALLGAARABEAGGFSLHPFYFNLABGARIAA	60				
DB	1	MAKRLCAGSALCVRGPRGAPALLVGLALLGAARABEAGGFSLHPFYFNLABGARIAA	60				
QY	61	SATCGEAPARGSPRTEDLYCKLVGGPVAGDPMQTIIRGOYCDICTAANSNKKAHPASNA	120				
DB	61	SATCGEAPARGSPRTEDLYCKLVGGPVAGDPMQTIIRGOYCDICTAANSNKKAHPASNA	120				
QY	121	IDGTERWQSPPLSRGLENYENVNVLIDGVPHVAVYLKFNANPRPOLWYLRSMDFGR	180				
DB	121	IDGTERWQSPPLSRGLENYENVNVLIDGVPHVAVYLKFNANPRPOLWYLRSMDFGR	180				
QY	181	TYQWQFFASSKDCLEERGPOTLERITDDAAICTTEYSRIVLPLENGEIVVSVLVNRP	240				
DB	181	TYQWQFFASSKDCLEERGPOTLERITDDAAICTTEYSRIVLPLENGEIVVSVLVNRP	240				
QY	241	AMNFSYPLLRFTKATNVLRLFLRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC	300				
DB	241	AMNFSYPLLRFTKATNVLRLFLRNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC	300				
QY	301	VCHGHADACDAKDPDTPFLQCTCOHNTCGGTCDRCPCGFENQCPKATANSANECOSCN	360				
DB	301	VCHGHADACDAKDPDTPFLQCTCOHNTCGGTCDRCPCGFENQCPKATANSANECOSCN	360				
QY	361	CYGHATDCYDDEVRDRRASQSLDGTYYGGVYDCQHHTAGVNCERCLPGFYRSPNHPL	420				
DB	361	CYGHATDCYDDEVRDRRASQSLDGTYYGGVYDCQHHTAGVNCERCLPGFYRSPNHPL	420				
QY	421	DSPHVCRRNCESDFTDGTCDLTCRCYCRPNFSGERCDCVCAEGFTGPPSCYTPPSSND	480				
DB	421	DSPHVCRRNCESDFTDGTCDLTCRCYCRPNFSGERCDCVCAEGFTGPPSCYTPPSSND	480				
QY	481	TREQVLPAQOIVNDCSAAGTQGNACRXDPRVGRCLCKPNFGQTHCBLCAPFGYGPQCP	540				
DB	481	TREQVLPAQOIVNDCSAAGTQGNACRXDPRVGRCLCKPNFGQTHCBLCAPFGYGPQCP	540				
QY	541	CCQSPGVADDCDPTQCRCRVFEATCDRCAPGVFHPFLCQLCGSCGAPGTLPEGCD	600				
DB	541	CCQSPGVADDCDPTQCRCRVFEATCDRCAPGVFHPFLCQLCGSCGAPGTLPEGCD	600				
QY	601	EAGRCLCOPEFAGPHCDRCRPGYHGFPCNQACTCDPRGALDQLCGAGGLCRCPGYTGTA	660				
DB	601	EAGRCLCOPEFAGPHCDRCRPGYHGFPCNQACTCDPRGALDQLCGAGGLCRCPGYTGTA	660				
QY	661	COECSPGHGPRSCVPHCSAEGSLHAACDPRSGQSCRPVTCGLRCDTCVPGAYNEPYC	720				
DB	661	COECSPGHGPRSCVPHCSAEGSLHAACDPRSGQSCRPVTCGLRCDTCVPGAYNEPYC	720				
QY	721	EAGSCHPAGLAPVDPALPEAVPCMCRAHVEGSPCDRCCKPGFGLSPSNPEGCTRCSCDL	780				
DB	721	EAGSCHPAGLAPVDPALPEAVPCMCRAHVEGSPCDRCCKPGFGLSPSNPEGCTRCSCDL	780				
QY	781	RGLTGLVAECQPGTQGCCKHVCGQACCKDGFGLDQADYEGCRSCDITGGALGQS	840				
DB	781	RGLTGLVAECQPGTQGCCKHVCGQACCKDGFGLDQADYEGCRSCDITGGALGQS	840				
QY	841	CSPTGVCRCRPNTOGPTCEPARDHYLPDLHLHLRLELEAAATPEGHAVRFGFNPLEFEN	900				
DB	841	CSPTGVCRCRPNTOGPTCEPARDHYLPDLHLHLRLELEAAATPEGHAVRFGFNPLEFEN	900				
QY	901	FSWRGVAQMAVQPRIVARLNLTSDDLFWLVFRVYVNRGAMSVGRVSVREGRSAACANC	960				
DB	901	FSWRGVAQMAVQPRIVARLNLTSDDLFWLVFRVYVNRGAMSVGRVSVREGRSAACANC	960				
QY	961	TAQSQFVAFPPSTEPAFITVQRFGEFVFLNPGTQWALRVEABGVLLDYVLLPSAYYEA	1020				
DB	961	TAQSQFVAFPPSTEPAFITVQRFGEFVFLNPGTQWALRVEABGVLLDYVLLPSAYYEA	1020				

QY	1021	ALLQLRVTEACTYRSASQSGDNCLLYTHLPDGFPSAAGLEALCRODNSLPRCPTEQL	1080				
DB	1021	ALLQLRVTEACTYRSASQSGDNCLLYTHLPDGFPSAAGLEALCRODNSLPRCPTEQL	1080				
QY	1081	SPSHPLITCTGSDVDVQVAVPOPGRYALVYANEDARQEVGVAVHTPQAPQOGLL	1140				
DB	1081	SPSHPLITCTGSDVDVQVAVPOPGRYALVYANEDARQEVGVAVHTPQAPQOGLL	1140				
QY	1141	SLHPLCLYSLTCRGATARDTQDLAVFHLDSASVRLTAEQARFFLHGVTLPVIEPSPFEV	1200				
DB	1141	SLHPLCLYSLTCRGATARDTQDLAVFHLDSASVRLTAEQARFFLHGVTLPVIEPSPFEV	1200				
QY	1201	EPVSCISSHGAFGPNASACLPSRFPKPPQPIILDCQVILPLPPGLPLTHAQDLTPATSP	1260				
DB	1201	EPVSCISSHGAFGPNASACLPSRFPKPPQPIILDCQVILPLPPGLPLTHAQDLTPATSP	1260				
QY	1261	AGPRPRPTAVDPDAEPTLLREPOATVVTHVTLGRYAPLLHGYOPAPHTPFEVILN	1320				
DB	1261	AGPRPRPTAVDPDAEPTLLREPOATVVTHVTLGRYAPLLHGYOPAPHTPFEVILN	1320				
QY	1321	AGRVWQHANASFCPHGYGCRTLVVCQALLDVTHTSELVTVRVPEGRMLWLDVYLVP	1380				
DB	1321	AGRVWQHANASFCPHGYGCRTLVVCQALLDVTHTSELVTVRVPEGRMLWLDVYLVP	1380				
QY	1381	ENVYSGYLREBPLDKSYDFISHCAAQYHISPSSSLFCENAAASLSLFYNGARPCGC	1440				
DB	1381	ENVYSGYLREBPLDKSYDFISHCAAQYHISPSSSLFCENAAASLSLFYNGARPCGC	1440				
QY	1441	HEVGATGTCFPGGQCPCHAHVIGRDCSRCATGYWGFPMCRPCDCGALCDELTGOCIC	1500				
DB	1441	HEVGATGTCFPGGQCPCHAHVIGRDCSRCATGYWGFPMCRPCDCGALCDELTGOCIC	1500				
QY	1501	PRRTIPDCLLCOPTGCHPLVGCBCNCSGPGIQELTDPCTDSDGQCKCPNVTGR	1560				
DB	1501	PRRTIPDCLLCOPTGCHPLVGCBCNCSGPGIQELTDPCTDSDGQCKCPNVTGR	1560				
QY	1561	CDTCSPGFHGPRCRPCDCHAGTAPGVCDPLTQCYCKENVQKPKCDQCSLGTSLDAA	1620				
DB	1561	CDTCSPGFHGPRCRPCDCHAGTAPGVCDPLTQCYCKENVQKPKCDQCSLGTSLDAA	1620				
QY	1621	NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWLLSTDQVVPHERQPTGTEMLRADLRH	1680				
DB	1621	NPKGTRCFCFGATERCRSSSYTRQEFVDMEGWLLSTDQVVPHERQPTGTEMLRADLRH	1680				
QY	1681	VPEAVPEAPFELYWOAPPSYLGDRVSSYGGTLRYELHSETQRGDVFVPMESRPDVVLQGN	1740				
DB	1681	VPEAVPEAPFELYWOAPPSYLGDRVSSYGGTLRYELHSETQRGDVFVPMESRPDVVLQGN	1740				
QY	1741	QMSITFLEPAYTPGHVHRGOLQIVEGNFRHTTNTVSEELMMVLASLEQLQIRALFS	1800				
DB	1741	QMSITFLEPAYTPGHVHRGOLQIVEGNFRHTTNTVSEELMMVLASLEQLQIRALFS	1800				
QY	1801	QISSAVSLRRVALEVASPAGOGALASNVELCLCPASVYRGDSQCECAPGFYRDYKGLFLGR	1860				
DB	1801	QISSAVSLRRVALEVASPAGOGALASNVELCLCPASVYRGDSQCECAPGFYRDYKGLFLGR	1860				
QY	1861	CVPCQCHGSDRCLPGSGVCDQHNTEGAHCRCQAGFMSSRDDPSAPCVSCPCPLSVP	1920				
DB	1861	CVPCQCHGSDRCLPGSGVCDQHNTEGAHCRCQAGFMSSRDDPSAPCVSCPCPLSVP	1920				
QY	1921	SNFPAEGCVLAGGRTQCLCKPGYAGASCERCAPGFNGNPLVLGSSCQPCDCSNGDPLNLL	1980				
DB	1921	SNFPAEGCVLAGGRTQCLCKPGYAGASCERCAPGFNGNPLVLGSSCQPCDCSNGDPLNLL	1980				
QY	1981	FSDCDPLTGACRGLRHTTGTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPSHGC	2040				
DB	1981	FSDCDPLTGACRGLRHTTGTGPRCEICAPGFYGNALLPGNCTRCDCCTPCGTEACDPSHGC	2040				
QY	2041	LCKAGVTGRRCDRCQEGHFGFNCGGCRPCACGPAAGSECHPQSGQCHCRPOTMGPOCR	2100				
DB	2041	LCKAGVTGRRCDRCQEGHFGFNCGGCRPCACGPAAGSECHPQSGQCHCRPOTMGPOCR	2100				

2101 ECAPGWGLPEOGRRCQPCGRCDPHTGRCNCPPGLSGERCDCSCQOHOVPPVPGVGH 2160  
2101 ECAPGWGLPEOGRRCQPCGRCDPHTGRCNCPPGLSGERCDCSCQOHOVPPVPGVGH 2160  
2161 SHCEVCDHCVVLLDDLERAGALLPAIHEQRLGINASSMAWARHLRLNASIADIQSOLR 2220  
2161 SHCEVCDHCVVLLDDLERAGALLPAIHEQRLGINASSMAWARHLRLNASIADIQSOLR 2220  
2221 SPLGPRHETAQOILEVLEBOGSTSLGQDARLGGQAVGTTRDOASOLLAGTEATIGHAKTLLA 2280  
2221 SPLGPRHETAQOILEVLEBOGSTSLGQDARLGGQAVGTTRDOASOLLAGTEATIGHAKTLLA 2280  
2281 ATRAVDRITSELMSOTGHILGLANASAPSGEQLLRTLAEVERLLWENRARDLGAPOAAAEA 2340  
2281 ATRAVDRITSELMSOTGHILGLANASAPSGEQLLRTLAEVERLLWENRARDLGAPOAAAEA 2340  
2341 ELAAAQRLARVOEQULSSWEENQALATOTDRRLAQHEAGLMDLRALNRAVDATREAOE 2400  
2341 ELAAAQRLARVOEQULSSWEENQALATOTDRRLAQHEAGLMDLRALNRAVDATREAOE 2400  
2401 LNSRNERLEALORQEISRDNATIQAATHARDTLASVFRLLHSLDOAKEELERLAAS 2460  
2401 LNSRNERLEALORQEISRDNATIQAATHARDTLASVFRLLHSLDOAKEELERLAAS 2460  
2461 LDGARTPLLRQMOTFSPAGSKLRLVEAAEAHAQOLQALNLSIIILDVNOQLTORAIE 2520  
2461 LDGARTPLLRQMOTFSPAGSKLRLVEAAEAHAQOLQALNLSIIILDVNOQLTORAIE 2520  
2521 ASNAYSRILOQAADAEADQAALQOQADHTWATVVRGLVDRAQOQLLANSTALEAMLOEQ 2580  
2521 ASNAYSRILOQAADAEADQAALQOQADHTWATVVRGLVDRAQOQLLANSTALEAMLOEQ 2580  
2581 ORLGLVWAALQOQARTLDRVRKDDQLEAHIQAQAMLAMMDTDETSKKIAHAKAVAAEAQ 2640  
2581 ORLGLVWAALQOQARTLDRVRKDDQLEAHIQAQAMLAMMDTDETSKKIAHAKAVAAEAQ 2640  
2641 DTATRVQSOLOAMQENVERVQOQVEGLRGQDLQAVLDAGHSYSTLEKTLPLQAKLSIL 2700  
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2701 ENRGVHNASIALSASIGRVELIAQARGAASKVPMKFNKRSQVQVLRPRDLADLAAYT 2760  
2701 ENRGVHNASIALSASIGRVELIAQARGAASKVPMKFNKRSQVQVLRPRDLADLAAYT 2760  
2761 ALKFYLOQPEPEPCQGTEDRFVMTMGSRQATGDMVGSRLDKKXVHWYQVLEAGPAVLSI 2820  
2761 ALKFYLOQPEPEPCQGTEDRFVMTMGSRQATGDMVGSRLDKKXVHWYQVLEAGPAVLSI 2820  
2821 DEDIGEPAAVSLDRTLOFGHMSVTVROMIQETKGTAVAPGAEGLLNLRPDDFVFVGG 2880  
2821 DEDIGEPAAVSLDRTLOFGHMSVTVROMIQETKGTAVAPGAEGLLNLRPDDFVFVGG 2880  
2881 YPSTFTPLPLRFPYRGCIEMDTLNEEWSLYNFERTFQDITAVDRPCARSKSTGDPWL 2940  
2881 YPSTFTPLPLRFPYRGCIEMDTLNEEWSLYNFERTFQDITAVDRPCARSKSTGDPWL 2940  
2941 TDGSYLDGTGPARISFDSQISTTKRFEQELNVSGLVFLKQOQSOFLCLAVOEGSLVL 3000  
2941 TDGSYLDGTGPARISFDSQISTTKRFEQELNVSGLVFLKQOQSOFLCLAVOEGSLVL 3000  
3001 LYDFGAGLKKAVPLOPPPLTSASKAIOVFLGGSRRKVLVRVERATVYSVEQNDLELA 3060  
3001 LYDFGAGLKKAVPLOPPPLTSASKAIOVFLGGSRRKVLVRVERATVYSVEQNDLELA 3060  
3061 DAYILGGVPPQOLPPSLRWLREPTGSGVRGCVKGIKALQKYVDLKLNTTGVSACTADLL 3120  
3061 DAYILGGVPPQOLPPSLRWLREPTGSGVRGCVKGIKALQKYVDLKLNTTGVSACTADLL 3120  
3121 VGRAMTEHGHFLRLALSNVAPLTONVYSGFGPHSAQDSALLYRYRASPDLGLCOVSLQOGR 3180  
3121 VGRAMTEHGHFLRLALSNVAPLTONVYSGFGPHSAQDSALLYRYRASPDLGLCOVSLQOGR 3180  
3181 VSLQLLRTEVTKOAGFADGAPHYAFYSNATGVMWLYDDQLQOMKPHRGPPPELQOPEG 3240

3181 VSLQLLRTEVTKOAGFADGAPHYAFYSNATGVMWLYDDQLQOMKPHRGPPPELQOPEG 3240  
3241 PPRLLGLGPESGTIYNFSGCISNVFQRLGQORVFDLQONLGSVNVSTGCPALQAOQT 3300  
3241 PPRLLGLGPESGTIYNFSGCISNVFQRLGQORVFDLQONLGSVNVSTGCPALQAOQT 3300  
3301 PGLGPRGLQATARKASRRSQPARHPACMLPPHLRTRDSYQFGGSLSSHLEFVGILARH 3360  
3301 PGLGPRGLQATARKASRRSQPARHPACMLPPHLRTRDSYQFGGSLSSHLEFVGILARH 3360  
3361 RNWPSLSMHWLPRSSRGLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRORS 3420  
3361 RNWPSLSMHWLPRSSRGLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLRAQSRORS 3420  
3421 RPSGWHKVSVRWEKNRILLVTDGARAWSQBGRHQHQAHPQPHITLFGVGLPASSHSSK 3480  
3421 RPSGWHKVSVRWEKNRILLVTDGARAWSQBGRHQHQAHPQPHITLFGVGLPASSHSSK 3480  
3481 LPVTGVSFGCVKRLRLHGRPLGAPTRVAGVTPCPLGLEAGLPPGSGGVITLDPGATL 3540  
3481 LPVTGVSFGCVKRLRLHGRPLGAPTRVAGVTPCPLGLEAGLPPGSGGVITLDPGATL 3540  
3541 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLRADDDGAGEFSTSVTRPSVL 3600  
3541 PDVGLLEVRPLAVTGLIFHLGQARTPPYLQVTEKQVLRADDDGAGEFSTSVTRPSVL 3600  
3601 CDGQWHLRANVMKSNVLRLEVDASQNHVTPGLLAAAAGAPAPLYLGLPEPMAVQMPWPPA 3660  
3601 CDGQWHLRANVMKSNVLRLEVDASQNHVTPGLLAAAAGAPAPLYLGLPEPMAVQMPWPPA 3660  
3661 YCGCMRRLANVRSPVAMTRSVVEHGVAGSGCPAA 3695  
3661 YCGCMRRLANVRSPVAMTRSVVEHGVAGSGCPAA 3695

RESULT 3

US-10-312-088-31  
; Sequence 31, Application US/10312088  
; Publication No. US20030219862A1  
; GENERAL INFORMATION:  
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; APPLICANT: Cogswell, John P.  
; APPLICANT: Kabnic, Karen S.  
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; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Strum, Jay C.  
; APPLICANT: Xiang, Zhaoqing  
; APPLICANT: Xie, Qing  
; APPLICANT: Rizni, Safia K.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50029  
; CURRENT APPLICATION NUMBER: US/10312,088  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/19929  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,161  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/213,156  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 3696  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-312-088-31

Query Match 99.7%; Score 20060.5; DB 15; Length 3696;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3687; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 MAXELCAGSALCVRGPRGPAPLLVGLALGAARAREEAGGFSLHPYFVNLAEARITAA 60  
DB 1 MAXELCAGSALCVRGPRGPAPLLVGLALGAARAREEAGGFSLHPYFVNLAEARITAA 60  
QY 61 SATCEAPARGSPRPTEDELYCKLVGPGVAGDPNQTIRGOVCDICTAANSKNAHPASNA 120  
DB 61 SATCEAPARGSPRPTEDELYCKLVGPGVAGDPNQTIRGOVCDICTAANSKNAHPASNA 120  
QY 121 IDGTERWQSPPLSRGLSEYNEVNVTLDLGVFHVAVVLIKFANSRPRDLWVLSRMDFR 180  
DB 121 IDGTERWQSPPLSRGLSEYNEVNVTLDLGVFHVAVVLIKFANSRPRDLWVLSRMDFR 180  
QY 181 TYQWQPFASKRDCLERPOFOTILERITRDDAAICTTEYSRIVPLENGEIVVLSVNGRPG 240  
DB 181 TYQWQPFASKRDCLERPOFOTILERITRDDAAICTTEYSRIVPLENGEIVVLSVNGRPG 240  
QY 241 AMNFSYPLREFTKATNVLRLRINTLLGLHMGKALRDPVTRRYYSIKDISIGRC 300  
DB 241 AMNFSYPLREFTKATNVLRLRINTLLGLHMGKALRDPVTRRYYSIKDISIGRC 300  
QY 301 VCHGHADACAKDPTDFRLOCTCOHNTCGTCDRCPCPGFNQOPWKPATANSANCQCN 360  
DB 301 VCHGHADACAKDPTDFRLOCTCOHNTCGTCDRCPCPGFNQOPWKPATANSANCQCN 360  
QY 361 CYGHATDCYDPEVDRRERASQSLDGTVQGGVVICDQHHTAGVNCERCLPGFYRSPNHL 420  
DB 361 CYGHATDCYDPEVDRRERASQSLDGTVQGGVVICDQHHTAGVNCERCLPGFYRSPNHL 420  
QY 421 DSPHVCRCNCESDFTDGTCEDEITGRCYCRPNFSGRCDVCAEGTGPSPCYPTSSND 480  
DB 421 DSPHVCRCNCESDFTDGTCEDEITGRCYCRPNFSGRCDVCAEGTGPSPCYPTSSND 480  
QY 481 TREOVLPAQIVNDCSAAQTQGNACRKPVRGRCLCKENFQGTCHCELCAFGYFGGQOP 540  
DB 481 TREOVLPAQIVNDCSAAQTQGNACRKPVRGRCLCKENFQGTCHCELCAFGYFGGQOP 540  
QY 541 CQCSRGVADRCDPTQOCRCRVGEGATCDRCABGYFHFPLCOLCGCSFAGTLPEGCD 600  
DB 541 CQCSRGVADRCDPTQOCRCRVGEGATCDRCABGYFHFPLCOLCGCSFAGTLPEGCD 600  
QY 601 EAGCLCOPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGSLCRCPGYTGA 660  
DB 601 EAGCLCOPEFAGPHCDRCRPGYHGFNCOACTCDPRGALDQLCGAGSLCRCPGYTGA 660  
QY 661 CQCSRGVADRCDPTQOCRCRVGEGATCDRCABGYFHFPLCOLCGCSFAGTLPEGCD 720  
DB 661 CQCSRGVADRCDPTQOCRCRVGEGATCDRCABGYFHFPLCOLCGCSFAGTLPEGCD 720  
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVGEFSCDRCRKPFWGLSPSNPEGCTRCSDL 780  
DB 721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVGEFSCDRCRKPFWGLSPSNPEGCTRCSDL 780  
QY 781 RGTLLGVVAECQGTGOCFKPHYCGOACASCKDGFGLDQADYFCRCRCRCDIGALGOS 840  
DB 781 RGTLLGVVAECQGTGOCFKPHYCGOACASCKDGFGLDQADYFCRCRCRCDIGALGOS 840  
QY 841 CEPRTGVCRPNTQGTCEPARDHYLPDLHLRLLELEAAATPEGHAVRFGFNPLEFEN 900  
DB 841 CEPRTGVCRPNTQGTCEPARDHYLPDLHLRLLELEAAATPEGHAVRFGFNPLEFEN 900  
QY 901 FSRGXYQAMAPQPRIVARLNLTSPLFVLYVNRGMSVSRVYREGRSNACANC 960  
DB 901 FSRGXYQAMAPQPRIVARLNLTSPLFVLYVNRGMSVSRVYREGRSNACANC 960  
QY 961 TAQSQPVAFPPSTEPAFITVPQRFGEFVFLNPGTVALRVEAEGLLDYVLLPSAYYEA 1020  
DB 961 TAQSQPVAFPPSTEPAFITVPQRFGEFVFLNPGTVALRVEAEGLLDYVLLPSAYYEA 1020  
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLYTHPLDGFPSAAGLEALCQDNLSRCPCTEOL 1080  
DB 1021 ALLQLRVTEACTYRPSAQSGDNCLYTHPLDGFPSAAGLEALCQDNLSRCPCTEOL 1080

QY 1081 SPSHPPLITCTGSDVDVQLQVAVPOPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140  
DB 1081 SPSHPPLITCTGSDVDVQLQVAVPOPGRYALVVEYANEDARQEVGVAVHTPQAPQOGLL 1140  
QY 1141 SLHPCLYSTLCRGTDARTQDHLAVPHLDSSEASVRLTAQARFFLHGVTLVPIEFSEFV 1200  
DB 1141 SLHPCLYSTLCRGTDARTQDHLAVPHLDSSEASVRLTAQARFFLHGVTLVPIEFSEFV 1200  
QY 1201 EPRVSCISSHGAFGPNASACLPSRFPKPPQPIILRDCQVILPLPGLPLTHAQDLTPATSP 1260  
DB 1201 EPRVSCISSHGAFGPNASACLPSRFPKPPQPIILRDCQVILPLPGLPLTHAQDLTPATSP 1260  
QY 1261 AGPRPPPTAVDPDAEPDLLREPOATVVTHTVFTLGRYAEFLHGYPAPHEFTFVEVLIN 1320  
DB 1261 AGPRPPPTAVDPDAEPDLLREPOATVVTHTVFTLGRYAEFLHGYPAPHEFTFVEVLIN 1320  
QY 1321 AGRVMQGHANAFCHGPGYGCRTLVVCEQALLDVTHSELTVTVRVPKGRMLWLDVYLVP 1380  
DB 1321 AGRVMQGHANAFCHGPGYGCRTLVVCEQALLDVTHSELTVTVRVPKGRMLWLDVYLVP 1380  
QY 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSLFCRNAASLSLFFNNGARPCGC 1440  
DB 1381 ENVYSGYLREBPLDKSYDFISHCAAQGYHISPSSSLFCRNAASLSLFFNNGARPCGC 1440  
QY 1441 HEVGATGPTCEBFGQGCPCCHAHVIGRDCSRCATGYWGFNPNCRPCDCGARLCELTGQCIC 1500  
DB 1441 HEVGATGPTCEBFGQGCPCCHAHVIGRDCSRCATGYWGFNPNCRPCDCGARLCELTGQCIC 1500  
QY 1501 PRPTTPDCLLCQPTGCHPLVGCCECNCSPGIGLTDPTCDTDSGCKRCRNVNTER 1560  
DB 1501 PRPTTPDCLLCQPTGCHPLVGCCECNCSPGIGLTDPTCDTDSGCKRCRNVNTER 1560  
QY 1561 CDTSPGPHGYPRCPCDCEAGTAGVGYDPLTQCCKENVOGPKCDQCGLTFSLDA 1620  
DB 1561 CDTSPGPHGYPRCPCDCEAGTAGVGYDPLTQCCKENVOGPKCDQCGLTFSLDA 1620  
QY 1621 NPKGCTRCFCGATCERCSSTYRQEFVDMEGWLLSTDQOVVPHRQPGTEMLRADLRH 1680  
DB 1621 NPKGCTRCFCGATCERCSSTYRQEFVDMEGWLLSTDQOVVPHRQPGTEMLRADLRH 1680  
QY 1681 VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQGRDVFVPMESRDPVVLQGN 1740  
DB 1681 VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQGRDVFVPMESRDPVVLQGN 1740  
QY 1741 QMSITFLEPAYTPGCHVHRGQOLQVNEGFRHTETNTVSRRELMVNLASLEQLQIRALFS 1800  
DB 1741 QMSITFLEPAYTPGCHVHRGQOLQVNEGFRHTETNTVSRRELMVNLASLEQLQIRALFS 1800  
QY 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPASVYRGDSQCECAPGFYRDVKGLFLGR 1860  
DB 1801 QISSAVSLRRVALEVASPAGQALASNVELCLCPASVYRGDSQCECAPGFYRDVKGLFLGR 1860  
QY 1861 CVPCCOCHGSDRCLPGSGVYVDCCQNTGEGACHCERCOAGFMSSRDDPSAPCVSCPLSVP 1920  
DB 1861 CVPCCOCHGSDRCLPGSGVYVDCCQNTGEGACHCERCOAGFMSSRDDPSAPCVSCPLSVP 1920  
QY 1921 SNNPAGCVLGRGTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDNLL 1980  
DB 1921 SNNPAGCVLGRGTQCLCKPGYAGASCRCAPGFFGNPLVLGSSCQPCDCSGNGDNLL 1980  
QY 1981 FSDCDPLTGACRGLRHTTGPCEICAPGFYGNALLPNCNTRCDCTPCGTEACDPHSGHC 2040  
DB 1981 FSDCDPLTGACRGLRHTTGPCEICAPGFYGNALLPNCNTRCDCTPCGTEACDPHSGHC 2040  
QY 2041 LCKAGVTGRRCDRCOEZGHFGPNCGGCRPCACGPAAESGECHPOSGOCHCRPGTMGQCR 2100  
DB 2041 LCKAGVTGRRCDRCOEZGHFGPNCGGCRPCACGPAAESGECHPOSGOCHCRPGTMGQCR 2100  
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DB 2101 ECAPGWGLPEQGRRCOCPCGRCDPHTGRNCNCPGLSGERCDTCSQOHOVVPFGGPGVGH 2160  
QY 2161 SIHCEVCDHCVVLLDDDLERAGALLPAIHEQLRGINASSMAWRLHRLNASIADLQSOQLR 2220

Db 2161 STHCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADIQSQR 2220  
QY 2221 SPLGRPHETAQOILEVLEQOSTSLGQDARELGGQ-AVGTRDQASOLLAGEATLGHAKTLL 2279  
Db 2221 SPLGRPHETAQOILEVLEQOSTSLGQDARELGGQAAVGTRDQASOLLAGEATLGHAKTLL 2280  
QY 2280 AAIKAVDRTLSELMSOTGHILGANASAPSGEQLLRTLAEVERLLWEMRARDIGAPQAAAE 2339  
Db 2281 AAIKAVDRTLSELMSOTGHILGANASAPSGEQLLRTLAEVERLLWEMRARDIGAPQAAAE 2340  
QY 2340 AELAAQRLLARVQEOQLSWEENQALATQTRDLAQHEAGLMDIREALNRAVDATREAO 2399  
Db 2341 AELAAQRLLARVQEOQLSWEENQALATQTRDLAQHEAGLMDIREALNRAVDATREAO 2400  
QY 2400 ELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKHEELERLAA 2459  
Db 2401 ELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKHEELERLAA 2460  
QY 2460 SLDGARTPLLORMQTESPAGSKLRLVEAABAHAQQLGQLALNLSIILDVNDRLTORAI 2519  
Db 2461 SLDGARTPLLORMQTESPAGSKLRLVEAABAHAQQLGQLALNLSIILDVNDRLTORAI 2520  
QY 2520 EASNAYSRILQVCAEDAGQALQADHTWATVVRQGLVDRQAQQLANSTALEEAMLQE 2579  
Db 2521 EASNAYSRILQVCAEDAGQALQADHTWATVVRQGLVDRQAQQLANSTALEEAMLQE 2580  
QY 2580 QQSLGLVMAALQAGARTQLDRVRAKQDLQEAHQAQAAMLMDTDETSKKIAHAKVAABA 2639  
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QY 2640 QDTATRVQSOLOAQMNVERWQOQYGLRGODLQOAVILDAGHSVSTLEKTLIPOLLAKLSI 2699  
Db 2641 QDTATRVQSOLOAQMNVERWQOQYGLRGODLQOAVILDAGHSVSTLEKTLIPOLLAKLSI 2700  
QY 2700 LENRGVHNASLALSASIGRVRELLIAQGAASKVYPMKFNRSQVQLRTPRDLADLAAY 2759  
Db 2701 LENRGVHNASLALSASIGRVRELLIAQGAASKVYPMKFNRSQVQLRTPRDLADLAAY 2760  
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Db 2761 TALKFYLGQPEPPGGOTEDRFWMYMGSRQATGDYNGVSLRDKKXHWYVQLGEAGPAVLUS 2820  
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Db 2821 IDEDIGEQFAAVSLDRTLQFGHMSVTVVEROMIQETKGDVAPQAEGLLNLRPDDFFVYVG 2880  
QY 2880 GYPSFTPTPPPLRFPYRGCIEMDTLNEEVSVLYNFERTFQDLDVDRPCARSKSTGDPW 2939  
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Db 2941 LTPGSLYLDGTCFARI SPDSQISTTKBPEQLRLVSVSGVLFLLKQOSQFLCLAVQSGSLV 3000  
QY 3000 LLYDFGAGLKKAVLPLOPPPLTSASKAIQVFLGGSRKXVLRVERATVYSVEQDNDLEL 3059  
Db 3001 LLYDFGAGLKKAVLPLOPPPLTSASKAIQVFLGGSRKXVLRVERATVYSVEQDNDLEL 3060  
QY 3060 ADAYILGGVPPDQIPSLRLWLPFTGSGVRGVKGIKALGXVYDLKRLNTGVSAGCTADL 3119  
Db 3061 ADAYILGGVPPDQIPSLRLWLPFTGSGVRGVKGIKALGXVYDLKRLNTGVSAGCTADL 3120  
QY 3120 LVGRAMTFHGHGFLRLALSNAVPLTGNVSGFGFHSQAQDSALLIYRASPDGLCQVSLQOQ 3179  
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QY 3180 RVSLQLLRTVKTOAGFADGAPHYVAFYSNATGWLYVDDQLQOMKPHRGPPELOPQPE 3239  
Db 3181 RVSLQLLRTVKTOAGFADGAPHYVAFYSNATGWLYVDDQLQOMKPHRGPPELOPQPE 3240  
QY 3240 GPPELLLGGIPESGTTYNFSGCISNVFVQRLQPVDFDQNLGSGVNVSTGCPALQAO 3299

Db 3241 GPPELLLGGIPESGTTYNFSGCISNVFVQRLQPVDFDQNLGSGVNVSTGCPALQAO 3300  
QY 3300 TPGGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVGILAR 3359  
Db 3301 TPGGLGPRGLQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSHLEFVGILAR 3360  
QY 3360 HRNWPISLMSMVLPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQROR 3419  
Db 3361 HRNWPISLMSMVLPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQROR 3420  
QY 3420 SRPGRMEKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAEHQPQHTLFGVGLPASHSS 3479  
Db 3421 SRPGRMEKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAEHQPQHTLFGVGLPASHSS 3480  
QY 3480 KLPVTYVFGSGVKRLRHGRPLGAPTRMAGVTTCILGPLEAGLFFPGSGGVITLDLPGAT 3539  
Db 3481 KLPVTYVFGSGVKRLRHGRPLGAPTRMAGVTTCILGPLEAGLFFPGSGGVITLDLPGAT 3540  
QY 3540 LPDVGLELEVRPLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGFSFSTVTRPSV 3599  
Db 3541 LPDVGLELEVRPLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGFSFSTVTRPSV 3600  
QY 3600 LCDQGMHRLAVMKSGNLYRLLEVDAQSNHTVGPPLLAAAAGAPAPLYLGLPEPMVAQVWPP 3659  
Db 3601 LCDQGMHRLAVMKSGNLYRLLEVDAQSNHTVGPPLLAAAAGAPAPLYLGLPEPMVAQVWPP 3660  
QY 3660 AYCGMRRLAVNRSPVAMTRSVVEHGVAGSGCPAA 3695  
Db 3661 AYCGMRRLAVNRSPVAMTRSVVEHGVAGSGCPAA 3696

RESULT 4  
US-10-112-944-347  
; Sequence 347, Application US/10112944  
; Publication No. US20040048249A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
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; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Zhiwei  
; TITLE OF INVENTION: NO. US20040048249A1el Nucleic Acids and  
; TITLE OF INVENTION: Secreted Polypeptides  
; FILE REFERENCE: 805A  
; CURRENT APPLICATION NUMBER: US/10/112,944  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: US 09/515,136  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: US 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 09/552,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/577,408  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 924  
; SOFTWARE: pt FL\_genes Version 5.0  
; SEQ ID NO 347  
; LENGTH: 3690

; TYPE: PRT									
; ORGANISM: Homo sapiens									
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Query Match									
Best Local Similarity 99.6%; Score 20035.5; DB 12; Length 3690;									
Matches 3682; Conservative									
Mismatches 5; Indels 5; Gaps 1;									
QY	1	MAKRLCAGSALCVRGPRGAPILLVGLALLGHAARAREAGGFSLHPYFNLAEAGARIAA	60						
DB	1	MAKRLCAGSALCVRGPRGAPILLVGLALLGHAARAREAGGFSLHPYFNLAEAGARIAA	60						
QY	61	SATCGEAPARGSPRPTEDLYCKLVGGPVAGGDPNQTIRGOVCDICTAANSNKAAHPASNA	120						
DB	61	SATCGEAPARGSPRPTEDLYCKLVGGPVAGGDPNQTIRGOVCDICTAANSNKAAHPASNA	120						
QY	121	IDGTERWWSPLSRGLFNEVNVNVLDLGOVPHVAYVLIKANSRPPDLWYERSMDFGR	180						
DB	121	IDGTERWWSPLSRGLFNEVNVNVLDLGOVPHVAYVLIKANSRPPDLWYERSMDFGR	180						
QY	181	TYQPMWFFASSKRDCLEREGPOTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
DB	181	TYQPMWFFASSKRDCLEREGPOTLERITRDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
QY	241	AMNFSYPLRFBFTKATNVLRLFTNTLLGHLAKALRDTVTTRYIYSIKDISIGRC	300						
DB	241	AMNFSYPLRFBFTKATNVLRLFTNTLLGHLAKALRDTVTTRYIYSIKDISIGRC	300						
QY	301	VCHGHADACADKDPDTPFLQCTCOHNTCCGTCDCRCCPGFNQCPWKPATANSANECOSCN	360						
DB	301	VCHGHADACADKDPDTPFLQCTCOHNTCCGTCDCRCCPGFNQCPWKPATANSANECOSCN	360						
QY	361	CYGHATDCYDVEVDRARRASQLDGTYYGGGVGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420						
DB	361	CYGHATDCYDVEVDRARRASQLDGTYYGGGVGVCIDCQHHTAGVNCERCLPGFYRSPNHPL	420						
QY	421	DSPHVCRRCNCESDFTDGTCEBLTGRCYCRRNFSGERCOCVCAEGFTGPPSCYPTPSSND	480						
DB	421	DSPHVCRRCNCESDFTDGTCEBLTGRCYCRRNFSGERCOCVCAEGFTGPPSCYPTPSSND	480						
QY	481	TREQVLPAGQIVNCDCSAAAGTCGNACRDPVGRCLCKPNTQGHCHCLCAPGFGPGCQP	540						
DB	481	TREQVLPAGQIVNCDCSAAAGTCGNACRDPVGRCLCKPNTQGHCHCLCAPGFGPGCQP	540						
QY	541	CQCSSPGVADDDCDPDTGQCRVCFEGATCDRCAPGYFHPFLQCLGCGSPAGTLPBGCD	600						
DB	541	CQCSSPGVADDDCDPDTGQCRVCFEGATCDRCAPGYFHPFLQCLGCGSPAGTLPBGCD	600						
QY	601	EAGRCLCQEPFAGPHCDRCRPGYHGFPGNCQACTCDPRGALDQLCGAGGLCRCPGYTGTA	660						
DB	601	EAGRCLCQEPFAGPHCDRCRPGYHGFPGNCQACTCDPRGALDQLCGAGGLCRCPGYTGTA	660						
QY	661	CQECSPGPHGFPSCVPCHCSABGSLHAACDPRSGQSCRPVTLGLRCDTCVPGAYNPPYC	720						
DB	661	CQECSPGPHGFPSCVPCHCSABGSLHAACDPRSGQSCRPVTLGLRCDTCVPGAYNPPYC	720						
QY	721	EAGSCHPAGLAVDPALPEAQVPCRAHVGPSCDRCKPGFWGLSPSNPEGCTRCSCDL	780						
DB	721	EAGSCHPAGLAVDPALPEAQVPCRAHVGPSCDRCKPGFWGLSPSNPEGCTRCSCDL	780						
QY	781	RGTGGVAECQPGTQCFCKPHVCQAACSKDGFGLDQADYFGCRSCRCIDIGGALGQS	840						
DB	781	RGTGGVAECQPGTQCFCKPHVCQAACSKDGFGLDQADYFGCRSCRCIDIGGALGQS	840						
QY	841	CEPRTGVCRCRNTGQPTCEPARDHYLPDLHLRLLELEAATPEGHAVRFGNPLEFEN	900						
DB	841	CEPRTGVCRCRNTGQPTCEPARDHYLPDLHLRLLELEAATPEGHAVRFGNPLEFEN	900						
QY	901	FSWRGVAQMAPQVPRIVARLNLTSDFLWLVFRVNRGAMSVSRVREGRSAACANC	960						
DB	901	FSWRGVAQMAPQVPRIVARLNLTSDFLWLVFRVNRGAMSVSRVREGRSAACANC	960						
QY	961	TAQSQPVAPPPSTEPAFITVQRGFGSPFVLNPGTMAIRVEAEGVLLDYVVLPSAYYEA	1020						

961	TAQSQPVAPPPSTEPAFITVQRGFGSPFVLNPGTMAIRVEAEGVLLDYVVLPSAYYEA	1020							
1021	ALLQLRVTEACTYRPSAOCSDGNCLLYTHLPDGFPSAAGLEALCRODNSIPRCPTEQL	1080							
1021	ALLQLRVTEACTYRPSAOCSDGNCLLYTHLPDGFPSAAGLEALCRODNSIPRCPTEQL	1080							
1081	SPSHPLTCTGSDVDVQVAVPQGRYALVWEYANEDARQEVGVAVHTPQAPQOGLL	1140							
1081	SPSHPLTCTGSDVDVQVAVPQGRYALVWEYANEDARQEVGVAVHTPQAPQOGLL	1140							
1141	SLHPCLYSTLCRGRTARDQDLHVLAVFHLDSSEASVELTAEQARFFLHGVTLPVIEFSPEFV	1200							
1141	SLHPCLYSTLCRGRTARDQDLHVLAVFHLDSSEASVELTAEQARFFLHGVTLPVIEFSPEFV	1200							
1201	EPVSCISHGAFGPNSSAACLPSPRPKPQBIILRDCQVPLPPGLPLTHAODLTPATSP	1260							
1201	EPVSCISHGAFGPNSSAACLPSPRPKPQBIILRDCQVPLPPGLPLTHAODLTPATSP	1260							
1261	AGPRPRPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYPAPHTFPEVVLIN	1320							
1261	AGPRPRPTAVDPDAEPTLLREPOATVVFTTHVPTLGRYAFLLHGYPAPHTFPEVVLIN	1320							
1321	AGRVWQHANASFCPHGCGRTLVVCGQALLDVTTHSELVTVTVRVPGRWLMDLYLVLP	1380							
1321	AGRVWQHANASFCPHGCGRTLVVCGQALLDVTTHSELVTVTVRVPGRWLMDLYLVLP	1380							
1381	ENVYSFGYLREBEPLDKSYDFIFISHCAAQYHISPSSSSLFCRNAASLSLFYNNGARPCGC	1440							
1381	ENVYSFGYLREBEPLDKSYDFIFISHCAAQYHISPSSSSLFCRNAASLSLFYNNGARPCGC	1440							
1441	HEVGATGTCTCFPGCGCHAHVIGRDCSCATGYWGFPCNCRPCDCGARLCLTGQCIC	1500							
1441	HEVGATGTCTCFPGCGCHAHVIGRDCSCATGYWGFPCNCRPCDCGARLCLTGQCIC	1500							
1501	PPRTIPDCLLQCPQTCGCHPLVGCBCNCSGPGIQBELTDPTCDTDSGQCKCRPNVTGR	1560							
1501	PPRTIPDCLLQCPQTCGCHPLVGCBCNCSGPGIQBELTDPTCDTDSGQCKCRPNVTGR	1560							
1561	CDTCSPGHGVPRCPDCHAGTAPGVCDPLTGOCYCKENVOGPKDCQSLGTFSLDAA	1620							
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1621	NPKGTRCFGFCGATERCRSSSYTRQBEFVDMEGWLLSTDQVVPHERPQGTETMLRADLRH	1680							
1621	NPKGTRCFGFCGATERCRSSSYTRQBEFVDMEGWLLSTDQVVPHERPQGTETMLRADLRH	1680							
1681	VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESSRDVVLQGN	1740							
1681	VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDVFPVMESSRDVVLQGN	1740							
1741	QMSITFLEPAVPTPGHVRGQQLVEGNFRHTTNTVSRSEELMVLASLEQLQIRALFS	1800							
1741	QMSITFLEPAVPTPGHVRGQQLVEGNFRHTTNTVSRSEELMVLASLEQLQIRALFS	1800							
1801	QISSAVSLRRVALEVASPAGGALASVVELCLCPASVYRGDSQCECAGFYRDKGLFLGR	1860							
1801	QISSAVSLRRVALEVASPAGGALASVVELCLCPASVYRGDSQCECAGFYRDKGLFLGR	1860							
1861	CVPCQCHGSDRCLPFGSGVCDQHNTEGAHCRCAQAGFVSSRDDPSAPCVSCPCPLSVP	1920							
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1921	SNNTAEGVLGGRTQCLCKPGVAGACERCAFGFNGNPLVLGSSQPCDCSNGDGNLL	1980							
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1981	FSDCDPLTGACRGLRHTTGTGPRCEICAPFGYGNALLPGNCTRCDCCTPCGTEACDPSHGHC	2040							
1981	FSDCDPLTGACRGLRHTTGTGPRCEICAPFGYGNALLPGNCTRCDCCTPCGTEACDPSHGHC	2040							
2041	LCKAGVTGRRCDRCQEGHFGFNGCGGRPCACGPAAGSECHPQSQOCHCRPQTMGPQCR	2100							

2041 LKAGVTGRRCDRCQBEHGFDFGCGGCRPCACGPAAGSECHPQSGQCHCRPGTMGPQR 2100  
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2161 SIHCEVCDHCVLLDDDLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSQLR 2220  
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2221 SPLGRPHRTAQOLEVLEEQSTISLGODARRLGGQAVGTEDQASQLLAGTEATLGHAKTLLA 2280  
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2281 AIRAVDRITLSLMSTGHLGLANASAPSGEQLLRTLAEBVRLLMEMRARDLGAPQAAAEA 2340  
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2341 ELAAQRLLARVBOELSSWEENQALATQTRDLRAQHEAGLMDREALNRAVDATREAOE 2400  
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2401 LNSRQERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEELERLAAS 2460  
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2461 LDGARTPLLRQMOTSPAGSKLRLVEAAEAAHAQOLGOLALNLSIIILDVNOQRILTQRAIE 2520  
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2581 QRLGLVMAALOGARTQLRDVRAKQOLEAHIQAAQAMLAMDTDETSKKIAHAKVAABEAQ 2640  
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2761 ALKFYLGPEPEPGQGTEDRFVYMGSROATGDYMGVSLRDKKHVWYQLGEGAPVLISI 2820  
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2821 DEDIGQFAAVSLDRTLQFGHMSVTVVERQMIQETKGDTPVAPGAEGLLNLRPDDFVYVGG 2880  
2821 DEDIGQFAAVSLDRTLQFGHMSVTVVERQMIQETKGDTPVAPGAEGLLNLRPDDFVYVGG 2880  
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3121 VGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQDSGALLYRASPDGLCQVSLQOQR 3180  
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3361 RNWPSLSMHLVPSSRGLLLFTARLRPPGSPSLALFLSNHGFVAQMEGLGTRLRAQSRQRS 3420  
3421 RPRGWHKVSVRKRNILLVTDGARAWSOEGPHRQHQGAHPQPHTLFVGGIPASSHSSK 3480  
3421 RPRGWHKVSVRKRNILLVTDGARAWSOEGPHRQHQGAHPQPHTLFVGGIPASSHSSK 3480  
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3541 PDVGLELEVRPLAVTGLIHLGQARTPPVYLQLOVTEKQVLLRADDGAGSFSTSVTRPSVL 3600  
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3661 YCGMRRLAVNRSPVAMTRSVVEVHGAVGASGCCPAA 3695  
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RESULT 5  
US-10-312-088-30  
; Sequence 30, Application US/10312088  
; Publication No. US20030219862A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Cogswell, John P.  
; APPLICANT: Kabnic, Karen S.  
; APPLICANT: Lai, Ying-Ta  
; APPLICANT: Martensen, Shelby A.  
; APPLICANT: Murdock, Paul R.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Strum, Jay C.  
; APPLICANT: Xiang, Zhaoxing  
; APPLICANT: Xie, Qing  
; APPLICANT: Rizni, Safia K.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50029  
; CURRENT APPLICATION NUMBER: US/10/312,088  
; PRIOR FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/19929  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/213,161  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 60/213,156  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 3705  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-312-088-30  
Query Match 99.6%; Score 20030; DB 15; Length 3705;



Best Local Similarity 99.4%; Pred. No. 0; Matches 3683; Conservative 3; Mismatches 9; Indels 10; Gaps 1;									
Qy	1	MAKRLCAGSALCVRGPRGAPLLVGLLIGALIGARAREEAGGFSLHPFYFLNLAEGARIAA	60						
Db	1	MAKRLCAGSALCVRGPRGAPLLVGLLIGALIGARAREEAGGFSLHPFYFLNLAEGARIAA	60						
Qy	61	SATCGEAPARGSPRTEDLYCKLVGVPVAGGDPNOTIRGOYCDICTAANSNKAHPASNA	120						
Db	61	SATCGEAPARGSPRTEDLYCKLVGVPVAGGDPNOTIRGOYCDICTAANSNKAHPASNA	120						
Qy	121	IDGTERWQSPPLSRGLEYNENVTLDLQGVHVAIVLKFANSRPPDLWLERSMDFGR	180						
Db	121	IDGTERWQSPPLSRGLEYNENVTLDLQGVHVAIVLKFANSRPPDLWLERSMDFGR	180						
Qy	181	TYQFWOFFASSKRDCLERFGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
Db	181	TYQFWOFFASSKRDCLERFGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG	240						
Qy	241	AMNFSYPLLEBKATNVLRLNLTLLGHMKALADPTVTRYYYSIKDISIGRC	300						
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Qy	301	VCHGHADACDAKDPDPRFRLQCTCOHNTCGGTCDRCPCGFNOQPMKPATANSANECQSCN	360						
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Qy	361	CYGHATDCYDPRVDRRASQSLDGTYYQGGVICIDCOHHTAGVNCERCLPGFYSPNHL	420						
Db	361	CYGHATDCYDPRVDRRASQSLDGTYYQGGVICIDCOHHTAGVNCERCLPGFYSPNHL	420						
Qy	421	DSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGPPSCYPTPSSND	480						
Db	421	DSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGPPSCYPTPSSND	480						
Qy	481	TRQVLPAGQIVNDCSAGTQGNACRKPDRVGRCLCKPNFOGTHCELCAPGFTGPGCQP	540						
Db	481	TRQVLPAGQIVNDCSAGTQGNACRKPDRVGRCLCKPNFOGTHCELCAPGFTGPGCQP	540						
Qy	541	CQCSSPGVADDRCDPTGTCRCRVGPEGATCDRCAPGVFHFPLCQCCSPAGTLPEGCD	600						
Db	541	CQCSSPGVADDRCDPTGTCRCRVGPEGATCDRCAPGVFHFPLCQCCSPAGTLPEGCD	600						
Qy	601	EAGRLCQBPAGFCHDCRCPGVHPPNCACTCDPRGALDQLCAGGLCRCRPGYGTGA	660						
Db	601	EAGRLCQBPAGFCHDCRCPGVHPPNCACTCDPRGALDQLCAGGLCRCRPGYGTGA	660						
Qy	661	CQCSFGFPGFPCVCHCSAEGSLHAACDPRSQCRCRPRVTGLRCDTVPGAYNPPYC	720						
Db	661	CQCSFGFPGFPCVCHCSAEGSLHAACDPRSQCRCRPRVTGLRCDTVPGAYNPPYC	720						
Qy	721	EAGSHPAGLAPVDPALPEAQPCKRAHVGPSCDRCKPGFWGLSPNPEGCTRCSCDL	780						
Db	721	EAGSHPAGLAPVDPALPEAQPCKRAHVGPSCDRCKPGFWGLSPNPEGCTRCSCDL	780						
Qy	781	RGLTGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDIIGALQGS	840						
Db	781	RGLTGGVAECQPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDIIGALQGS	840						
Qy	841	CEBRTGVCRCRPNTOGPTCSBPARDHYLDLHLHLELEEAATPEGHAVRFGFNPLEFN	900						
Db	841	CEBRTGVCRCRPNTOGPTCSBPARDHYLDLHLHLELEEAATPEGHAVRFGFNPLEFN	900						
Qy	901	FSWRGAQAPVQPRIVARLNLTSPLFWLVFRYVNRGAMSVSRGVSVRBEGRSAACANC	960						
Db	901	FSWRGAQAPVQPRIVARLNLTSPLFWLVFRYVNRGAMSVSRGVSVRBEGRSAACANC	960						
Qy	961	TAQSQVAPPPSTEPAFITVPORGFGEPPVLPNGTWALRVBAEGLLDYVLLPSAYYEA	1020						
Db	961	TAQSQVAPPPSTEPAFITVPORGFGEPPVLPNGTWALRVBAEGLLDYVLLPSAYYEA	1020						
Qy	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPPSAAGLEALCRQDNLSPRCPTEQ	1080						

Db	1021	ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPPSAAGLEALCRQDNLSPRCPTEQ	1080						
Qy	1081	SPSHPLITCTGSDVDVQLOVAVPQGRYALVWYBANEADARQEVGVAVHTPQAPQOGLL	1140						
Db	1081	SPSHPLITCTGSDVDVQLOVAVPQGRYALVWYBANEADARQEVGVAVHTPQAPQOGLL	1140						
Qy	1141	SLHPCLYSLCRGTARDTQDHLAVFHLDSSEASVLTABQARFFLHGVTLVPIEFPSPFV	1200						
Db	1141	SLHPCLYSLCRGTARDTQDHLAVFHLDSSEASVLTABQARFFLHGVTLVPIEFPSPFV	1200						
Qy	1201	EPVSCISSHGAFGNSAACLPSPRPKPQPIIILDCQVILPPLGCLPLTHAQDUTPATSP	1260						
Db	1201	EPVSCISSHGAFGNSAACLPSPRPKPQPIIILDCQVILPPLGCLPLTHAQDUTPATSP	1260						
Qy	1261	AGPRRPPTAVDPDAEPTLLREPQATVVTTHVPTLGRYAFLLHGYPAPHTFFVEVLIN	1320						
Db	1261	AGPRRPPTAVDPDAEPTLLREPQATVVTTHVPTLGRYAFLLHGYPAPHTFFVEVLIN	1320						
Qy	1321	AGRVWQHANASFCPHGVCRTLVVCEQALLDVTHSELTVTVRVPEGRWLWLYLVVP	1380						
Db	1321	AGRVWQHANASFCPHGVCRTLVVCEQALLDVTHSELTVTVRVPEGRWLWLYLVVP	1380						
Qy	1381	ENVYSGYLREPLDKSYDFISHCAAQGYHISPSSSLFCRNAASLSLFYNNGARPCGC	1440						
Db	1381	ENVYSGYLREPLDKSYDFISHCAAQGYHISPSSSLFCRNAASLSLFYNNGARPCGC	1440						
Qy	1441	HEVGATGPTCEBFGQCCCHAHVIGRDCSRCATGYWGFPPNCRPCDCGALCDELTGQCIC	1500						
Db	1441	HEVGATGPTCEBFGQCCCHAHVIGRDCSRCATGYWGFPPNCRPCDCGALCDELTGQCIC	1500						
Qy	1501	PRPTIPDCLLQCPOTFGCHPLVGCENCSGPGIQBELTPTCDTDSGQCKRPNVTGRR	1560						
Db	1501	PRPTIPDCLLQCPOTFGCHPLVGCENCSGPGIQBELTPTCDTDSGQCKRPNVTGRR	1560						
Qy	1561	CDTCSFGHGYPRCPDCHCAGTAGVCDPLTQCYCKENVOGPKDCQSLGTFSLDAA	1620						
Db	1561	CDTCSFGHGYPRCPDCHCAGTAGVCDPLTQCYCKENVOGPKDCQSLGTFSLDAA	1620						
Qy	1621	NPKGTRCFGFCGATERCRRSSSYTRQEFVDMEGWLLSTDROVPHRQPGTEMLRADLRH	1680						
Db	1621	NPKGTRCFGFCGATERCRRSSSYTRQEFVDMEGWLLSTDROVPHRQPGTEMLRADLRH	1680						
Qy	1681	VPEAVPEAPPELYWQAPSYLGDVSSVGGTLRLVELHSETQRGDVFPVMSRDPVVLQGN	1740						
Db	1681	VPEAVPEAPPELYWQAPSYLGDVSSVGGTLRLVELHSETQRGDVFPVMSRDPVVLQGN	1740						
Qy	1741	QMSITFLFPAYPTPGHVRGQLQVVEGNFRHTETRTNTVSRREELMMVLASLEQLRALFS	1800						
Db	1741	QMSITFLFPAYPTPGHVRGQLQVVEGNFRHTETRTNTVSRREELMMVLASLEQLRALFS	1800						
Qy	1801	QISSAVSLRRVALVAVASAGOGALASVVELCLCPASVYRGDSQCEBGFYVDVKGLFLGR	1860						
Db	1801	QISSAVSLRRVALVAVASAGOGALASVVELCLCPASVYRGDSQCEBGFYVDVKGLFLGR	1860						
Qy	1861	CVPCCCHGHSRCLPGSGVCVDCQHNTEGAHCRCQAGFMSSRDPDAPCVSCPCPLSVP	1920						
Db	1861	CVPCCCHGHSRCLPGSGVCVDCQHNTEGAHCRCQAGFMSSRDPDAPCVSCPCPLSVP	1920						
Qy	1921	SNNFAGCVLGRGTQCLCKPGYAGASCERCAPGFNGNPLVLGSSCPCDCSNGNDNL	1980						
Db	1921	SNNFAGCVLGRGTQCLCKPGYAGASCERCAPGFNGNPLVLGSSCPCDCSNGNDNL	1980						
Qy	1981	FSDCDPLTGACRGLRHTTGPRCICAPGFYGNALLPGNCTRCDCPTCGTEACDPHSGHC	2040						
Db	1981	FSDCDPLTGACRGLRHTTGPRCICAPGFYGNALLPGNCTRCDCPTCGTEACDPHSGHC	2040						
Qy	2041	LCKAGVTGRCDRCOBEGHFGNGCGCRPCACGPAASGSRCHQSGOCHCRPGTMGPQCR	2100						
Db	2041	LCKAGVTGRCDRCOBEGHFGNGCGCRPCACGPAASGSRCHQSGOCHCRPGTMGPQCR	2100						
Qy	2101	ECAPGYWGLPQGGRCRCQPGCRCDPHTGRNCNCPPLGSGRCDTCSQHQVVPVPGPVGH	2160						
Db	2101	ECAPGYWGLPQGGRCRCQPGCRCDPHTGRNCNCPPLGSGRCDTCSQHQVVPVPGPVGH	2160						



QY 2161 SIRCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMWARHLRLNASIADLQSQLR 2220  
Db 2161 SIRCEVCDHCVVLLDDLERAGALLPAIHEQLRGINASSMWARHLRLNASIADLQSQLR 2220  
QY 2221 SPLGPHETAQOQLEVLBOQSTSLGDARLGGQAVGTRD-----OASOLLAGTEA 2270  
Db 2221 SPLGPHETAQOQLEVLBOQSTSLGDARLGGQAVGTRD-----OASOLLAGTEA 2280  
QY 2271 TLGHAKTLLAAIRAVDRTLSLMSQTHGLGLANASAPSGEQLLRTLAEBERLILWENRARD 2330  
Db 2281 TLGHAKTLLAAIRAVDRTLSLMSQTHGLGLANASAPSGEQLLRTLAEBERLILWENRARD 2340  
QY 2331 LGAPAAAAEALAAARLLARVOEQLSSWENQALATOTRDLAHEAGLMDLREALNR 2390  
Db 2341 LGAPAAAAEALAAARLLARVOEQLSSWENQALATOTRDLAHEAGLMDLREALNR 2400  
QY 2391 AVDATREAOELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDOA 2450  
Db 2401 AVDATREAOELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDOA 2460  
QY 2451 KEELERLAASLDGARTPLLOMQTTFSPAGSKLRLVEAAEHAQQLQALNLSIIILDVN 2510  
Db 2461 KEELERLAASLDGARTPLLOMQTTFSPAGSKLRLVEAAEHAQQLQALNLSIIILDVN 2520  
QY 2511 QDRLTQRAIEASNAYSRILOQAAEDAAQALQQADHTWATVVOGLVDRAOQLLANST 2570  
Db 2521 QDRLTQRAIEASNAYSRILOQAAEDAAQALQQADHTWATVVOGLVDRAOQLLANST 2580  
QY 2571 ALBEAMLEQOQRLGLVWAALQGARTQLRDYRAKKDQLEAHIQAAQAWLAMDDETSEKIA 2630  
Db 2581 ALBEAMLEQOQRLGLVWAALQGARTQLRDYRAKKDQLEAHIQAAQAWLAMDDETSEKIA 2640  
QY 2631 HAKAVAAEAOATRVOSQLOQAOENVERWQOYEGIRGODLGQAVLDAGHSVSTLEKTL 2690  
Db 2641 HAKAVAAEAOATRVOSQLOQAOENVERWQOYEGIRGODLGQAVLDAGHSVSTLEKTL 2700  
QY 2691 POLLAKLSILENRGVHNASLALSASIGRVRELLAQAGAAKVKPKMKNRSGVQLRTP 2750  
Db 2701 POLLAKLSILENRGVHNASLALSASIGRVRELLAQAGAAKVKPKMKNRSGVQLRTP 2760  
QY 2751 RDLADLAAYTALKFYLOGPEPQGTEDRPFVYMGSRQATGDMYGSVLSRDKKVVHYQL 2810  
Db 2761 RDLADLAAYTALKFYLOGPEPQGTEDRPFVYMGSRQATGDMYGSVLSRDKKVVHYQL 2820  
QY 2811 GEAGPAVLSDIDEDIGEQAFAVSLDRTLQFGHMSVTVVERQMIQETKGDTPVAPGAEGLNLNR 2870  
Db 2821 GEAGPAVLSDIDEDIGEQAFAVSLDRTLQFGHMSVTVVERQMIQETKGDTPVAPGAEGLNLNR 2880  
QY 2871 PDDFVYVGGYPSFTTTPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFOLDTAVDRPCA 2930  
Db 2881 PDDFVYVGGYPSFTTTPPLLRFPYRGCIEMDTLNEEVVSLYNFERTFOLDTAVDRPCA 2940  
QY 2931 RSKSTGDPMLTDGSLYDGTGFARTSPDSQISTTKRFEQELRLVSYSGVLFELKQSQOFLC 2990  
Db 2941 RSKSTGDPMLTDGSLYDGTGFARTSPDSQISTTKRFEQELRLVSYSGVLFELKQSQOFLC 3000  
QY 2991 LAVOEGSLVLLYDFGAGLKKAVPLQPPPPPLTSASKAIQVFLGGSRRKVLVRVERATVYS 3050  
Db 3001 LAVOEGSLVLLYDFGAGLKKAVPLQPPPPPLTSASKAIQVFLGGSRRKVLVRVERATVYS 3060  
QY 3051 VEQNDLELADAYILGVPDPQLPPSLRWLPPTGSGVRGCVKGIKALGKXVDLKRINTTG 3110  
Db 3061 VEQNDLELADAYILGVPDPQLPPSLRWLPPTGSGVRGCVKGIKALGKXVDLKRINTTG 3120  
QY 3111 VSAGCTADLLVGRANTPHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDG 3170  
Db 3121 VSAGCTADLLVGRANTPHGHGFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYRASPDG 3180  
QY 3171 LCQVSLQOQGRVSLQLLTKTEVKTOAGFADGAPHHVAFYFYSNATGWLIVYDDQLQOMKPHRG 3230  
Db 3181 LCQVSLQOQGRVSLQLLTKTEVKTOAGFADGAPHHVAFYFYSNATGWLIVYDDQLQOMKPHRG 3240

QY 3231 PPELOQOPEGPRLILGLPESGTYINFGCISNVFVQRLIGPORVFDLQONLGSVNVST 3290  
Db 3241 PPELOQOPEGPRLILGLPESGTYINFGCISNVFVQRLIGPORVFDLQONLGSVNVST 3300  
QY 3291 GCAPALQAQTPGLGPRGLQATARKASRRSRQPAFHPACMLPPHLRTRTTRDSYQFGGSLSSH 3350  
Db 3301 GCAPALQAQTPGLGPRGLQATARKASRRSRQPAFHPACMLPPHLRTRTTRDSYQFGGSLSSH 3360  
QY 3351 LEFVGILARHNWPSLSNVLPSSRGLLFTABRLRPGSPSLALFLNSGHFVAQMEGLGT 3410  
Db 3361 LEFVGILARHNWPSLSNVLPSSRGLLFTABRLRPGSPSLALFLNSGHFVAQMEGLGT 3420  
QY 3411 RLRAQSRORSRPPGRHWKVSVRWEXNRILLVTDGARAMSQEGPHRQHQGAEPHPQHTLTVFG 3470  
Db 3421 RLRAQSRORSRPPGRHWKVSVRWEXNRILLVTDGARAMSQEGPHRQHQGAEPHPQHTLTVFG 3480  
QY 3471 GLPASHSSSKLPVTVGSGGCVKRLRLHGRPLIGASTRMAGVTPCILGLEAGLFFPGSGGV 3530  
Db 3481 GLPASHSSSKLPVTVGSGGCVKRLRLHGRPLIGASTRMAGVTPCILGLEAGLFFPGSGGV 3540  
QY 3531 ITLDDLPGATLDPVGLLEVRPLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEF 3590  
Db 3541 ITLDDLPGATLDPVGLLEVRPLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEF 3600  
QY 3591 STSVTRPSVLCDGGWHRLAVNMKSGNVLRLEVDASQNSHTVGPFLAAAGAPAPLYLGGULPE 3650  
Db 3601 STSVTRPSVLCDGGWHRLAVNMKSGNVLRLEVDASQNSHTVGPFLAAAGAPAPLYLGGULPE 3660  
QY 3651 PMAVQWPWPAYCGCMRRRLAVNRSPVAMTRSVEVHGAVGASGCPAA 3695  
Db 3661 PMAVQWPWPAYCGCMRRRLAVNRSPVAMTRSVEVHGAVGASGCPAA 3705

RESULT 6

US-10-037-417-2  
; Sequence 2, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Pattarajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Sciore, Paul  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Stone, David J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shency, Suresh G  
; APPLICANT: Anderson, David W  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Miller, Charles E  
; APPLICANT: Eisen, Andrew J  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260, 018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260, 360  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/272, 411

Qy	707	--CDT	VC	PGAYN	FP	CE	AGS	CH	PAG	L	AVD	PA	BP	AC	RAH	VE	GS	CD	CR	K	PG	FW	G	764																																	
Db	690	HVC	PV	TT	S	T	A	K	P	L	F	T	A	S	C	H	P	A	G	L	A	V	D	PA	BP	AC	RAH	VE	GS	CD	CR	K	PG	FW	G	749																					
Qy	765	L	S	P	N	E	G	T	R	C	S	D	L	R	G	T	L	G	V	A	B	E	C	O	F	C	K	P	H	V	C	G	A	C	A	S	K	D	G	F	L	D	O	A	D	Y	F	824									
Db	750	L	S	P	N	E	G	T	R	C	S	D	L	R	G	T	L	G	V	A	B	E	C	O	F	C	K	P	H	V	C	G	A	C	A	S	K	D	G	F	L	D	O	A	D	Y	F	808									
Qy	825	G	C	R	S	C	D	I	G	G	A	L	G	O	S	C	E	P	R	T	G	V	C	R	P	N	T	O	G	P	T	C	S	E	P	A	R	D	H	V	L	P	D	L	H	L	R	L	E	L	E	A	A	T	P	884	
Db	809	G	C	R	S	C	D	I	G	G	A	L	G	O	S	C	E	P	R	T	G	V	C	R	P	N	T	O	G	P	T	C	S	E	P	A	R	D	H	V	L	P	D	L	H	L	R	L	E	L	E	A	A	T	P	868	
Qy	885	E	G	H	A	V	E	F	G	N	P	L	E	F	N	F	S	W	R	G	A	O	M	A	P	O	P	R	I	V	A	R	L	N	L	T	S	P	D	L	F	M	L	V	F	R	Y	N	R	G	A	M	S	V	G	944	
Db	869	E	G	H	A	V	E	F	G	N	P	L	E	F	N	F	S	W	R	G	A	O	M	A	P	O	P	R	I	V	A	R	L	N	L	T	S	P	D	L	F	M	L	V	F	R	Y	N	R	G	A	M	S	V	G	928	
Qy	945	R	V	S	V	R	E	G	S	A	C	A	N	C	T	A	O	S	O	P	V	A	P	P	S	T	E	P	A	F	I	T	V	P	O	R	G	F	E	P	F	V	L	N	P	G	T	W	A	L	R	V	E	A	E	G	1004
Db	929	R	V	S	V	R	E	G	S	A	C	A	N	C	T	A	O	S	O	P	V	A	P	P	S	T	E	P	A	F	I	T	V	P	O	R	G	F	E	P	F	V	L	N	P	G	T	W	A	L	R	V	E	A	E	G	988
Qy	1005	V	L	D	Y	V	L	P	S	A	Y	E	A	L	L	O	L	R	V	T	E	A	C	T	T	R	P	S	A	O	G	D	N	C	L	I	Y	T	H	L	P	D	G	F	P	S	A	A	G	L	E	A	L	1064			
Db	989	V	L	D	Y	V	L	P	S	A	Y	E	A	L	L	O	L	R	V	T	E	A	C	T	T	R	P	S	A	O	G	D	N	C	L	I	Y	T	H	L	P	D	G	F	P	S	A	A	G	L	E	A	L	1048			
Qy	1065	C	R	O	N	S	L	P	R	C	P	T	E	O	L	S	P	S	H	P	L	I	T	C	G	S	D	V	D	V	O	L	Q	V	A	P	O	G	R	A	L	V	V	E	A	N	E	D	A	R	Q	E	V	1124			
Db	1049	C	R	O	N	S	L	P	R	C	P	T	E	O	L	S	P	S	H	P	L	I	T	C	G	S	D	V	D	V	O	L	Q	V	A	P	O	G	R	A	L	V	V	E	A	N	E	D	A	R	Q	E	V	1108			
Qy	1125	G	V	A	H	T	P	O	R	A	P	O	G	L	L	S	H	P	C	L	Y	S	T	L	C	R	G	T	A	R	D	T	O	H	L	A	V	F	H	L	D	S	A	S	V	L	T										

Db 1769 MYLASLEQLOIRALFSQISSAVFLRRVALEVASPAGQALASNVELCLCPASYRGDSQCE 1828  
Qy 1845 CAPGFYRDVKGLFGRVCPQCHGHSRCLPBGSGVCDVCHNTGAGHCERCAQFMSRD 1904  
Db 1829 CAPGFYRDVKGLFGRVCPQCHGHSRCLPBGSGVCDVCHNTGAGHCERCAQFMSRD 1887  
Qy 1905 DPSAPCVSCPCLSPVSPNNFAEGCVLRGGRTQCLCKPGYACACERCAPGFFGNPLVLGS 1964  
Db 1888 DPSAPCVSCPCLSPVSPNNFAEGCVLRGGRTQCLCKPGYACACERCAPGFFGNPLVLGS 1920  
Qy 1965 SCQPCDCSGNGDNPLFLPSDCDPLTGACRGCLRHITGPRCEICAPGFYGNALLPGNCTRCD 2024  
Db 1921 SCQPCDCSGNGDNPLFLPSDCDPLTGACRGCLRHITGPRCEICAPGFYGNALLPGNCTRCD 1980  
Qy 2025 CTPCCTEACDPSHGCHLCKAGVTGRCDRCQEGHFGNGCGCRPCACGPAEAGSECHPQ 2084  
Db 1981 CTPCCTEACDPSHGCHLCKAGVTGRCDRCQEGHFGNGCGCRPCACGPAEAGSECHPQ 2040  
Qy 2085 SQQCHCRFGTMGPQCRECAPGYWGLPEQGCRCRCQPGCRCDPHTRGNCNCPPLGSGERCDT 2144  
Db 2041 SQQCHCRFGTMGPQCRECAPGYWGLPEQGCRCRCQPGCRCDPHTRGNCNCPPLGSGERCDT 2100  
Qy 2145 CSQCHQVPPGPGVGHSHCEVCHCVLLDDLEERAGALLPAIHEQURGINASMAWAR 2204  
Db 2101 CSQCHQVPPGPGVGHSHCEVCHCVLLDDLEERAGALLPAIHEQURGINASMAWAR 2160  
Qy 2205 LHLNASTADL-----OSQLRSPGLPRHETAQOQLEVLQOOST 2241  
Db 2161 LHLNASTADLQVLSVLAFFPPQPGVQAFTRFLPOSQLRSPGLPRHETAQOQLEVLQOOST 2220  
Qy 2242 SLGQDARRLGGQAVTRDQASQILAGTEATLGAKTLLAAITRAVDRTLSLMSQGTGHLG 2301  
Db 2221 SLPP-----QAVGTRDQASQILAGTEATLGAKTLLAAITRAVDRTLSLMSQGTGHLG 2273  
Qy 2302 ANASAPSGQLLRTLAEVERLLWEWARDLGAPOAAAEALAAOQLLARVOEQLSLWE 2361  
Db 2274 ANASAPSGQLLRTLAEVERLLWEWARDLGAPOAAAEALAAOQLLARVOEQLSLWE 2333  
Qy 2362 ENQALATQTRDLAQEAGLMDLREALNAVDAITREAOELNSRQERLEALQKQELSR 2421  
Db 2334 ENQALATQTRDLAQEAGLMDLREALNAVDAITREAOELNSRQERLEALQKQELSR 2393  
Qy 2422 DNATLOATLHAARDTLASVRLHSLDQAK--BELERLAASLDGARTPLQRMOTESPAGS 2480  
Db 2394 DNATLOATLHAARDTLASVRLHSLDQAK--BELERLAASLDGARTPLQRMOTESPAGS 2453  
Qy 2481 KLRLVEAAEAHAQQLGQALNLSIILDVNDRLTQRAIEASNAYSRILOAVQAAEDAAG 2540  
Db 2454 KLRLVEAAEAHAQQLGQALNLSIILDVNDRLTQRAIEASNAYSRILOAVQAAEDAAG 2512  
Qy 2541 QALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQOQLGL--VWA---ALQGART 2595  
Db 2513 QALQQAADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQOQLGLGECWAPNGALURPAGT 2572  
Qy 2596 QLRDVRAXKDDOLEAHTQAAQAMAMDITDTSKKIAHAKAVAAEAQDTATRVQSQLOAMQE 2655  
Db 2573 QLRDVRAXKDDOLEAHTQAAQAMAMDITDTSKKIAHAKAVAAEAQDTATRVQSQLOAMQE 2632  
Qy 2656 NVERWQOGEVGRQDGLQAVLDAGHSVSTLEKTLIPOLLAKLSILENRRGVNVALSAS 2715  
Db 2633 NVERWQOGEVGRQDGLQAVLDAGHSVSTLEKTLIPOLLAKLSILENRRGVNVALSAS 2692  
Qy 2716 IGVRELLIAQARGAASK-KVPMKFNKRGSGVOLTRPDLADLAAYTALKFYLGQPEPEFG 2774  
Db 2693 IGVRELLIAQARGAASK-KVPMKFNKRGSGVOLTRPDLADLAAYTALKFYLGQPEPEFG 2752  
Qy 2775 QGTEDRFVVMGSRQATGDMVGSRLRDKKVVHVVYQLGEAGPAVLSIDEDIGQFPAVSLD 2834  
Db 2753 QGTEDRFVVMGSRQATGDMVGSRLRDKKVVHVVYQLGEAGPAVLSIDEDIGQFPAVSLD 2812  
Qy 2835 RTLOFGHMSVTVVEROMIQETKGTAVPAGAGLLNLRPDDFVFGYGPSTFTPPPLLRFP 2894

Db 2813 RTLOFGHMSVTVVEROMIQETKGTAVPAGAGLLNLRPDDFVFGYGPSTFTPPPLLRFP 2872  
Qy 2895 GYRGCIEMDTLNEEVSVLYNFERTTQLDTAVDRPCARSKSTGDPWLTDGSIYLDGTGFARI 2954  
Db 2873 GYRGCIEMDTLNEEVSVLYNFERTTQLDTAVDRPCARSKSTGDPWLTDGSIYLDGTGFARI 2932  
Qy 2955 SPSQSISTTKRFEQELRLVSYSGVLFLLKQOQOFICLAVQEGSLVLLYDFGAGLKKAVPL 3014  
Db 2933 SPSQSISTTKRFEQELRLVSYSGVLFLLKQOQOFICLAVQEGSLVLLYDFGAGLKKAVPL 2992  
Qy 3015 QPPPLTSAKAIQVFPLLGGSRKRVLRVERATVTVSVEQNDLELADAYYLGVPPDQPL 3074  
Db 2993 QPPPLTSAKAIQVFPLLGGSRKRVLRVERATVTVSVEQNDLELADAYYLGVPPDQPL- 3051  
Qy 3075 PSRLWLPFGTGGSVRGCVKGIKALGKIVDLKRLNTTQVSAGCTADLLVGRAMTFHGGFLR 3134  
Db 3052 PSRLWLPFGTGGSVRGCVKGIKALGKIVDLKRLNTTQVSAGCTADLLVGRAMTFHGGFLR 3111  
Qy 3135 LALSNVAPLTGNVYSGFGFHSQDSALLVYRASPDLCOVSLQOQGRVSIQLLRTVEVKTQA 3194  
Db 3112 LALSNVAPLTGNVYSGFGFHSQDSALLVYRASPDLCOVSLQOQGRVSIQLLRTVEVKTQA 3171  
Qy 3195 GFADGAPHYVAFYSNATGNVLYVDQLOQMKPHRGPPPELQPOPEGPRLLLGGLPESGT 3254  
Db 3172 GFADGAPHYVAFYSNATGNVLYVDQLOQMKPHRGPPPELQPOPEGPRLLLGGLPESGT 3231  
Qy 3255 IYFSGCISNVFORLLGQPVDFDLOONLGSVNVSTGCAPALQAOPTGLGPRGLQATARK 3314  
Db 3232 IYFSGCISNVFORLLGQPVDFDLOONLGSVNVSTGCAPALQAOPTGLGPRGLQATARK 3284  
Qy 3315 ASRRSQAPARHPACMLPPHLLRTTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLPKS 3374  
Db 3285 ASRRSQAPARHPACMLPPHLLRTTRDSYQFGGSLSSHLEFVGILARHNWPSLSMHVLPKS 3332  
Qy 3375 SRGILLFTARLRPGSPSLALFLSNGHFVAQMEGLGTRLAQSRQSRPGRWHKVSVRWEK 3434  
Db 3333 -----VSVRWEK 3339  
Qy 3435 NRILLVTDGARAWSQBPHRQHOGAHPQHTLFGVGLPASSHSSKLPVTVFGSGCVKRL 3494  
Db 3340 NRILLVTDGARAWSQBPHRQHOGAHPQHTLFGVGLPASSHSSKLPVTVFGSGCVKRL 3399  
Qy 3495 RLHGRPLGATPRMAGVTPCILGPLEAGLFPFGSGGVITLDPQATLPDVGLELEVPLAV 3554  
Db 3400 RLHGRPLGATPRMAGVTPCILGPLEAGLFPFGSGGVITLDPQATLPDVGLELEVPLAV 3459  
Qy 3555 TGLIFHLGOARTPPYLOQVTEKOVLLRADDDGAGEFSTSVTRPSVLCDDGOWHRLAVMKSG 3614  
Db 3460 TGLIFHLGOARTPPYLOQVTEKOVLLRADDDGAGEFSTSVTRPSVLCDDGOWHRLAVMKSG 3519  
Qy 3615 NVLRLEVDACSNTVGPPLAAAGAPAPLYLGLPEPMAVQPPMPAYCGCMRRLAVNRSP 3674  
Db 3520 NVLRLEVDACSNTVGPPLAAAGAPAPLYLGLPEPMAVQPPMPAYCGCMRRLAVNRSP 3579  
Qy 3675 VAMTRSEVHGAVGASGCPAA 3695  
Db 3580 VAMTRSEVHGAVGASGCPAA 3600

RESULT 7  
US-10-037-417-6  
; Sequence 6, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E

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; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothensberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCES: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3597
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-037-417-6

Query Match          90.6%; Score 18231; DB 12; Length 3597;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 3428; Conservative 18; Mismatches 108; Indels 184; Gaps 21;

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QY      61  SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNOTIRGOYCDICTAANSNKAHPASNA 120
DB      40  SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNOTIRGOYCDICTAANSNKAHPASNA 99
QY      121  IDGTERWQSPSLRGLEYNEVNTLDLGQVHVAYVYLKIPANSRPDLWVLSRSMDFGR 180
DB      100  IDGTERWQSPSLRGLEYNEVNTLDLGQVHVAYVYLKIPANSRPDLWVLSRSMDFGR 159
QY      181  TYQWQOFFASRDCCLERGPOTLERITRDAAICTEYSRIVPLENGEIVSVLVNRP 240
DB      160  TYQWQOFFASRDCCLERGPOTLERITRDAAICTEYSRIVPLENGEIVSVLVNRP 219
QY      241  AMNFSYSPLLREFTKATVNRFLRFTNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC 300
DB      220  AMNFSYSPLLREFTKATVNRFLRFTNTLLGLHMGKALRDPVTTRYYYSIKDISIGRC 279
QY      301  VCHGHADACADKDPDTPFLQCTCGTCDRCCEGFGNQPKPATANSANECOSCN 360

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DB      339  CYGHATDCYDPEVDRRARSOSLDGTYGGGVGVCIDCOHHTAGVNCERCLFGFYSSPNHPL 398
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DB      399  DSPHVRCNCESDFTDGTCEBTLGRCYCRPNFSGERCDCVCAEGFTGFCYSPYTPSSND 458
QY      481  TREQVLPAGQIVNDCSAAAGTQGNACRDKPRVGRCLCKPNFQGTCHCBLCAPGYGQCQP 540
DB      459  TREQVLPAGQIVNDCSAAAGTQGNACRDKPRVGRCLCKPNFQGTCHCBLCAPGYGQCQP 517
QY      541  CQCSS---PGVADDRCDPDGTGQCRVGFEGATCDRCAPGYF-----HPPLCQLCGCSP 591
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QY      592  AGTLPEGCDDEAGRCCLCOPEFAGPCHDCRCPGYHGFNCOACTCDPRGALDQLCGAGLGR 651
DB      575  AGTLPEGCDDEAGRCCLCOPEFAGPCHDCRCPGYHGFNCACTCDPRGALDQLCGAGLGR 634
QY      652  CRPGYTGATACQRCSPGFHGFPPSPVCHCSABGSIHAAC-----DPRGQCSRCRPRVTGLRC 707
DB      635  CRPGYTGATACQRCSPGFHGFPPSPVCHCSABGSIHAAC-----DPRGQCSRCRPRVTGLRC 688
QY      708  DTCVPGAYNPPYCBAGSCHPAGLAPALPEAQVPCMCRAHVGEPSDCRCKPFGWGLSP 767
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QY      768  SNPGCTRCSCDLRGTLGGVAECOPGTGQCFCFPHVCGQACASCCKGFFGLDOADYFGCR 827
DB      749  SNPGCTRCSCDLRGTLGGVAECOPGTGQCFCFPHVCGQACASCCKGFFGLDOADYFGCR 808
QY      828  SCRCDIGALQSCSEPRTGVCRCRPNPTGPTCSEPARDHVLPDLHLRLLEBEAATPEGH 887
DB      809  SCRCDIGALQSCSEPRTGVCRCRPNPTGPTCSEPARDHVLPDLHLRLLEBEAATPEGH 868
QY      888  AVREGNPLEBENFESWEGYACMAPVOPRIVARLNTSPDLFWLVRYVNRGAMSVGRVS 947
DB      869  AVREGNPLEBENFESWEGYACMAPVOPRIVARLNTSPDLFWLVRYVNRGAMSVGRVS 928
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DB      929  VREGRSAACANCTAQOPVAFPPSTEPATITVQORGFGEPFVLNPGTVALVEAGVLL 988
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DB      989  DYVLLPSAYVEALQLRVTEACTVYRPSAQSGDNCLLYTHPLDLPFSPSAAGLEALCQ 1048
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DB      1169  TLVPIEFSEFVEPRVSCISSHGAFGPNSAACLPSPRPKPQPIILRDCQVPIPPGLP 1228
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DB      1229  LTHAQDLTPATSPAGPRPPTAVDDPDEPTLLREBQATVVTHTVPTLGRVAFILLHQY 1288
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DB      1289  PAHPTTFVVELINAGRWOQHANASCPRGYGCRTLVWCEGQALLDVTHSELTVTVRVE 1348
QY      1368  GRWLWLDVVLVENVYVFCYLREELDKSYDFISHCAAQGYHISPSSSSLFCRNAASL 1427
DB      1349  GRWLWLDVVLVENVYVFCYLREELDKSYDFISHCAAQGYHISPSSSSLFCRNAASL 1408

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RESULT 8  
US-09-845-583-2  
; Sequence 2, Application US/09845583  
; Patent No. US200201429541  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583-2

Query Match 78.7%; Score 15839; DB 9; Length 3635;  
Best Local Similarity 79.4%; Pred. No. 0;  
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;  
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Qy 139 YNEVNTLDLQVPHVAYLLKFAANSRDLWLERSMDRGTQVQWOPFASSKRCDLER 198  
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Qy 379 ASQSLDGYQGGVCIQDQHTAGVNCERCLPGYRSPNPLDPSPHYCRNCNCSPTDG 438  
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Qy 1638 RSSSTYRQFVDMEGWLLSTDRQVPHRQPGTETMLRADLHRVPEAVPEAFPELYWQAP 1697  
Db 1560 GNSNLARHEFVDMEGWLLSSDRQVPHRQPGTETMLRADLHRVPEAVPEAFPELYWQAP 1615

1698 PSYLGDRVSSYGGTLYRYELHSSTQGDVFPVPMESRPDVLVQNMQSIITFLEPAYTPGHV 1757  
1616 PSYLGDRVSSYGGTLYRYELHSSTQGDIPIPYESRPDVLVQNMQSIIFLELAYPPGV 1675  
1758 HGOLOLVGEGNHRHTETRTNVSREELMMVLALEOLOIRALFSQISSAVSLRRVALEVAS 1817  
1676 HGOLOLVGEGNFRHLETHNVPREELMMVLALEOLOIRALFSQISSAVSLRRVALEVAS 1735  
1818 PAQOQALANVELCLCPASIRYSDSCQECAPFYRDVKGFLGRCVPCQCHGSHDCLPGS 1877  
1736 EAGRGPPASNVCLCMCPANIRYSDSCQECAPFYRDVKGFLGRCVPCQCHGSHDCLPGS 1795  
1878 GYVDCOHNTEGAHCERCAQGWSS--RDDPSAPCVSCPCPLSPVBNFAEGCVLRGGRTQ 1936  
1796 GICVGCQHNTEGDCQERCPCPGFVSSDPSNPASPCVSCPCPLSPVBNFAEGCVLRGGRTQ 1855  
1937 CLCKPGYAGASERCAPGFGFNPLVLGSSCCPCDCSGNGDPLNLFSDCDPLTGACRGCLR 1996  
1856 CLCKPGYAGASERCAPGFGFNPLVLGSSCCPCDCSGNGDPLNLFSDCDPLTGACRGCLR 1915  
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1916 HTTGPRCEICAPGYFNALLPNCITRCDCPCGTETCDPQSGRCLCKAGVTGRRCDRCOE 1975  
2057 GHFGNGCGCRPCACGPAAGSECHPQSQGCHCRPGTGMPCRECAPGYWGLPBGQCR 2116  
1976 GYFGFQCQCRPCACGPAAGSECHPQSQGCHCRPGTGMPCRECAPGYWGLPBGQCR 2035  
2117 CQCPGRCDBHTGRNCPCPLGSERCOTCSQHQVPPVPGPGVHSHCEVCHCVLLID 2176  
2036 CQCPGRCDBHTGRNCPCPLGSERCOTCSQHQVPPVPGPGVHSHCEVCHCVLLID 2095  
2177 DLBRAGALLPAIHEOLRGINASSMAWARHLRLNASIADLQSLRSPGLGRHETAQOQLEVL 2236  
2096 DLBRAGALLPAIHEOLRGINASSMAWARHLRLNASIADLQSLRSPGLGRHETAQOQLEVL 2155  
2237 EQOSTSLGQDARELGQAVTRDQASQLLAGTEATLGHAKTLLAIARAVDRITLSELMQOT 2296  
2156 EQOSTSLGQDARELGQAVTRDQASQLLAGTEATLGHAKTLLAIARAVDRITLSELMQOT 2215  
2297 GHGLNANASPGFOLLRTLAVERLLWEMBRARDLGAPOAAAEALAAORILLARVQEO 2356  
2216 GQSPGDALVPSEGEURWALAEVERLLWEMBRARDLGAPOAAAEALAAORILLARVQEO 2275  
2357 SSLWEENQALATDRDLAHEAGLMDLREALNRAVDATREAOELNSRNOERLEBALQK 2416  
2276 TSPWEENQALATDRDLAHEAGLMDLREALNRAVDATREAOELNSRNOERLEBALQK 2335  
2417 QELSRNATLQATLHAARDTLASVFLHSLDOAKEELERLAASLDGATPILLOQMOTPS 2476  
2336 QELSRNATLQATLHAARDTLASVFLHSLDOAKEELERLAASLDGATPILLOQMOTPS 2395  
2477 PAGSKRLRVEAAHAHQQLQALNLSIIIDVNDRLTQRAIEASNAYSRIQARVQAAE 2536  
2396 PASSKVDLVEAAHAHQQLQALNLSIIIDVNDRLTQRAIEASNAYSRIQARVQAAE 2455  
2537 DAAGQALQADHTWATVROGLVDRAQOLLANSTALEBAMLEQOQRLGLVWALQARTQ 2596  
2456 DAAGQALQADHTWATVROGLVDRAQOLLANSTALEBAMLEQOQRLGLVWALQARTQ 2515  
2597 LRDVRAKQOLEAHIQAAQAMLANDTDETSKTIHAKAVAAEAQDATTAVQSOLOQAMQEN 2656  
2516 LHNWARKQOLAAQIQEAQAMLANDTDETSKTIHAKAVAAEAQDATTAVQSOLOQAMQEN 2575  
2657 VERWQOQYEGRLGODLQQAQVLDAGHVSLEKTLIPOLLAKLSILENVRGVHNASLALSBI 2716  
2576 VERWQOQYEGRLGODLQQAQVLDAGHVSLEKTLIPOLLAKLSILENVRGVHNASLALSBI 2635  
2717 GYRELIQAARGAASKVVKPMKNGSGVQLRTPRLADLAAVYALKFYLOG--PEPEPG 2774  
2636 GRVKKLIAQARSAAASKVVKPMKNGSGVQLRTPRLADLAAVYALKFYLOG--PEPEPG 2695

2775 QGTEDREVTMGSRQATGDTMGVSLRDKKVVHVVYQLEAGPAVLSDIDEGEQAFAVSLD 2834  
2696 KNTGDHVLVINGRQATGDTMGVSLRDKKVVHVVYQLEAGPAVLSDIDEGEQAFAVSLD 2755  
2835 RTLOFGHMSVTVPERQMIQETKGTVAPEAGELNLRPDDPFVYVGGYPSFTTTPPPLRFP 2894  
2756 RTLOFGHMSVTVPERQMIQETKGTVAPEAGELNLRPDDPFVYVGGYPSFTTTPPPLRFP 2815  
2895 GYRCIEMDTLNEBVSINPFTFQDQTAVDPRCARSKSTGDPWLTGDSYLDGOTGPARI 2954  
2816 GYLCIEMDTLNEBVSINPFTFQDQTAVDPRCARSKSTGDPWLTGDSYLDGOTGPARI 2875  
2955 SFDQISQITTKRFQELRLVSVGLPFLKQCSQFLCLAVQEGSLVLLYDFGAGLKAAPVL 3014  
2876 SFEKQFNSTKRFQELRLVSVGLPFLKQCSQFLCLAVQEGSLVLLYDFGAGLKAAPVL 2935  
3015 OPPPLTSASKATOYFLLGSRKRVLRVERATVSVYQDNLDLEADAVYLGVPDPQLP 3074  
2936 OPPQALTAASKATOYFLLGSRKRVLRVERATVSVYQDNLDLEADAVYLGVPDPQLP 2995  
3075 PSLRLWLPFTGSGVRGCVKIGKALGVYDLKRLNNTTGSAGCTADLLVGRAMTFHGHFLR 3134  
2996 LSLRLWLPFTGSGVRGCVKIGKALGVYDLKRLNNTTGSAGCTADLLVGRAMTFHGHFLR 3055  
3135 LALSNVAPLTGNTVYSGFGFHSADSALLYYRASPDGLCQVSLQOGRVSLQLLATEVTKQA 3194  
3056 LALPDVAPITTEVYVSGFGFHSADSALLYYRASPDGLCQVSLQOGRVSLQLLATEVTKQA 3115  
3195 GFADGAPHYVAFTSNAGVWLYYDDLOQOMKPRGPPPELPQEPGPRLLGLLGLPESGT 3254  
3116 VFADGAPHYVAFTSNAGVWLYYDDLOQOMKPRGPPPELPQEPGPRLLGLLGLPESGT 3175  
3255 IYNSFGCISNVFQRLGPRVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQATARK 3314  
3176 FHNFSGCISNVFQRLGPRVFDLQONLGSVNVSTGCAPALQATPGLGPRGLQATARK 3228  
3315 ASRSSROPASHPACMLPHLRTTRDSYQFGGSLSSHLEFVGLARHNPSPSLSMHVLPR- 3373  
3229 VRSRSPQSLACTTTPWLPCTQDAYQFGGSLSSHLEFVGLARHNPSPSLSMHVLPR- 3288  
3374 SSRGLLFTARLRPSPSLALFLSNHGFVAQMEGLGTRLSAQSRQRSPGRMHKVSVRWE 3433  
3289 ASQGLLSTAPMSGRSPSLVFLNHHGFVAQMEGLGTRLSAQSRQRSPGRMHKVSVRWE 3348  
3434 KNRILLVTDGARANOSGRPHRQHQGAHPOPHTLFVCGLPASSHSSKLPVTVGSGCVKR 3493  
3349 MQQILVVDGSGTQMSQALHHRVPRABRPQPYTLVSGGLPASSYSSKLPVTVGSGCVKR 3408  
3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFPFGSGGVITLDPGATLDPVGLLEVRPLA 3553  
3409 LQDLKQPLRTPTQNVGTVPCVSGGLEDLFPFGSGGVITLDPGATLDPVGLLEVRPLA 3468  
3554 VTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEFSTVTPSPVLCQGWRLAVMKS 3613  
3469 AAGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEFSTVTPSPVLCQGWRLAVMKS 3527  
3614 GNVLRLEVDAQSNHTVGPFLAAAGAPAPLYLGLPEPMAVQVPPPAYCGCMRRLAVNRS 3673  
3528 RDTLRLEVDQSNHTVGPFLAAAGAPAPLYLGLPEPMAVQVPPPAYCGCMRRLAVNRS 3587  
3674 PVAMTRSVHEHGAAGSGCPA 3694  
3588 PVAMTRSVHEHGAAGSGCPA 3608

## RESULT 9

US-10-037-417-47  
; Sequence 47, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Keskula, Ramesh  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Tchernev, Velizar T





Db 1320 YDFISHCATQGYHISFSSSPFCRANATSLSLFYNGALPCOCHEVGVASVPCEPFGQC 1379  
QY 1458 PCHAVHIGRDCRCATGYWGFNCRPCDCGRLCDBELTGQCICPRTTIPDDCLLQCPQTF 1517  
Db 1380 PCRGHVIGRDCRCATGYWGFNCRPCDCGRLCDBELTGQCICPRTTIPDDCLVCPQSF 1439  
QY 1518 GCHPLVGCBECCSGGIGIELDPTCDTDSGCKCRPNVTRGCRDTCSPGFHGYRCPRC 1577  
Db 1440 GCHPLVGCBECCSGGIGVQSLDPTCDMDSGCQCRPNVAGRRCDTCAFGFYGSCRCPC 1499  
QY 1578 DCHAGTAGVGCDDPLTGQCYCKENVGPKDCDCLGTFSLDAANPKGTCTRCFCFGATERC 1637  
Db 1500 DCHAGTAGVGCDDPLTGQCHCKENVGSRCDQCRVGTFSLDAANPKGTCTRCFCFGATERC 1559  
QY 1638 RSSYTRQBFVDMGFWLLSTDRQVPHRQPGTEMLRADLHVPEAVPEAPPELYWQAP 1697  
Db 1560 GNSNLARHEFVDMGFWLLSSDRQVPHRPEIELLHADLR----SVADTFESELWQAP 1615  
QY 1698 PSYLGDRVSYGGLIYELHSETQRCGVFVPMESRDPVVLQGNQMSITFLEPAYTPGHV 1757  
Db 1616 PSYLGDRVSYGGLIYELHSETQRCGVFIPESRDPVVLQGNQMSIAFELAYPPGVQ 1675  
QY 1758 HRGQLOLVEGNFRHTTRNTVSRREELMMVLASLEQIQIRALFSQISSAVSLRRVALEVAS 1817  
Db 1676 HRGQLOLVEGNFRHTTRNTPSVRREELMMVLASLEQIQIRALFSQISSAVSLRRVLEVAS 1735  
QY 1818 PAGOGALASVELCLCPASVRGDSQCECAPFYRDKGLFLGRCVPCQCHGSDRCLPGS 1877  
Db 1736 EAGRGPPASVELCMCPANVRGDSQCECAPFYRDKGLFLGRCVPCQCHGSDRCLPGS 1795  
QY 1878 GVCVDCOHNTEGAHCRCQAGFMSS--RDDPSAPCVSCPCPLSPVSNFAEGCVLRGRTO 1936  
Db 1796 GICVGCQHNTEGAHCRCQAGFMSS--RDDPSAPCVSCPCPLSPVSNFAEGCVLRGRTO 1855  
QY 1937 CLCKPGVAGASCRCAPGFFGNPLVLGSSQPCDCSGNGDPLNLPSCDPLTGACRGCLR 1996  
Db 1856 CLCKPGVAGASCRCAPGFFGNPLVLGSSQPCDCSGNGDPLNLPSCDPLTGACRGCLR 1915  
QY 1997 HTTGPCEICAPGYGNALLPGNCTRCDCPTEACDPSHCHLCKAGVTGRRCDRCQE 2056  
Db 1916 HTTGPCEICAPGYGNALLPGNCTRCDCPTEACDPSHCHLCKAGVTGRRCDRCQE 1975  
QY 2057 GHFGNCGGCRPCACGPAAGSECHPQSGQCHRCRPGTGMQPCRECAPGWGLPBOGCR 2116  
Db 1976 GHFGNCGGCRPCACGPAAGSECHPQSGQCHRCRPGTGMQPCRECAPGWGLPBOGCR 2035  
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Db 2036 CQCPGRCDEHTGRCNCPGLSBERCDTCSQHQVPPVPGFVGHSHCEVCDHCVVLLD 2095  
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Db 2096 DLERAGALLPAIHEQLRGINASSMAWARLHRLNASIADLQSLRSPGPRHETAQOLEVL 2155  
QY 2237 EQOSTSLGODARLGGVAGTRDOASOLLAGTEATLGHAKTLLAAITRAVDRTLSLMSOT 2296  
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QY 2297 GHLGLANASAPSGQLLRTLAVERLLWEMRARDLGAPOAAAEALAAQRLARVOEQL 2356  
Db 2216 GQSGPGLDALVPSGQLWALAEVERLLWEMRARDLGAPOAAAEALAAQRLARVOEQL 2275  
QY 2357 SSLWEENQALATQTRDLAHEAGLMDIREALNPAVDATREAOFLNSRNOERLEALORK 2416  
Db 2276 TSFWEENQSLATHIRDQLAQYESGLMDLREALNOAVNTTREAELNSRNOERLEALORK 2335  
QY 2417 QELSRDNATLQATLHAARDTILASVFRLLHSDQAKBEELERLASLDGARTPLLRMQTFS 2476  
Db 2336 QELSRDNATLQATLHAARDTILASVFRLLHSDQAKBEELERLASLDGARTPLLRMQTFS 2395  
QY 2477 PAGSKLRLVEAAEHAHQLOLALNLSIILDVNQDRLTORAEASNAYSRILOAQVAAE 2536

Db 2396 PASSKVDLVEAAEHAHQLOLALNLSIILGINQDRF:QRAVEASNAYSRILOAQVAAE 2455  
QY 2537 DAAGQALQOQADHTWATTVROGLVDRAQOQLLANSTALEEAMLOEQORLGLVWAAALQOARTQ 2596  
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Db 2636 GRVRELLAQARGAASKVKVPMKFNKRSQVLRPRDLADLAAYTALKFYLG--PEPEPG 2695  
QY 2775 QGTEDRFVWNGSRQATGDMVSLRDKKVVHVYOLGSEAPVLSIDEDIGEQAFAASLD 2834  
Db 2696 KNTGDHFVWNGSRQATGDMVSLRDKKVVHVYOLGSEAPVLSIDEDIGEQAFAASLD 2755  
QY 2835 RTLOFGHMSVTVRQMIQETKGTAVAPGAEGLNLNRPDDFVYVGGYPSFTTTPPLLRFP 2894  
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QY 2895 GYRGCIEMDTLNEEVSILYNPFTFQDQAVDRPCARSKSTGDPMLTGDGSLDGTGTARI 2954  
Db 2816 GYRGCIEMDTLNEEVSILYNPFTFQDQAVDRPCARSKSTGDPMLTGDGSLDGTGTARI 2875  
QY 2955 SFDQISITTKRFEQELRLVSYGVFLFKQOSQFLCLAVOGSLVLLYDFGAGLKKAVPL 3014  
Db 2876 SFDQISITTKRFEQELRLVSYGVFLFKQOSQFLCLAVOGSLVLLYDFGAGLKKAVPL 2935  
QY 3015 QPPPLPLTSASKAIQVFLGGSRKELVVRVERATVYSVEQDNDLEBLADAYILGGVPPDOLP 3074  
Db 2936 QPPPLPLTSASKAIQVFLGGSRKELVVRVERATVYSVEQDNDLEBLADAYILGGVPPDOLP 2995  
QY 3075 PSLRMLPFTGSGVSGVKGKIKALGYVDLKLNTTGVSACTADLLVGRAMTFHGHGFLR 3134  
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QY 3135 LALSNAVLTCNVYSGFHSQAQDSALLYRASPDGLCQVSLQOGRVSLQLLRTEVTKQA 3194  
Db 3056 LALSNAVLTCNVYSGFHSQAQDSALLYRASPDGLCQVSLQOGRVSLQLLRTEVTKQA 3115  
QY 3195 GFADGAPHYVAFYFNATQVWLYDDOLOQMKPHRGPPELOQOPEGPRLILGLPESGT 3254  
Db 3116 GFADGAPHYVAFYFNATQVWLYDDOLOQMKPHRGPPELOQOPEGPRLILGLPESGT 3175  
QY 3255 IYNFSGCISNVFVORLLGPQVFDLQOQLGNSVNVSTGCAPALQATPGLGPRGLQATARK 3314  
Db 3176 IYNFSGCISNVFVORLLGPQVFDLQOQLGNSVNVSTGCAPALQATPGLGPRGLQATARK 3228  
QY 3315 ASRRRQRPARHPACMLPHLRTTRDSYQFGSLSHLEFVGLIARHNMWPSLSHVLPR- 3373  
Db 3229 VSRRSRQSPQDLACTTPWLPGTIQDAYQFGGLPSYQFVGSFHSRNLHLMLVRPHA 3289  
QY 3374 SRRGILLTARLPGSPSIALFLNSGHFVAQMEGLGTRLRQAQRORSRPRGHWKYSVRWE 3433  
Db 3289 ASQGLLSTAPNSGRSPSLVFLNHGHFVAQTEGPGFLOVQSRQHSRAGQHWVSVRWG 3348  
QY 3434 KNRILLVTDGARAWSQEGPHEHQGAHPQPHUFTVGLPASSSHSSKLPVTVGSGCCVKR 3493  
Db 3349 MQOIQLVWDGSGTWESQKALHHRVPRAPRPPQPYTLTVSGGLPASSYSSKLPVSVGSGCCLK 3408  
QY 3494 LBLHRGPGLAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLDPVGLLEVRPLA 3553  
Db 3409 LQLDQOPLRTQMVGVTPCVSGPGLDGLFFPGSGGVITLDPGATLDPVGLLEVRPLA 3468  
QY 3554 VTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEFSTSVTRPSVLCGQWHLRANVMS 3613  
Db 3469 AAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTPK-LCDGRWHRVAVIMG 3527



1698 QY PSYLGDRVSSYGGTULRYELHSETQRTQGVFVPMESRPDVVLQGNQMSITFLFPAYTPGHV 1757  
1616 Db PSYLGDRVSSYGGTULRYELHSETQRTQGVFVPMESRPDVVLQGNQMSITFLFPAYTPGHV 1675  
1758 QY HRGQQLQVEGFRHETENTVSRBELMMVLASLEQLQIRALFSGTSSAVSRVVALEVAS 1817  
1676 Db HRGQQLQVEGFRHETENTVSRBELMMVLASLEQLQIRALFSGTSSAVSRVVALEVAS 1735  
1818 QY PAGQALASNVLCPLCPASRYGDSQCECAPFYRDVKGFLTGRVPCOCHGSHDRCLPGS 1877  
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1878 QY GVCVDCQNTGHAHCERCOAGPMSS- RDDPSAPCVSCPCPLSVSNFNAECVLRGRTQ 1936  
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1997 QY HTTGPRCEITCAPGFGYNALLPNCNTRCDCTPCGTEACDPHSGHCLCKAGVTGRRCDRCOE 2056  
1916 Db HTTGPRCEITCAPGFGYNALLPNCNTRCDCTPCGTEACDPHSGHCLCKAGVTGRRCDRCOE 1975  
2057 QY GHFGFNGCGGRCPCACGPAAGSECHPQSGQCHCRPGTMGQCRCACFYWGLPEQGCR 2116  
1976 Db GHFGFNGCGGRCPCACGPAAGSECHPQSGQCHCRPGTMGQCRCACFYWGLPEQGCR 2035  
2117 QY CQCPGRCDPHTGRCNCPGLSGERCDCSCQOHQVVPVPGGVGHSIHCEVCHCVLLLD 2176  
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2177 QY DIERGALLPALTHEOLRGINASMAWARLHRLNASIADLQSLRSPGLPRHETHAQLEVL 2236  
2096 Db DIERGALLPALTHEOLRGINASMAWARLHRLNASIADLQSLRSPGLPRHETHAQLEVL 2155  
2237 QY EQOSTSLQDARLGGQAVGTQDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSLSMQT 2296  
2156 Db EQOSTSLQDARLGGQAVGTQDQASQLLAGTEATLGHAKTLLAAIRAVDRTLSLSMQT 2215  
2297 QY GHGLGANASAPGEOLRTLASVERLLMEMRADLGAPOAAEAELAAQRLARVQBOL 2356  
2216 Db GHGLGANASAPGEOLRTLASVERLLMEMRADLGAPOAAEAELAAQRLARVQBOL 2275  
2357 QY SSLWEENQALATCTDRRLAQHAGLMDUREALNRAVDATREAOELNSNRQERLEALQK 2416  
2276 Db SSLWEENQALATCTDRRLAQHAGLMDUREALNRAVDATREAOELNSNRQERLEALQK 2335  
2417 QY QELSRDNATLQATLHAARDTLASVFLHLSLDOAKEELERLAASLDGARTPLLRQMOTFS 2476  
2336 Db QELSRDNATLQATLHAARDTLASVFLHLSLDOAKEELERLAASLDGARTPLLRQMOTFS 2395  
2477 QY PAGSKRLVYEAABAAHQQLGQALANLSSIILDVNQDRLTQRAIEASNAYSRILOVQAAE 2536  
2396 Db PAGSKRLVYEAABAAHQQLGQALANLSSIILDVNQDRLTQRAIEASNAYSRILOVQAAE 2455  
2537 QY DAAGQALQADHTWATVYRQGLVDRQAQQLANSTALEEAMLOEQOQLGLVWAAQAGARTQ 2596  
2456 Db DAAGQALQADHTWATVYRQGLVDRQAQQLANSTALEEAMLOEQOQLGLVWAAQAGARTQ 2515  
2597 QY LRDVRAKQDLQEAHQAAQAMLANDTETSXKIAHAKVAABEAQDTATRVOSQLQAMQEN 2656  
2516 Db LRDVRAKQDLQEAHQAAQAMLANDTETSXKIAHAKVAABEAQDTATRVOSQLQAMQEN 2575  
2657 QY VERWQOQYGLRGQDLQGOAVLDAGHSVSTLEKTLFOLLAKLSILENRGVHNASIALSASI 2716  
2576 Db VERWQOQYGLRGQDLQGOAVLDAGHSVSTLEKTLFOLLAKLSILENRGVHNASIALSASI 2635  
2717 QY GAVRELIAGARGAASVKVPMKFNRSQVQLTPRDLADLAAYTALKFYLOQ--PEPEPG 2774  
2636 Db GAVRELIAGARGAASVKVPMKFNRSQVQLTPRDLADLAAYTALKFYLOQ--PEPEPG 2695  
2775 QY QGTEDRFVYMGSRQATGDMYGSURDKKVVHVVYQLGEAGPAVLSDIDEDIGEQQFAAVSLD 2834

2696 Db KNTGDHFVLYMGSRQATGDMYGSURDKKVVHVVYQLGEAGPAVLSDIDEDIGEQQFAAVSLD 2755  
2835 QY RTLOFQGHMSVTVVERQMIQETKGTAVAPGAEGILNLRPDDFVYVGGYPTFTPPPLLRPP 2894  
2756 Db RTLOFQGHMSVTVVERQMIQETKGTAVAPGAEGILNLRPDDFVYVGGYPTFTPPPLLRPP 2815  
2895 QY GYEGCIEMTDLAEEVVSILYNEFBRTFOLDTAVRPPCARSKSTGDPWLTDCSYLDGTGFARI 2954  
2816 Db GYEGCIEMTDLAEEVVSILYNEFBRTFOLDTAVRPPCARSKSTGDPWLTDCSYLDGTGFARI 2875  
2955 QY SPDSQISTTKRPEQELRLVSYSGVLFPFLKQOQFCLAVQEGSLVLLYDFGAGLKAIVPL 3014  
2876 Db SPDSQISTTKRPEQELRLVSYSGVLFPFLKQOQFCLAVQEGSLVLLYDFGAGLKAIVPL 2935  
3015 QY OPPPPLTSKATQOVFLLGSRKRVLRVERATVYSVEODNDLELADAYVYLGVPVPPDQLP 3074  
2936 Db OPPPPLTSKATQOVFLLGSRKRVLRVERATVYSVEODNDLELADAYVYLGVPVPPDQLP 2995  
3075 QY PSRLWLPFTGGSYRGCVKGIKALGVYDVKRLNTTQVSAGCTADLLVGRAMTHGHGFLR 3134  
2996 Db PSRLWLPFTGGSYRGCVKGIKALGVYDVKRLNTTQVSAGCTADLLVGRAMTHGHGFLR 3055  
3135 QY LALSNTAPLTGNTVYSGFGHSAQDSALLYRASPDGLCOVSLQOQGRVSLQLLATEVKTQA 3194  
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3195 QY GFADGAPHYVAFYSNATGVMLYVDDQLQOMKPHRGPPPELQPOPEGPPRLLLGGLPESGT 3254  
3116 Db GFADGAPHYVAFYSNATGVMLYVDDQLQOMKPHRGPPPELQPOPEGPPRLLLGGLPESGT 3175  
3255 QY IYFSGCISNVFQRLGPGORVFDLQONLGSUNVSTGCAPALQAOPTGLGPRGLQATARK 3314  
3176 Db IYFSGCISNVFQRLGPGORVFDLQONLGSUNVSTGCAPALQAOPTGLGPRGLQATARK 3328  
3315 QY ASRRSROPARHPACMLPHLRTTRDSVQFGGSLSSHLEFVGIILARHNPWPSLSMHVLP 3373  
3229 Db ASRRSROPARHPACMLPHLRTTRDSVQFGGSLSSHLEFVGIILARHNPWPSLSMHVLP 3288  
3374 QY SSRGLLFTARLPSPSALFLSNHGFVAQMEGLGTRLAQSRQSRPQRWHKVSURWE 3433  
3289 Db SSRGLLFTARLPSPSALFLSNHGFVAQMEGLGTRLAQSRQSRPQRWHKVSURWE 3348  
3434 QY KNRILTAVDCARAWSOBGRHQHQPHTLVFGGLPASPSSHSLKPLVTVGFGSCVKR 3493  
3349 Db KNRILTAVDCARAWSOBGRHQHQPHTLVFGGLPASPSSHSLKPLVTVGFGSCVKR 3408  
3494 QY LRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLA 3553  
3409 Db LRLHGRPLGAPTRMAGVTPCILGLEAGLFFPGSGGVITLDPGATLPDVGLELEVRPLA 3468  
3554 QY VTGLIFHLQOARTPPYLOQVTEKQVLLRADGAGEFSTSVTEPSVLCDGQWHLAVMKS 3613  
3469 Db VTGLIFHLQOARTPPYLOQVTEKQVLLRADGAGEFSTSVTEPSVLCDGQWHLAVMKS 3527  
3614 QY GNVLRLEVDQAQSNHTVGPILAAAAGAPAPLYLGLPEPMAVQPPPAYCGCMRLAVNRS 3673  
3528 Db GNVLRLEVDQAQSNHTVGPILAAAAGAPAPLYLGLPEPMAVQPPPAYCGCMRLAVNRS 3587  
3674 QY PVMTSRVVEHGVAGVAGCCPA 3694  
3588 Db PVMTSRVVEHGVAGVAGCCPA 3608

RESULT 11

US-10-037-182-36  
; Sequence 36, Application US/10037182  
; Publication No. US20030044899A1  
; GENERAL INFORMATION:  
; APPLICANT: Tryggvason, Karl  
; APPLICANT: Doi, Masayuki  
; APPLICANT: Thyboll, Jill  
; TITLE OF INVENTION: Recombinant Laminin 10

```
; FILE REFERENCE: 99-274-F
; CURRENT APPLICATION NUMBER: US/10/037,182
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,449
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/279,282
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 36
; LENGTH: 2743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-182-36

Query Match      75.2%; Score 15120; DB 14; Length 2743;
Best local similarity 100.0%; Pred. No. 0;
Matches 2743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGAPALLVGLLGHARAREAGGGSFSLHPYFNLAEGARIAA 60
Db 1 MAKRLCAGSALCVRGPRGAPALLVGLLGHARAREAGGGSFSLHPYFNLAEGARIAA 60
QY 61 SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120
Db 61 SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120
QY 121 IDGTERWQSPPLSRGLEYNVNTLDIGQVHVAVVLIKEANSRPDLWYERSMDFGR 180
Db 121 IDGTERWQSPPLSRGLEYNVNTLDIGQVHVAVVLIKEANSRPDLWYERSMDFGR 180
QY 181 TYQPMOFFASSKRDCLERPGQTLERITRDDAAICTTEYSRIVPLENGEIVSLVNGRPG 240
Db 181 TYQPMOFFASSKRDCLERPGQTLERITRDDAAICTTEYSRIVPLENGEIVSLVNGRPG 240
QY 241 AMNFSYSPLLREFTKATNVRLEFNTNLLGHLMKALRDEPTVRRVYYSIKDISIGRC 300
Db 241 AMNFSYSPLLREFTKATNVRLEFNTNLLGHLMKALRDEPTVRRVYYSIKDISIGRC 300
QY 301 VCHGHADAADKPTDPPFLQCTOHNCTCGTCRCRCCPGNQCPWKATANSANECOSCN 360
Db 301 VCHGHADAADKPTDPPFLQCTOHNCTCGTCRCRCCPGNQCPWKATANSANECOSCN 360
QY 361 CYGHATDCYDVEVDRRASQSLDTYGGGVGVCIDQHTTAGVNCERCLGFFVRSNHL 420
Db 361 CYGHATDCYDVEVDRRASQSLDTYGGGVGVCIDQHTTAGVNCERCLGFFVRSNHL 420
QY 421 DSPHVCRRNCESDFTDGTCDLTCRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND 480
Db 421 DSPHVCRRNCESDFTDGTCDLTCRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND 480
QY 481 TREQVLPAQIYNCDCSAAGTQGNACRDPVRGRLCKPNFQGTCHCELCAPEGVGCQP 540
Db 481 TREQVLPAQIYNCDCSAAGTQGNACRDPVRGRLCKPNFQGTCHCELCAPEGVGCQP 540
QY 541 CQCSGPGVADDCDPTDGTQCRVGFEGATCDRCAPGYFHPPLCQLCGCSPAGTLPBEGCD 600
Db 541 CQCSGPGVADDCDPTDGTQCRVGFEGATCDRCAPGYFHPPLCQLCGCSPAGTLPBEGCD 600
QY 601 EAGRLCQPEFAGPCDCRCRPGYHFNQCACTCDPRGALDOLCAGGLCRCPGYGTGA 660
Db 601 EAGRLCQPEFAGPCDCRCRPGYHFNQCACTCDPRGALDOLCAGGLCRCPGYGTGA 660
QY 661 CQCSGPGHGFPSVCPCHSAEGLSAAACDPRSGQCSRPRVTGLRCDTICVGAYNFFYC 720
Db 661 CQCSGPGHGFPSVCPCHSAEGLSAAACDPRSGQCSRPRVTGLRCDTICVGAYNFFYC 720
QY 721 EAGSCHPAGLAPVDLPALPEAQVPCMCRAHVGPSCDRCKPFWGLSPSNPEGTCRSCDL 780
Db 721 EAGSCHPAGLAPVDLPALPEAQVPCMCRAHVGPSCDRCKPFWGLSPSNPEGTCRSCDL 780
QY 781 RTGLGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCIDGALGQS 840
Db 781 RTGLGVAECQPGTGQCFCKPHVCGQACASCKDGGFFGLDQADYFGCRSCRCIDGALGQS 840
QY 841 CEPRTGVCRCRNTQPTCSEPADRDHYLPDLHLRLLEBAATPEGHAVRFGFNPLEFEN 900
Db 841 CEPRTGVCRCRNTQPTCSEPADRDHYLPDLHLRLLEBAATPEGHAVRFGFNPLEFEN 900
QY 901 FSWRGYAQMAVPQPRIVARLNLTSPLDFWLIVRVNNGAMSVSRVSRVREGSAAACANC 960
Db 901 FSWRGYAQMAVPQPRIVARLNLTSPLDFWLIVRVNNGAMSVSRVSRVREGSAAACANC 960
QY 961 TAQSQPVAFPPSTPEAFITVQRCFGFBPVLPNPTWALRVABGVLLDYVVLPSAYEEA 1020
Db 961 TAQSQPVAFPPSTPEAFITVQRCFGFBPVLPNPTWALRVABGVLLDYVVLPSAYEEA 1020
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDLGFPSPAAGLEALCRQDNLSLRPCPTQEL 1080
Db 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDLGFPSPAAGLEALCRQDNLSLRPCPTQEL 1080
QY 1081 SPSSHPLATCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQRAPOGGLL 1140
Db 1081 SPSSHPLATCTGSDVDVQLQVAVPQGRYALVVEYANEDARQEVGVAVHTPQRAPOGGLL 1140
QY 1141 SLHPCLYSTLCRGARTDQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVIEEFSPEFV 1200
Db 1141 SLHPCLYSTLCRGARTDQDHLAVFHLDSASVRLTAEQARFFLHGVTLPVIEEFSPEFV 1200
QY 1201 EPRVSCISSHGAFGPNSAACLPSRFPKPPQIILRDCQVILPPLGCLPLTHAQDLTPATSP 1260
Db 1201 EPRVSCISSHGAFGPNSAACLPSRFPKPPQIILRDCQVILPPLGCLPLTHAQDLTPATSP 1260
QY 1261 AGPRPRPTAVDPAEPTLLREPOATVVTHTVPTLGRYAFLLHGYPQAPHTFPVEVLIN 1320
Db 1261 AGPRPRPTAVDPAEPTLLREPOATVVTHTVPTLGRYAFLLHGYPQAPHTFPVEVLIN 1320
QY 1321 AGRVWQGHANASFCPHGVGCGRTLVVCGQALLDVTHSELVTVRVPEGRWLVDYVLPV 1380
Db 1321 AGRVWQGHANASFCPHGVGCGRTLVVCGQALLDVTHSELVTVRVPEGRWLVDYVLPV 1380
QY 1381 ENVYSFGYLRBEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNNGARPCGC 1440
Db 1381 ENVYSFGYLRBEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNNGARPCGC 1440
QY 1441 HEVATGTCFPGGQCPCHAHVIGRDCRCATGYMGFNCRCDCGARLDELTCQCIC 1500
Db 1441 HEVATGTCFPGGQCPCHAHVIGRDCRCATGYMGFNCRCDCGARLDELTCQCIC 1500
QY 1501 PPRTIPDCLLCQPTFGCHPLVGCCECNCSGPGIOELTDPTCDTSDGCKCRPNVTGRR 1560
Db 1501 PPRTIPDCLLCQPTFGCHPLVGCCECNCSGPGIOELTDPTCDTSDGCKCRPNVTGRR 1560
QY 1561 CDTCSPGHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVOGPKDCQCSLGTFFSLDAA 1620
Db 1561 CDTCSPGHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVOGPKDCQCSLGTFFSLDAA 1620
QY 1621 NPKGTCRCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680
Db 1621 NPKGTCRCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVVPHERQPGTEMLRADLRH 1680
QY 1681 VPEAVPAFPELYWQAPPSYLGDRVSSYGGTFLVHLHSETQRCGDVFPVRESRDVVLQGN 1740
Db 1681 VPEAVPAFPELYWQAPPSYLGDRVSSYGGTFLVHLHSETQRCGDVFPVRESRDVVLQGN 1740
QY 1741 QMSITTFLEPAYPTPGVHRGQQLVCEGNFRHTETRTNVSREELMMVLASLEQIQIRALFS 1800
Db 1741 QMSITTFLEPAYPTPGVHRGQQLVCEGNFRHTETRTNVSREELMMVLASLEQIQIRALFS 1800
QY 1801 QISSAVLSLRVALVAVSPAGGALANVELCLCPASVYRGDSQCECAPGFFVDRVKGFLGR 1860
Db 1801 QISSAVLSLRVALVAVSPAGGALANVELCLCPASVYRGDSQCECAPGFFVDRVKGFLGR 1860
QY 1861 CVPQCCHGHSRCLPGSGVGVCDQHNTEGARHCRCQAGFMSRRDPSAPCVSCPCPLSYV 1920
Db 1861 CVPQCCHGHSRCLPGSGVGVCDQHNTEGARHCRCQAGFMSRRDPSAPCVSCPCPLSYV 1920
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Db 541 CGARTQLRVRKQQLQLEAHIQAAQAMLANMDTETSKTIAHAKAVAAEAQDTATRVOSQL 600  
Qy 2651 QAMQENVERQGOYEGRLGQDLQAOAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 2710  
Db 601 QAMQENVERQGOYEGRLGQDLQAOAVLDAGHSVSTLEKTLPLLAKLSILENRGVHNASL 660  
Qy 2711 ALSASGRVRELLTAQARGAASKVKVPMKENGSGVQLRTPRDLADLAAYTALKFYLOQPE 2770  
Db 661 ALSASGRVRELLTAQARGAASKVKVPMKENGSGVQLRTPRDLADLAAYTALKFYLOQPE 720  
Qy 2771 PEPQGTEDRFVYMGSRQATGDMYGLSRDKKXVHWYQLGEAGPAVLSDIDEDIGEOPAA 2830  
Db 721 PEPQGTEDRFVYMGSRQATGDMYGLSRDKKXVHWYQLGEAGPAVLSDIDEDIGEOPAA 780  
Qy 2831 VSLDRILQGHMSVTVVERQWIBETKGDVAPGAEGLANLRDPDFVYVGGYPSFTFPPL 2890  
Db 781 VSLDRILQGHMSVTVVERQWIBETKGDVAPGAEGLANLRDPDFVYVGGYPSFTFPPL 840  
Qy 2891 LRPGVRCIEMDTLNEEVVSLYNFERTPQDTAVDRPCARSKSTGDPWLTDGSLDGTG 2950  
Db 841 LRPGVRCIEMDTLNEEVVSLYNFERTPQDTAVDRPCARSKSTGDPWLTDGSLDGTG 900  
Qy 2951 FARISFDSQISTTKRFEQELRLVSYSGVLFELKQSQFCLAVQSGSLVLYLDFGAGLKK 3010  
Db 901 FARISFDSQISTTKRFEQELRLVSYSGVLFELKQSQFCLAVQSGSLVLYLDFGAGLKK 960  
Qy 3011 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDELADAYLGGVPP 3070  
Db 961 AVPLQPPPLTSASKAIQVFLGGSRKRVLRVERATVYSVEQDNDELADAYLGGVPP 1020  
Qy 3071 DQLPPLRLWFFPTGGVGRGVKXKALGXKVDLKLNTTGVSACTADLLVGRAMTTHGH 3130  
Db 1021 DQLPPLRLWFFPTGGVGRGVKXKALGXKVDLKLNTTGVSACTADLLVGRAMTTHGH 1080  
Qy 3131 GFRLALSNVAPLITGVYSGFPHSAQDSALLYRASPDGLQVSLQGRVSLQLLRTEV 3190  
Db 1081 GFRLALSNVAPLITGVYSGFPHSAQDSALLYRASPDGLQVSLQGRVSLQLLRTEV 1140  
Qy 3191 KTAGFADGAPHVAVYSNATGVWLVDDQLQMKPHRGPPELQPEGPRLILGLPL 3250  
Db 1141 KTAGFADGAPHVAVYSNATGVWLVDDQLQMKPHRGPPELQPEGPRLILGLPL 1200  
Qy 3251 ESGTIYFSGCISNVVQRLLPQVFDLQNLGSLVNVSTGCAPALQATPGLGPRGLQA 3310  
Db 1201 ESGTIYFSGCISNVVQRLLPQVFDLQNLGSLVNVSTGCAPALQATPGLGPRGLQA 1260  
Qy 3311 TAKASRRSQPARHPACVLPHELRTDSDYQFGSLSSHLEFVGLARHNNWPSLSHV 3370  
Db 1261 TAKASRRSQPARHPACVLPHELRTDSDYQFGSLSSHLEFVGLARHNNWPSLSHV 1320  
Qy 3371 LPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQSRORSRPRGWHKVS 3430  
Db 1321 LPRSSRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQSRORSRPRGWHKVS 1380  
Qy 3431 RWEKNRILLVTDGARAWSEGRHROHGAHPQHTLFGVGLPASSHSSKLPVTVGSGC 3490  
Db 1381 RWEKNRILLVTDGARAWSEGRHROHGAHPQHTLFGVGLPASSHSSKLPVTVGSGC 1440  
Qy 3491 VKRLRHGRPLGAPTRMAGVTPCIIPLGPLEAGLFFPGSGGVITLDPGATLPDVGLLEVR 3550  
Db 1441 VKRLRHGRPLGAPTRMAGVTPCIIPLGPLEAGLFFPGSGGVITLDPGATLPDVGLLEVR 1500  
Qy 3551 PLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEFSTVTRPSVLCDGQWHRLAV 3610  
Db 1501 PLAVTGLIFHLGQARTPPYLOQVTEKQVLLRADDGAGEFSTVTRPSVLCDGQWHRLAV 1560  
Qy 3611 MKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQPPWPPAYCGCMRRLAV 3670  
Db 1561 MKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQPPWPPAYCGCMRRLAV 1620  
Qy 3671 NRS-PVANTRSVEHGAASGCPA 3694  
Db 1621 NRSPPVNTRSVEHGAASGCPA 1645

## RESULT 13

US-10-037-417-8

Sequence 8, Application US/10037417

Publication No. US20040052806A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Patturajan, Meera

APPLICANT: Grosse, William M

APPLICANT: Lepley, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Vernet, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malyankar, Uriel M

APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J

APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia

APPLICANT: Shency, Suresh G

APPLICANT: Anderson, David W

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Miller, Charles E

APPLICANT: Eisen, Andrew J

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-235

CURRENT APPLICATION NUMBER: US/10/037.417

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,018

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/272,411

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/272,817

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/291,186

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/303,231

PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/305,060

PRIOR FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 60/318,405

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/318,700

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 1640

TYPE: PRT

ORGANISM: Homo sapiens

US-10-037-417-8

Query Match 42.2%; Score 8499.5; DB 12; Length 1640;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1640; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 2051 CDRCQEGHFGNGCGGCRPCACGPAAGSGECHPQSGCHCRPGTMTGPOCRCAFGTWGLP 2110

Db 1 CDRCQEGHFGNGCGGCRPCACGPAAGSGECHPQSGCHCRPGTMTGPOCRCAFGTWGLP 60

Qy 2111 EOGCERCOCPGRCDDPHTRGNCNCPPLSGBCDCTCSOQHOVPPVGGPVGHSIHCEVCDHC 2170



Db 61 BQCRRCOCPOGRCDPHTGRNCNCPPLSGBERCDTCSQOQVVPVGGPVGHSIHCEVCHDC 120  
Qy 2171 VVLLDDDLERAGALLPAIHEQLRGINASSMAWALHRLNASIADLQSOQRSPLGRHETA 2230  
Db 121 VVLLDDDLERAGALLPAIHEQLRGINASSMAWALHRLNASIADLQSOQRSPLGRHETA 180  
Qy 2231 QOLEVLEQOSTSLGQDARLGGQAVGTQDASOLLAGTEATLGHAKTLLAIRAIVDRTL 2290  
Db 181 QOLEVLEQOSTSLGQDARLGGQAVGTQDASOLLAGTEATLGHAKTLLAIRAIVDRTL 240  
Qy 2291 ELMSTQTHLGLANASAPSGEQLLRTLAEVERLLMEMRARDLGAPOAAAEALAAQRLLA 2350  
Db 241 ELMSTQTHLGLANASAPSGEQLLRTLAEVERLLMEMRARDLGAPOAAAEALAAQRLLA 300  
Qy 2351 RVQOELSSWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAOELNSRNOBLE 2410  
Db 301 RVQOELSSWEENQALATQTRDLAQHEAGLMDLREALNRAVDATREAOELNSRNOBLE 360  
Qy 2411 BALQRKQELSRNATLQATLHAARTDLASVFFLLHSLDQAEELERLAASLDGARTPLQ 2470  
Db 361 BALQRKQELSRNATLQATLHAARTDLASVFFLLHSLDQAEELERLAASLDGARTPLQ 420  
Qy 2471 RMOFTSPAGSKLRLVEABAHAAQOLGOLALNLSIIIDVNOQRLTORAIBASNAYSRILO 2530  
Db 421 RMOFTSPAGSKLRLVEABAHAAQOLGOLALNLSIIIDVNOQRLTORAIBASNAYSRILO 480  
Qy 2531 AVQRAEDAGQALQOADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQORGLVWAAAL 2590  
Db 481 AVQRAEDAGQALQOADHTWATVVRQGLVDRAQQLLANSTALEEAMLOEQORGLVWAAAL 540  
Qy 2591 QGARTQLDRVRAKQOQLEAHIQAAQAMLANOTDETSSKITAHAKAVAAEAQDTATRVQSQL 2650  
Db 541 QGARTQLDRVRAKQOQLEAHIQAAQAMLANOTDETSSKITAHAKAVAAEAQDTATRVQSQL 600  
Qy 2651 QAMQENVERWQOGEGLRGDQGOAVLDAGHSVSTLEKTLPOALLKLSILENRGVHNASL 2710  
Db 601 QAMQENVERWQOGEGLRGDQGOAVLDAGHSVSTLEKTLPOALLKLSILENRGVHNASL 660  
Qy 2711 ALSASIGRVRELIJAARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLOQPE 2770  
Db 661 ALSASIGRVRELIJAARGAASKVKVPMKFNRSRGVQLRTPRDLADLAAYTALKFYLOQPE 720  
Qy 2771 PEPGQGTEDRFVNYGMSRQATGYMGVSLRDKKHVVYOLGEAGPAVLSIDEDIGEQFAA 2830  
Db 721 PEPGQGTEDRFVNYGMSRQATGYMGVSLRDKKHVVYOLGEAGPAVLSIDEDIGEQFAA 780  
Qy 2831 VSLDRILQFGHMSVTVVERQMIQETKGDTVAPAGELNLRPDDFVYVGYSTPTTPEPL 2890  
Db 781 VSLDRILQFGHMSVTVVERQMIQETKGDTVAPAGELNLRPDDFVYVGYSTPTTPEPL 840  
Qy 2891 LRFPFGYRCIEMDTLNEEVSVLYNFERTFQDTPAVDRPCARSKSTGDPWLTGSLDGTG 2950  
Db 841 LRFPFGYRCIEMDTLNEEVSVLYNFERTFQDTPAVDRPCARSKSTGDPWLTGSLDGTG 900  
Qy 2951 FARISFDSQISTTKRFEQELRLVSYSGVLFLLKQSQOFLCLAVQEGSLVLLYDFGAGLKK 3010  
Db 901 FARISFDSQISTTKRFEQELRLVSYSGVLFLLKQSQOFLCLAVQEGSLVLLYDFGAGLKK 960  
Qy 3011 AVPLQPPPLTSASKAIQVFLGGSRRKVLVRVERATVYSVEQNDLLEADAYYLGGVPP 3070  
Db 961 AVPLQPPPLTSASKAIQVFLGGSRRKVLVRVERATVYSVEQNDLLEADAYYLGGVPP 1020  
Qy 3071 DQLPSSLRWLPPTGGSVRGCVKGIKALGVYDLKRLNTTGVSAAGTADLLVGRAMTFHGH 3130  
Db 1021 DQLPSSLRWLPPTGGSVRGCVKGIKALGVYDLKRLNTTGVSAAGTADLLVGRAMTFHGH 1080  
Qy 3131 GFRLALSNVAPLTGNVYSGFGFHSQADSALLYRASPDGLCQVSLQOQKRVSLQLLRTEV 3190  
Db 1081 GFRLALSNVAPLTGNVYSGFGFHSQADSALLYRASPDGLCQVSLQOQKRVSLQLLRTEV 1140  
Qy 3191 KTOAGFADGAPHYVAFVSNATGWLYYDDQLQOMKPHRGPPPELOQPGPPELLLGGPL 3250  
Db 1141 KTOAGFADGAPHYVAFVSNATGWLYYDDQLQOMKPHRGPPPELOQPGPPELLLGGPL 1200

Qy 3251 ESCTIYNFSGCISNVFVQRLGPQVFDLQONLGSVNVSTGCAPALQAOPTGLGPRGLQA 3310  
Db 1201 ESCTIYNFSGCISNVFVQRLGPQVFDLQONLGSVNVSTGCAPALQAOPTGLGPRGLQA 1260  
Qy 3311 TARKASRRSRQPARHPACMLPHELRTTRDSYQFGSLSHLEFVGLIASHRNWPSLSMEV 3370  
Db 1261 TARKASRRSRQPARHPACMLPHELRTTRDSYQFGSLSHLEFVGLIASHRNWPSLSMEV 1320  
Qy 3371 LPSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLTRLRQAQRQRSRPGRMHKVS 3430  
Db 1321 LPSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLTRLRQAQRQRSRPGRMHKVS 1380  
Qy 3431 RWEKNRILLVTDGARAWSOEGPHROHQAEPHPOPHTLFVGGLPASSHSSKLPVTVGFSGC 3490  
Db 1381 RWEKNRILLVTDGARAWSOEGPHROHQAEPHPOPHTLFVGGLPASSHSSKLPVTVGFSGC 1440  
Qy 3491 VKRLRLHGRPLGAPTRMAGVTTCILGLPGLAGLFFPGSGGVITLIDLPGATLPDVGLELEVR 3550  
Db 1441 VKRLRLHGRPLGAPTRMAGVTTCILGLPGLAGLFFPGSGGVITLIDLPGATLPDVGLELEVR 1500  
Qy 3551 PLAVTGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGSFSTSVTRPSVLCQOWHRLAV 3610  
Db 1501 PLAVTGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGSFSTSVTRPSVLCQOWHRLAV 1555  
Qy 3611 MKSGNVLRLVEDAQSNHTVCPILAAAGAPAPLYLGLPEPMAVQPPAYCCGMRLAV 3670  
Db 1556 MKSGNVLRLVEDAQSNHTVCPILAAAGAPAPLYLGLPEPMAVQPPAYCCGMRLAV 1615  
Qy 3671 NRSVPAMTRSVVEHGAAGSCCPAA 3695  
Db 1616 NRSVPAMTRSVVEHGAAGSCCPAA 1640

RESULT 14

US-10-037-417-49  
; Sequence 49, Application US/10037417  
; Publication No. US20040052806A1  
; GENERAL INFORMATION:  
; APPLICANT: Keskuda, Ramesh  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Sciore, Paul  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Stone, David J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Anderson, David W  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Miller, Charles E  
; APPLICANT: Eisen, Andrew J  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260,018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260,360  
; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411  
 ; PRIOR FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: 60/272,817  
 ; PRIOR FILING DATE: 2001-03-02  
 ; PRIOR APPLICATION NUMBER: 60/291,186  
 ; PRIOR FILING DATE: 2001-05-15  
 ; PRIOR APPLICATION NUMBER: 60/303,231  
 ; PRIOR FILING DATE: 2001-07-05  
 ; PRIOR APPLICATION NUMBER: 60/305,060  
 ; PRIOR FILING DATE: 2001-07-12  
 ; PRIOR APPLICATION NUMBER: 60/318,405  
 ; PRIOR FILING DATE: 2001-09-10  
 ; PRIOR APPLICATION NUMBER: 60/318,700  
 ; PRIOR FILING DATE: 2001-09-12  
 ; NUMBER OF SEQ ID NOS: 227  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 49  
 ; LENGTH: 1634  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-037-417-49

Query March 38.8%; Score 7804.5; DB 12; Length 1634;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1533; Conservative 1; Mismatches 5; Indels 13; Gaps 1;

QY	2157	PVCHSTHC-----EVCDCVVLDDLERAGALLPAIHEOLGINASSMAWA	2203
DB	83	PAASSIRCLFQAGLNATATVVCDCVVLDDLERAGALLPAIHEOLGINASSMAWA	142
QY	2204	RLHRLNASIADQSLRSPLGRHETAQOQLEVEEQSTSLGQDARRLGGQAVGTRDQASQ	2263
DB	143	RLHRLNASIADIQSLRSPLGRHETAQOQLEVEEQSTSLGQDARRLGGQAVGTRDQASQ	202
QY	2264	LLAGTEATGAKHTLLAATRAVDRTLSLMSOTGHLGNASAPSGEOLLTLAEVERLL	2323
DB	203	LLAGTEATGAKHTLLAATRAVDRTLSLMSOTGHLGNASAPSGEOLLTLAEVERLL	262
QY	2324	WEMRARDLGAPOAAAEALAAQRLARVQEQSLSLWEENQALATQTRDRLAQAHEAGLMD	2383
DB	263	WEMRARDLGAPOAAAEALAAQRLARVQEQSLSLWEENQALATQTRDRLAQAHEAGLMD	322
QY	2384	LREALNRADTAEQELNSRNOERLEALQKQELSDONATLOATLHAARDTLASVRL	2443
DB	323	LREALNRADTAEQELNSRNOERLEALQKQELSDONATLOATLHAARDTLASVRL	382
QY	2444	LHSLDQAEELERLAASLDGARTPLLQRMOTFSPAGSKRLRVEAAEAHAQQLQALNLS	2503
DB	383	LHSLDQAEELERLAASLDGARTPLLQRMOTFSPAGSKRLRVEAAEAHAQQLQALNLS	442
QY	2504	SIILDVNDRLTORATEASNAYSRILOAVQAAEDDAAGALQOQADHTWATVROGLVDRQA	2563
DB	443	SIILDVNDRLTORATEASNAYSRILOAVQAAEDDAAGALQOQADHTWATVROGLVDRQA	502
QY	2564	QLLANSTALEEAMLOEQQRGLVWAALQOQARTQLRDVRAKDDQLEAHTQAAQAMLMDTD	2623
DB	503	QLLANSTALEEAMLOEQQRGLVWAALQOQARTQLRDVRAKDDQLEAHTQAAQAMLMDTD	562
QY	2624	ETSKKTAHAKAVAAEAQDTRATVQSLQAMQENVERWQOYEGLRGDLQAVLDAGHSV	2683
DB	563	ETSKKTAHAKAVAAEAQDTRATVQSLQAMQENVERWQOYEGLRGDLQAVLDAGHSV	622
QY	2684	STLEKTLPLLAKLSILENRGVNRSALASISIGVRELIQAARGAASKVKVPMKFNRS	2743
DB	623	STLEKTLPLLAKLSILENRGVNRSALASISIGVRELIQAARGAASKVKVPMKFNRS	682
QY	2744	GVOLRTPRLADLAATALKFYLOQPEPEPGQGTEDRFVWYMGSRQATGDTYMGVSLRDKK	2803
DB	683	GVOLRTPRLADLAATALKFYLOQPEPEPGQGTEDRFVWYMGSRQATGDTYMGVSLRDKK	742
QY	2804	VHVVYQLGAGPAVLSDIDEGEQAFAVSLDRTLQFGHMSVTVRQMIQETKGTVAPGA	2863
DB	743	VHVVYQLGAGPAVLSDIDEGEQAFAVSLDRTLQFGHMSVTVRQMIQETKGTVAPGA	802

QY	2864	EGHNLNRDDDFVYVGGYSTFTTTPPILLRPFYGCIEMDTLEEVVSLYNFERTFOLDT	2923
DB	803	EGHNLNRDDDFVYVGGYSTFTTTPPILLRPFYGCIEMDTLEEVVSLYNFERTFOLDT	862
QY	2924	AVDRFCARSKSTGDPWLTGDSYLDGTGFARISFDSQISTTKRFFQELRLVSYSGVLFELK	2983
DB	863	AVDRFCARSKSTGDPWLTGDSYLDGTGFARISFDSQISTTKRFFQELRLVSYSGVLFELK	922
QY	2984	QOSQFLCLAVQEGSLVLLYDFGAGLKKAVPLOPPPLTSASKATQVFLGGSRRKRLVRV	3043
DB	923	QOSQFLCLAVQEGSLVLLYDFGAGLKKAVPLOPPPLTSASKATQVFLGGSRRKRLVRV	982
QY	3044	ERATVYSVEQNDLELADAYYLGVPDQPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPL	3103
DB	983	ERATVYSVEQNDLELADAYYLGVPDQPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPL	1042
QY	3104	KELNTTGVSACTADLLNGRAWTFHGHFLALSNVAPLTGNTVYSGFGHSAQDSALLY	3163
DB	1043	KELNTTGVSACTADLLNGRAWTFHGHFLALSNVAPLTGNTVYSGFGHSAQDSALLY	1102
QY	3164	YRASPDGLCQVSLQOQGRVSLQLLRTVEYKTAQAGFADGAPHYVAFYSNATGVMLYVDDQLQ	3223
DB	1103	YRASPDGLCQVSLQOQGRVSLQLLRTVEYKTAQAGFADGAPHYVAFYSNATGVMLYVDDQLQ	1162
QY	3224	MKPHGSGPPELQOPEGPRLLLGLPESGTYNFSGCISNVFVORLLGPORVFDLQNL	3283
DB	1163	MKPHGSGPPELQOPEGPRLLLGLPESGTYNFSGCISNVFVORLLGPORVFDLQNL	1222
QY	3284	GSVNVSTGCAPALQATPGLGPRGLQATARKASRRSQPARHPACMLPPLHRTTRDSYQF	3343
DB	1223	GSVNVSTGCAPALQATPGLGPRGLQATARKASRRSQPARHPACMLPPLHRTTRDSYQF	1282
QY	3344	GGSLSHLEFVGIILARHNWPSLSMHLPRSSRGLLFTARLRPGSPSLALFLSNGHFVA	3403
DB	1283	GGSLSHLEFVGIILARHNWPSLSMHLPRSSRGLLFTARLRPGSPSLALFLSNGHFVA	1342
QY	3404	QMEGLGTLRAQSRQSRGRWVKVSVRWEKNRILLVTDGARAWSQEGPHRQGAHPQ	3463
DB	1343	QMEGLGTLRAQSRQSRGRWVKVSVRWEKNRILLVTDGARAWSQEGPHRQGAHPQ	1402
QY	3464	PHLTFVGLGPASSHSSKLPVTGFGGCVKRLHLGRPLGAPTRMAGVTPCILGPLEAGLF	3523
DB	1403	PHLTFVGLGPASSHSSKLPVTGFGGCVKRLHLGRPLGAPTRMAGVTPCILGPLEAGLF	1462
QY	3524	PFSGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGOARTPPYLOQVTEKQVLLRA	3583
DB	1463	PFSGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGOARTPPYLOQVTEKQVLLRA	1522
QY	3584	DDGAGEPSTVTRPSVLCDDQWHRLAVKSGNVLRLVDAQSNHTVGPLLAAAAGAPPL	3643
DB	1523	DDGAGEPSTVTRPSVLCDDQWHRLAVKSGNVLRLVDAQSNHTVGPLLAAAAGAPPL	1582
QY	3644	YLGGLPEPMVQPPPPAYCGCMRRLAVNRSPVAMTRSVVHGAVGASGCPAA	3695
DB	1583	YLGGLPEPMVQPPPPAYCGCMRRLAVNRSPVAMTRSVVHGAVGASGCPAA	1634

RESULT 15  
 US-10-037-417-48  
 ; Sequence 48, Application US/10037417  
 ; Publication No. US20040052806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Alsbrook II, John P  
 ; APPLICANT: Tchernev, Velizar T  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Spytek, Kimberly A  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Grosse, William M  
 ; APPLICANT: Lepley, Denise M  
 ; APPLICANT: Burgess, Catherine E  
 ; APPLICANT: Vernet, Corine A.M.

Query Match	25.3%	Score 5097;	DB 12;	Length 3712;
Best Local Similarity	31.7%;	Pred. No. 2.4e-288;		
Matches 1248;	Conservative 609;	Mismatches 1541;	Indels 540;	Gaps 122;
QY	45	LHPYENLAEGARTAASTACGEEAPAGSGSRPRTEDLYCKLVGPVAGGDPN-QTIRGGVC	103	
DB	24	LTPPFNLATGRKIYATATCG---PDTDGP---ELYCKLVGANTBHDHIDYSVIQGGVC	76	
QY	104	DICTAANGKNKAHPASNAIDGTERWQSQPPLSRGLEYNEVNVTLDLQGFHVAYVLKCAN	163	
DB	77	DYCDTPTVERNHPPENALDGTAEWQSQPPLSRGKMEVNVLTINFEQGFHVAYLIRWGN	136	
QY	164	SPRPDLVLEKSMDFGRTYQPMQGFASKKDCULERFGPOTLEIRTRDDAAICTTYSYRIV	223	
DB	137	SPRPLMTLEKSTGYGKTWTQWHSFTPADCETYFGKDTYKPIRTDDDVICTTYSYKIV	196	
QY	224	PLENGEIVVSVLNGRPGAMGPSYSPILARETKATNVRLRFLRNTLLGHLMKALRDPTV	283	
DB	197	PLENGEIVPMNLNERPSTNIFNSVLQEWTRATNVRIRLRTKLLGLHLMVSAQDEPTV	256	
QY	284	TRRYYSIKDLSIGRCVCHGHADCAKADFTDPPR-LQCTCOHNTCGGTCDRCGCGFNQ	342	
DB	257	TRRYFYSIKDLSIGRCWCNCGHADTCVDKPKSPVAILACRQOHTCGIQCNECCPGFEQ	316	
QY	343	QPKWEPATANGANEQSCNCGVGHATDCYVDDEVDRRAASQSLDGTGYGGGVGVCIDCQHTTAG	402	
DB	317	KKWRQNTNARPFNCEPCNCHGSHNECKYSDDEVNRKGLSLDIHGHDYDGGVCVCNCOHNTVG	376	

1455 GOCPCAHVIGRDCRCATGYWFFNCRPCDC--GARLDELGTGOCICPPRTIPPDCLLCQ 1513  
1392 GOCQCKPNIWIERTCGRSRYGFFDKCKPCPSANCEPTTGECKMPPNVIQDLCEKCA 1451  
1514 POTFGCHPLVGBEENCSCGPGIQLTDTCDTDSQCKCRNVNTRCDDTSCPGFHYPR 1573  
1452 PNTYGFHQVIGCEBACACNPMGIAN--GNSQCCLFNGTCECRNIEGRACDVCSNGYFNFP 1510  
1574 CRPCDCHAGTAGVCDPLTGOCYCKENVOGPKCDQCSLGTFSFDAANPKGCTRCFCFGA 1633  
1511 CFCQCSCHKPGTELEVCDKIDGACFKKNVGRDCQCVDTGTYNLOESNPDGCTTCFCFG 1570  
1634 TERCSSSYTROEFVDMEGWLLSTDTRQVVPHERQ-----PGTEM-----LRAD-- 1677  
1571 TSCR--DSAYLRVYVNSLLKHYSITTFEF---HEESIKFDMWVPADILLNETTLKADFT 1626  
1678 LRHVPEAVPEAPPELYWQAPPSYL---GDRVSSVGGTLRYELHSETQRGVDFVPMESRPD 1734  
1627 LREAVDERPAYFGVL-----DYLNNQNNHLSAYGGDLAYTLHFTSGFDGKYI---VAPD 1677  
1735 VVLQGNQMSITPLEPAYTPGHVHRGLOLVGEGFRHTETRTNVSREELMWLASLOLQ 1794  
1678 VILFSEHNALVHTSYEQFSRNEPFTNRYNIVESFQ--TISGKPVSRADFMVWLRLDKVIF 1736  
1795 IRALFSQISSAVSLRRVALEVASPAGQA-----LASNVLCCLCPASYRGDSQCECAPGF 1849  
1737 ISANYEQTLVTHLSDVYTLADEADGTGEYQFLA--VERCSCPFGYSGHSCDCAPGY 1794  
1850 YRDVKGFLGRVCPQCHGHSRDLPGSGVCDVCHNTEGACHRCOAGFM--SRDDPSA 1908  
1795 YRDPSPGYGVCIPCECNGHSETCDATGICSKQCHGTGHDHCRCVSGYGNATNGTPG 1854  
1909 PCVSCPCPLSVSPNNFASGCVL---RGRTQCLCPGYAGASCERCAPGFGNPLVLGSSC 1966  
1855 DCWICACPLPDPNPNFATSCISBSGQIHCECKPGYTGPRCESCANGFYGEPIGQVC 1914  
1967 QPCDCSNGNDPMLFSDCDPTGTACRGCLRTTGPCEICAPGPHYGNALLPGNTRCDCT 2026  
1915 KPCECSGNINPEDQGS--CDTGTGECRLNNTFGAANCNLCPAGFYGDAIKLKNQCSCDCD 1973  
2027 PGCTEACDPHSGHCLCKAGVTGRRCDRCQEGHFGNCGCRPCACGPAAGSEGECHPQSG 2086  
1974 DLGTQTCDFPVGVCCTCHENVIGDRCDCKPDHYFESGVGCRACDCGAASNSTQCDPHG 2033  
2087 QCHCPGTMGQCRECAPGYWGLPEQGRRCQCPGG-----RCDPHGTGRNCFPGLSGER 2141  
2034 HCACKSGVTGRCQRCADVDHWKYBKDGCTPCNCGQYSRGFGCNPNTGKQCLPGVIGDR 2093  
2142 CDTCSQCHQVPVGGFVGHSHCEVCDCRVLLDDLERAGALLPATHEQLRGINASSVA 2201  
2094 CDACPNRWLIKDEG-----CQECNCHALLDVTDRMYQIDSV---LEDFNSVTLA 2143  
2202 WARLHRLN-----ASIALQSLRSPGLPHRET-AQOL 2233  
2144 FFTSQKLYYQDLADELPKVKLLDPNSVDSLSPSKANSSELSDAKSYAKQVNTLANAF 2203  
2234 EYLEQOSTSLGQDARRLGQAVGTRDQASQLLACTEATLGHAKTL-LAAIRAVDRTLSEL 2292  
2204 DIRERSSTLIG-NITVAYDEAVKSADQAKEAIAVEAL---SKNLEAAASTKIDAALEQA 2259  
2293 MSQTGHLGLANAPSGEOLLRTLAVERLLWEMRARDLGAPQAAAEALAAQRLARV 2352  
2260 QHILQINGTSIELTPNEQVL-----EKARKLYE--EYNTLVLPITKAQNKSNALNKNDIGEF 2314  
2353 QEQLSSLEENQALOTRDLRAQHEAGLMDLREALN-RAVDATREAOELNSNQBRLLEE 2411  
2315 SDHLEDLFNWESEASQAKSAD-----VERRNVANOKAFD-----NSKFDVTSBQ 2357  
2412 ALQKQOEL--SRDNATLQNTLHAARDTLASVFRLLHSLDQAKELERLASLDGARTPLIQ 2470  
2358 KLOAKENIKDAGNFINGDL-----TLNQINQKLDNLDALNELSNFNKVD--BELPVRE 2411  
2471 RMQTFSPAGSKRLRVERAAEAHAQGLQALNLSLSSILDVNQDRLTORATEASNAYSRIQ 2530

2412 DQHKREADA-----LTDQAEQKAAELAIAQDLAAQYDWTAS--ABEPAKAAATAYSGIVE 2464  
2531 AVQAAEDAAQALQAOADHTWATVVRQGLVDRAQOLLANSTALEEAMLQSOQ----- 2581  
2465 AVEAAQKLSODAISAAGN--ATDKTDGIBERAHADTGSTDLQORAROSLQKQVDDLEBR 2522  
2582 -----RLGLVWAALQOARTQLDRVRAKQDLQZAHQA-----AQAMLAMDTDETSKK 2628  
2523 LNASAGKVQKISAVNNATEHQLKDINKLIDOLPAESQDRMKNNSANASDALEILKNVLE 2582  
2629 IAHAKAVAAEAQ--DTATRVOSOLOQMOENVERWQGVQEGRLGQDLQOAVLDAGHSVSTLE 2687  
2583 ILEPVSVOITPKELKAHGINRDLDLTNNKQVSQANKQLDDVEG-----SVSKLN 2630  
2688 KTLPOLAKSILENRGVHNASLASISIGRVELIAQARGAASKVKVPMKFNRSQVQL 2747  
2631 B-----LAEDIEEQHRVGSOSQRLQGEIENLKAQVEAAQLANSIKGVNPKFSTILEL 2685  
2748 RTPRDLADLAATKALYLOGPPEPGQGTEDFVVMYG-----SRQATGYMGSVLRDKK 2803  
2686 KTBKTKLLATRTNLSTYFRITTEP-----SGLLYLGNNDKNTAKONNDFVAIVEINGY 2738  
2804 VHWYVQGEAGPAVLSDIEDI--GEOPAAVSLDRTLQFGHMSVTVERQMIQETKGTV-- 2859  
2739 PILTIDLGN--GPERITSDKYVADGRWYQAV--VDR--MGPNAKLTIREEL---PNGDVVEH 2791  
2860 -----APAGEGLNLRRDDDFVYGVGP--STTFPBLRLFFPGYRCIEMDTLINEEWSL 2912  
2792 SKSGYLEGSONILHVDKNKSLF--VGGYEGISDFNAPDPTLTNFSFGDIEDLKIGDESGL 2850  
2913 YNF-----ERTFQDVTADRPCARSKSTGDPMLTDSYLDGTGTFARISFDSQIS 2961  
2851 WNFVYGDNDQOARERDVLLEKKKPTGLRFKNGVYVQLNATSNLKSRSISQSFPAKADK 2910  
2962 TTKEPEQELRLVSVGVLPFLKQOSQFLCLAVOEGSLVLLYDFGAGLKKAVLPQPPPLT 3021  
2911 TS-----NGULFFYGRDKXNSTEMIDGAIFFNISLGEQ-----ATVYSVBQNDLELA 2944  
3022 SASKAIQVFLIGGSRKEV-----LVYRVER-----ATVYSVBQNDLELA 3060  
2945 ---GGVQ---SGSQDRYNDNQWHKQAEARENGLLKVDIVISRTNAPLEADLELPKL 2997  
3061 DAYYLGVPDPDOLPPLSLRWLPFTGGSVRCVKIKALKKVVLDLKRNT--TGVSACTADL 3119  
2998 RRLYFGG--HPRRLNTSIS--LQP---NPDGICDNNVINQGVVDLTETVYGGVEEGSARF 3052  
3120 LVGRAMTFHGHGFLRLALSNAVPLTGNVYSGFGFHSQADSALLYVRASPD--GLCQVSLQ 3177  
3053 STVSVYAPHEVGFLR--MNVVSS--DNNLHVLFHKTTPNGVLFYAANHDAQSSTIGLSLQ 3109  
3178 QGRVSLQOLLSTE-VKTOAGFADGAPHYVAFYSNATGVWLYVDDLOQOMKPHRGPPPELOP 3236  
3110 DGLLKNMSGQLVIDDRILNDGEDHVTVQHTQGBELRTVDDVDNKRUG-----SP 3161  
3237 QP---EGPRLLLGGLPES-----GTIYNPFGCISNVFVQRLIGPQRFDL---QQ 3281  
3162 QPLILEGGD--IPFAGLPDNYRTPRNALASLAYFVGICSDVTYN---BEINFANSAEK 3215  
3282 NLGSVNSTCCALQAOTPELOP----- 3305  
3216 KNGNIN---GCPPHVLAYESLVPYSYPSGDNVESPSWNSADTLPLPKPDIESTLPPTTP 3272  
3306 -----RGLQATARKASRRSROPAR-----HFA 3327  
3273 TTTTTTTTTTTTTTTTTTTTTTPSIVIDESEKEIETKTPQKILTRTPAKNLNPSDR 3332  
3328 CMLPBP-----LRTRDSYQFGSLSHLSFVGLAHARNWPSLSMHVLPSSRGILLFTA 3383  
3333 CKUPEQNFVDVTEAGYRYPGLREORQLINSPLPVKRHHOIGISFTRTERNGLLIY-A 3391  
3384 RLREGSPSLALFSLNGHFAQMEGLTRLRAQ--SRQSRPGRWHKVSVRWEKNRILVIT 3441

Db 3392 GSKQDDFIAYLLDGRVTYR-VGAQLOAKITTEALNDGTWHTVTVVTRQKVSLLI 3450  
Qy 3442 DGAFAWQEGPHRQCHQAEHPQ-----HTLFVGG-----PASSHSSKLPVTVGF 3487  
Db 3451 D-----KLEQPGSVDLNAERSAPVLAVELPIYLGGVNKFLESEVKNLTDEKTEVPY---P 3502  
Qy 3488 SGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFPFGSGGVITLDPGATLPDVGLEL 3547  
Db 3503 NGCLNLIKFDAMDLETPEEPFGVVC-SEQVERGLFFNNQKAFVKI-----FDHFDVGT 3557  
Qy 3548 EV----EPLAVTGLIHLQARTPPYLOLQVTEKQVLLRADDGAGEPSTSVTRPS--VLC 3601  
Db 3558 KISDFPRDPNGLLFSVHGKNSVAILLEL-VDNLYFTVKTDLKNIVSTNYKLPNNESEC 3616  
Qy 3602 DGQWHLAVMKSNGVNLREVD-AQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQWPW-- 3658  
Db 3617 DGKTENVAIKSKFVINIAVDFISSNPGVNEGSVITRTNRPLFLGG---HVAFAQPAPI 3673  
Qy 3659 ---PAYCGMRRLAVNRSFVAMTRSVEVHGAVGASGCP 3693  
Db 3674 KTKSFKGCISKVEVQNRMINITPMVY-GDIWQGYCP 3710

Search completed: May 18, 2004, 15:41:36  
Job time : 133.004 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 14:29:28 ; Search time 100.235 Seconds

(without alignments)  
11631.021 Million cell updates/sec

Title: US-10-037-182-2

Perfect score: 2018

Sequence: 1 MAKRLCAGSLCVRGPRGA.....AMTRSEVHGAVGAGCGPAA 3695

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_25.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_prodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20118	100.0	3695	4 Q8TDF8	Q8tdf8 homo sapien
2	5093	25.3	3712	5 Q9VRW0	Q9vrw0 drosophila
3	4964	24.7	3704	5 P91904	P91904 caenorhabdi
4	4010	19.9	1486	4 O14637	O14637 homo sapien
5	3360.5	16.7	670	4 Q9BTT3	Q9btt3 homo sapien
6	2715.5	13.5	734	11 Q8R3Y7	Q8r3y7 mus musculu
7	2601	12.9	3102	5 O45614	O45614 caenorhabdi
8	2566	12.8	1806	4 Q96TG0	Q96tgo homo sapien
9	2467.5	12.3	3375	5 Q8IP51	Q8ip51 drosophila
10	2438.5	12.1	3367	5 Q9XZC9	Q9xzc9 drosophila
11	2302	11.4	1725	6 Q867A1	Q867a1 canis famli
12	2249	11.2	1735	11 P70570	P70570 rattus norv
13	2160.5	10.7	2731	5 Q9VJT5	Q9vjt5 drosophila
14	1630.5	8.1	1792	13 O57484	O57484 gallus gall
15	1624	8.1	1799	11 Q8R0Y0	Q8r0y0 mus musculu
16	1556.5	7.7	1761	4 Q86XN2	Q86xn2 homo sapien

17 1552.5 7.7 1785 13 Q8JHV7  
18 1510.5 7.5 1827 13 Q8JHV6  
19 1426.5 7.1 1631 4 Q9Y6U6  
20 1393 6.9 1264 11 Q91VW0  
21 1374.5 6.8 1623 5 Q93U7  
22 1274.5 6.3 452 11 Q80VE8  
23 1266.5 6.3 1593 13 Q8UHV8  
24 1212 6.0 695 11 Q8C9J2  
25 1153 5.7 1007 13 Q90ZN3  
26 1147.5 5.7 1546 4 Q9NS27  
27 1139.5 5.7 1546 4 Q75445  
28 1106 5.5 1461 11 Q9JLP3  
29 1090.5 5.4 1067 5 O44565  
30 1077.5 5.4 885 11 Q8ESJ0  
31 1063 5.3 1512 11 Q8XK1  
32 1046 5.2 254 11 P70636  
33 1004.5 5.0 1574 11 Q88281  
34 985 4.9 1664 5 Q9TVQ2  
35 959 4.8 4223 5 Q8MPN3  
36 958 4.8 4228 5 Q8IRV8  
37 947.5 4.7 4117 5 Q8IRV9  
38 935.5 4.7 4179 5 Q9W4Y4  
39 929 4.6 1190 6 Q8HZ19  
40 924 4.6 1086 4 Q8TAS6  
41 913 4.5 1196 6 Q867A2  
42 901.5 4.5 1026 5 Q8SWY0  
43 894 4.4 1168 5 Q967S8  
44 882 4.4 1168 11 Q91V90  
45 881 4.4 2447 5 Q9NEF9

#### ALIGNMENTS

#### RESULT 1

Q8TDF8

ID Q8TDF8 PRELIMINARY; PRT; 3695 AA.

AC Q8TDF8; (1)

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Laminin alpha5 chain precursor.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=21933381; PubMed=11821406;

RA Doi M., Thyboll J., Kortegaa J., Jansson K., Iivanainen A.,

RA Parvadeh M., Timpl R., Hedin U., Swedenborg J., Tryggvason K.,

RA "Recombinant Human Laminin-10 (alphasbeta1gamma1). Production,

RT Purification, and Migration-Promoting Activity on Vascular Endothelial

RT Cells."

RL J. Biol. Chem. 277:12741-12748 (2002)..

DR EMBL; AF443072; AAM12527.1; -

DR GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0030288; C:cytoplasmic space (sensu Gram-negative Bact. .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0003743; F:translation initiation factor activity; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006413; P:translational initiation; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR008985; ConA like lec\_gl.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR000034; Laminin\_B.

DR InterPro; IPR002049; Laminin\_EGF.

DR InterPro; IPR001791; Laminin\_G.

DR InterPro; IPR008211; LamNT.

DR InterPro; IPR008212; Lam N2.

DR InterPro; IPR001638; SHF\_bac\_3.

DR InterPro; IPR001950; TIF\_SUI1.

Q8jhw7 brachydanio  
Q8jhw6 brachydanio  
Q9y6u6 homo sapien  
Q91vv0 mus musculu  
Q9u3u7 anopheles g  
Q80ve8 mus musculu  
Q8jhw8 brachydanio  
Q8c9j2 mus musculu  
Q90zn3 gallus gall  
Q9ne27 homo sapien  
Q75445 homo sapien  
Q91lp3 mus musculu  
Q44565 caenorhabdi  
Q8bej0 mus musculu  
Q8xk1 rattus norv  
P70636 rattus norv  
Q88281 rattus norv  
Q9tvq2 caenorhabdi  
Q8mpn3 drosophila  
Q8irv8 drosophila  
Q8irv9 drosophila  
Q9w4y4 drosophila  
Q8hz19 equus cabal  
Q8tas6 homo sapien  
Q867a2 canis famli  
Q8swy0 drosophila  
Q967s8 schistocerc  
Q91v90 mus musculu  
Q9nef9 drosophila

DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00052; laminin\_B; 1.  
 DR Pfam; PF00053; laminin\_EGF; 18.  
 DR Pfam; PF00054; laminin\_G; 2.  
 DR Pfam; PF00055; laminin\_Nterm; 1.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR ProDom; PD003031; Laminin\_B; 1.  
 DR ProDom; PD002082; Lam\_N2; 1.  
 DR SMART; SM00180; EGF\_Lam; 20.  
 DR SMART; SM00281; LamB; 1.  
 DR SMART; SM00282; LamG; 5.  
 DR SMART; SM00136; LamNT; 1.  
 DR PROSITE; PS00022; EGF\_1; 19.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 19.  
 DR PROSITE; PS00025; LAMININ\_DOMAIN; 5.  
 DR PROSITE; PS01039; SBP\_BACTERIAL\_3; 1.  
 DR PROSITE; PS01118; SUI1\_1; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
 KW Laminin EGF-like domain; Signal.  
 FT SIGNAL 1 35 POTENTIAL.  
 FT CHAIN 36 3695 LAMININ ALPHAS CHAIN.  
 SQ SEQUENCE 3695 AA; 399642 MW; 69703B52536EFOA3 CRC64;

Query Match 100.0%; Score 20118; DB 4; Length 3695;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGAPALLVGLALLGAARAREAGGFSLLHPYFLAEGARIAA 60  
 DB 1 MAKRLCAGSALCVRGPRGAPALLVGLALLGAARAREAGGFSLLHPYFLAEGARIAA 60

QY 61 SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120  
 DB 61 SATCGEAPARGSPRTEDLYCKLVGGPVAGGDPNQTIRGOYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWAGSPPLSRGLENEVNTLDLGQVPHAVYLIKFNANPRDLWLESMDFGR 180  
 DB 121 IDGTERWAGSPPLSRGLENEVNTLDLGQVPHAVYLIKFNANPRDLWLESMDFGR 180

QY 181 TYQPMQFFASSKEDCLEREGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240  
 DB 181 TYQPMQFFASSKEDCLEREGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYSPLLREFTKATNVRLFLRNTLLGLHGKALRDPVTTRYIYSIKDISIGRC 300  
 DB 241 AMNFSYSPLLREFTKATNVRLFLRNTLLGLHGKALRDPVTTRYIYSIKDISIGRC 300

QY 301 VCHGHADACDAKDPTDFRLOCTCOHNTCGGTCDRCPCGPNQCPKATANSANECOSCN 360  
 DB 301 VCHGHADACDAKDPTDFRLOCTCOHNTCGGTCDRCPCGPNQCPKATANSANECOSCN 360

QY 361 CYGHATDCYDPEVDRRASQSLDGTYYGGVCTDCQHTAGVNCERCLPGFYRSPNHPL 420  
 DB 361 CYGHATDCYDPEVDRRASQSLDGTYYGGVCTDCQHTAGVNCERCLPGFYRSPNHPL 420

QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND 480  
 DB 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTPSSND 480

QY 481 TREQVLPAQOI VNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGTCHBLCPAGFYGECQP 540  
 DB 481 TREQVLPAQOI VNCDCSAAGTQGNACRDKPRVGRCLCKPNFQGTCHBLCPAGFYGECQP 540

QY 541 CQCSPFGVADRDPTDGTQCRVGFEGATCDRCAPGYFHPFLCQLCGCSFAGTLPEGCD 600  
 DB 541 CQCSPFGVADRDPTDGTQCRVGFEGATCDRCAPGYFHPFLCQLCGCSFAGTLPEGCD 600

QY 601 EAGRLCQEPFAGHCDRCRGYHGFNCOACTCDPRGALDQLCGAGGLCRCPGTYGTA 660  
 DB 601 EAGRLCQEPFAGHCDRCRGYHGFNCOACTCDPRGALDQLCGAGGLCRCPGTYGTA 660

QY 661 COECSPGFHGRPSVCPCHCSAEGSLHAACDPRSGQSCRPRVTGLRCDTCTVPGAYNPPYC 720  
 DB 661 COECSPGFHGRPSVCPCHCSAEGSLHAACDPRSGQSCRPRVTGLRCDTCTVPGAYNPPYC 720

QY 721 EAGSCHPAGLAPVDPALPEAQVPCRAHVEGSPCDRCKPGFWGLSPNPEGCTRCSCDL 780  
 DB 721 EAGSCHPAGLAPVDPALPEAQVPCRAHVEGSPCDRCKPGFWGLSPNPEGCTRCSCDL 780

QY 781 RGTGLGVAECOPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDDIGALGQS 840  
 DB 781 RGTGLGVAECOPGTGQCFCKPHVCGQACASCKDGFGLDQADYFGCRSCRCDDIGALGQS 840

QY 841 CEPRTGVCRCRPNTOGPTCSEPARDHYLPDLHHLRLEBAATPEGHAVRFGFNPLEFEN 900  
 DB 841 CEPRTGVCRCRPNTOGPTCSEPARDHYLPDLHHLRLEBAATPEGHAVRFGFNPLEFEN 900

QY 901 FSWRGYAQWAPVQPRIVARLNLTSFDLFWLVRVYVNRGAMSVSRVSRVEGSAACANC 960  
 DB 901 FSWRGYAQWAPVQPRIVARLNLTSFDLFWLVRVYVNRGAMSVSRVSRVEGSAACANC 960

QY 961 TAQSQPVAFPPSTEPAFITVPQRFGBPFVLPNGTWRVAREAGVLLDYVLLPSAYEEA 1020  
 DB 961 TAQSQPVAFPPSTEPAFITVPQRFGBPFVLPNGTWRVAREAGVLLDYVLLPSAYEEA 1020

QY 1021 ALLQLRVTEACTYRPSAQCGDNCLLYTHLPLDGFPSAAGLEALCRODNLSPRCPTQEL 1080  
 DB 1021 ALLQLRVTEACTYRPSAQCGDNCLLYTHLPLDGFPSAAGLEALCRODNLSPRCPTQEL 1080

QY 1081 SPSHPPLTCTGSDVDVOLQVAVPQGRYALVVEYANEDARQEVGVAVHTPOAPQOGLL 1140  
 DB 1081 SPSHPPLTCTGSDVDVOLQVAVPQGRYALVVEYANEDARQEVGVAVHTPOAPQOGLL 1140

QY 1141 SLHPLCLYTLCRGTARTQDHLAVFHLDSBASVRLTAEQARFFLHGVTLPVIEEFSPFV 1200  
 DB 1141 SLHPLCLYTLCRGTARTQDHLAVFHLDSBASVRLTAEQARFFLHGVTLPVIEEFSPFV 1200

QY 1201 EPRVSCISSHGAFGNSAACLPSPFPQPIILRDCQVILPPLPGLPLTHAOLTPATSP 1260  
 DB 1201 EPRVSCISSHGAFGNSAACLPSPFPQPIILRDCQVILPPLPGLPLTHAOLTPATSP 1260

QY 1261 AGPRPRPTAVDPAEPDLLREPOATVVFTHPTLGRYAFLLHGYPQAHPTFPVEVLIN 1320  
 DB 1261 AGPRPRPTAVDPAEPDLLREPOATVVFTHPTLGRYAFLLHGYPQAHPTFPVEVLIN 1320

QY 1321 AGRVWQHANASFCPHYGCRCTLVCEGOALLDVTHSELTVTVRVEGRMLWLDYLVVP 1380  
 DB 1321 AGRVWQHANASFCPHYGCRCTLVCEGOALLDVTHSELTVTVRVEGRMLWLDYLVVP 1380

QY 1381 ENVYSFGYLREBPLDKSYDPTISHCAQGYHISPSSSSLFCRNAASLSLYFNNGARPCGC 1440  
 DB 1381 ENVYSFGYLREBPLDKSYDPTISHCAQGYHISPSSSSLFCRNAASLSLYFNNGARPCGC 1440

QY 1441 HEVGATGTCPEPFGGQCPCHAHVIGRDCSCATGYWGFNCRPCDCGARLDBELTGQCIC 1500  
 DB 1441 HEVGATGTCPEPFGGQCPCHAHVIGRDCSCATGYWGFNCRPCDCGARLDBELTGQCIC 1500

QY 1501 PPRTIPDCLLCQPQTFCGCHPLVGCBECCNSGPGIQLTDPCTDSDGCKCRPNVTGRR 1560  
 DB 1501 PPRTIPDCLLCQPQTFCGCHPLVGCBECCNSGPGIQLTDPCTDSDGCKCRPNVTGRR 1560

QY 1561 CDTCSPGHGYPRCPCDCEAGTAPGVCDPLTGQCYCKENWGCPKDCQCSLGTFFSLDAA 1620  
 DB 1561 CDTCSPGHGYPRCPCDCEAGTAPGVCDPLTGQCYCKENWGCPKDCQCSLGTFFSLDAA 1620

QY 1621 NPKGCTRCFCFGATERCRSSSYTRQBFVDMEGWVLLSTDQVVPHERQGTGEMLRADLRH 1680  
 DB 1621 NPKGCTRCFCFGATERCRSSSYTRQBFVDMEGWVLLSTDQVVPHERQGTGEMLRADLRH 1680

QY 1681 VPEAVPAFELWQAPPSYLGDRVSYGGTYELHSETQGDGVPEVESPDVVLQGN 1740  
 DB 1681 VPEAVPAFELWQAPPSYLGDRVSYGGTYELHSETQGDGVPEVESPDVVLQGN 1740

QY 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTRTNVTVSREELMMVLALEQLQIRALPS 1800



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2004, 14:25:32 ; Search time 100.235 Seconds  
(without alignments)  
10415.614 Million cell updates/sec

Title: US-10-037-182-2  
Perfect score: 20118  
Sequence: 1 MAKRLCAGSALCVRGPGPA.....AMTRSEVHGAVGASGCPAA 3695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20118	100.0	3695	5	Abb81588 Human lam
2	20060.5	99.7	3696	5	Aae17310 Human lam
3	20030	99.6	3705	5	Aae17309 Human lam
4	18754.5	90.7	3600	5	Abb09501 Human lam
5	18231	90.6	3597	5	Abb09503 Human lam
6	15839	78.7	3635	5	Abb81589 Mouse lam
7	15839	78.7	3635	5	Aam50357 Mouse lam
8	15120	75.2	2743	5	Abb81598 Human lam
9	8499.5	42.2	1640	5	Abb09504 Human lam
10	8255	41.0	1601	4	Aam39009 Human pol
11	6915	34.4	3332	7	Ade08094 Novel pro
12	5093	25.3	3712	4	Abb64954 Drosophil
13	5002	24.9	953	5	Aam50358 Human lam
14	4756.5	23.6	908	5	Abb89502 Human lam
15	4058	20.2	1486	7	Ade09114 Novel pro
16	3141.5	15.6	3106	3	Aab19795 Mouse lam
17	3141.5	15.6	3106	7	Ade61792 Rat Prote
18	3133.5	15.6	3084	3	Aab19796 Mouse lam
19	3123.5	15.5	3122	7	Ade61794 Human Pro
20	3103.5	15.4	3110	2	Aar71730 Merosin m
21	3103.5	15.4	3110	2	Aay15460 Human lam
22	3103.5	15.4	3110	3	Aab19793 Human lam
23	3103.5	15.4	3110	5	Aau84345 Protein L
24	3101.5	15.4	3110	3	Aab19791 Human lam
25	3099.5	15.4	3088	3	Aab19794 Human lam

26	3097.5	15.4	3089	3	AAB19792	Aab19792 Human lam
27	3069.5	15.3	3070	5	AAO17359	Aao17359 Human lam
28	2998	14.9	3150	4	ABG20414	Abg20414 Novel hum
29	2933	14.6	3084	4	AAE11215	Aae11215 Mouse lam
30	2923	14.5	3084	2	AAW50891	Aaw50891 Mouse lam
31	2854	14.2	3075	2	AAW50892	Aaw50892 Human lam
32	2598	12.9	2901	4	ABG09763	Abg09763 Novel hum
33	2342.5	11.6	3319	4	ABB70376	Abb70376 Drosophil
34	2260.5	11.2	1693	3	ABA848459	Aab48459 Human lam
35	2260.5	11.2	1693	3	ABA848457	Aab48457 Human lam
36	2260.5	11.2	1713	3	ABA848458	Aab48458 Human lam
37	2260.5	11.2	1713	6	ABR92102	Abrr92102 Human cer
38	2260.5	11.2	1713	7	ADD29904	Add29904 Human lam
39	2260.5	11.2	1724	3	AAA48456	Aab48456 Human lam
40	2249	11.2	1694	3	AAA48461	Aab48461 Rat lamin
41	2249	11.2	1725	3	AAA48460	Aab48460 Rat lamin
42	2228.5	11.1	1713	2	AAR70148	Aar70148 Deduced s
43	2155.5	10.7	3084	1	AAP94758	Aap94758 Sequence
44	2153.5	10.7	1816	7	ADC01879	Adc01879 Human lam
45	2149	10.7	1823	5	ABP63020	Abp63020 Human pol

ALIGNMENTS

RESULT 1  
ABB81588  
ID ABB81588 standard; protein; 3695 AA.  
XX ABB81588;  
AC ABB81588;  
XX  
DT 19-SEP-2002 (first entry)  
XX  
DE Human laminin alpha 5 protein SEQ ID NO:2.  
XX

Laminin alpha 5; laminin 10; vulnery; cell growth; differentiation;  
tissue repair development; laminin; healing; vascular tissue;  
re-endothelialisation; vascular injury; cell attachment; cell stasis;  
proliferation; migration.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FT Peptide 1..35  
FT Protein /label= signal  
FT Protein 36..3695  
FT Protein /label= laminin\_alpha\_5  
XX WO200250111-A2.  
XX  
XX PD 27-JUN-2002.  
XX  
XX PF 21-DEC-2001; 2001WO-US051035.  
XX  
XX PR 21-DEC-2000; 2000US-0257449P  
XX PR 28-MAR-2001; 2001US-0279282P  
XX PR 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX  
XX PI Tryggvason K, Doi M, Thyboll J;  
XX DR WPI: 2002-557650/59.  
XX DR N-PSDB; ABQ72906.

New human laminin-10 proteins, useful for accelerating the healing of  
vascular tissue, improving the biocompatibility of grafts, or for  
promoting re-endothelialization at the site of vascular injuries.  
XX  
XX Claim 5; Page 68-79; 23lpp; English.  
XX  
XX The present sequence represents human laminin alpha 5. Also described is  
an isolated laminin 10. Laminin 10 has vulnerary activity. Laminins are

CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grats useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, and promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration  
XX  
SQ Sequence 3695 AA;

Query Match 100.0%; Score 20118; DB 5; Length 3695;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGAPALLVGLALLGAARAEAGGFSLHPPYFNLAEGARIAA 60  
DB 1 MAKRLCAGSALCVRGPRGAPALLVGLALLGAARAEAGGFSLHPPYFNLAEGARIAA 60  
QY 61 SATCEEAPARGSPPTEDLYCKLVGGPVAGGDNQITRGQYCDICTAANSNKAHPASNA 120  
DB 61 SATCEEAPARGSPPTEDLYCKLVGGPVAGGDNQITRGQYCDICTAANSNKAHPASNA 120  
QY 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLIKFANSPRDLWTLERSMDFG 180  
DB 121 IDGTERWQSPPLSRGLEYNVNTLDLQGVFHVAYVLIKFANSPRDLWTLERSMDFG 180  
QY 181 TYQWQFQFASXRDCLEFPGQTLERITRDAAICTTEYSRIVPLENGEIVWSLVNRP 240  
DB 181 TYQWQFQFASXRDCLEFPGQTLERITRDAAICTTEYSRIVPLENGEIVWSLVNRP 240  
QY 241 AMNFSYSPLLREFTKATNVRFLRTNTLLGLHMGKALRDPVTTRYYIKDISIGGR 300  
DB 241 AMNFSYSPLLREFTKATNVRFLRTNTLLGLHMGKALRDPVTTRYYIKDISIGGR 300  
QY 301 VCHGHADACDAKDPDPRLOCTOHNCTGTCRCCPGFNOQWPKPATANSNEQCSN 360  
DB 301 VCHGHADACDAKDPDPRLOCTOHNCTGTCRCCPGFNOQWPKPATANSNEQCSN 360  
QY 361 CYGHATDCYDPEVDRREASQSLDGTQGGGVCIQCOHHTAGVNCERCLPGFVRSNHP 420  
DB 361 CYGHATDCYDPEVDRREASQSLDGTQGGGVCIQCOHHTAGVNCERCLPGFVRSNHP 420  
QY 421 DSPHVCRCNCESDPTDGTCTDLTGRCYCRNFNSGERCDVCAEGFTGFPSCYTPSSND 480  
DB 421 DSPHVCRCNCESDPTDGTCTDLTGRCYCRNFNSGERCDVCAEGFTGFPSCYTPSSND 480  
QY 481 TREQVLPAGQIVNCDCAAGTQGNACRDPVGRCLCKPNFQTHCELCAPGFYGGCOP 540  
DB 481 TREQVLPAGQIVNCDCAAGTQGNACRDPVGRCLCKPNFQTHCELCAPGFYGGCOP 540  
QY 541 COCSSPGVADRDCTDQCRVGFEGATCDRCAPGYFHPPLCOLCGSPAGTLP 600  
DB 541 COCSSPGVADRDCTDQCRVGFEGATCDRCAPGYFHPPLCOLCGSPAGTLP 600  
QY 601 EAGRCLCQPEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGTGTA 660  
DB 601 EAGRCLCQPEFAGPHCDRCRPGYHGFNQCQACTDPRGALDQLCGAGGLCRCPGTGTA 660  
QY 661 COECSPGPHGPPSCVPCHCSAEGSLHAACDPRSOCSRPRVTGLRCDTCVPAYNFYC 720  
DB 661 COECSPGPHGPPSCVPCHCSAEGSLHAACDPRSOCSRPRVTGLRCDTCVPAYNFYC 720  
QY 721 EAGSCHPAGLAPVDPALPEAQVPCWRAHVGPSCDRCKPFGWGLSPNPEGCTRCSCDL 780  
DB 721 EAGSCHPAGLAPVDPALPEAQVPCWRAHVGPSCDRCKPFGWGLSPNPEGCTRCSCDL 780  
QY 781 RGTLLGVABECOPGTGQCECKPHVCGQACSKDGFGLDQADYFGCSCRCDTGGALGOS 840  
DB 781 RGTLLGVABECOPGTGQCECKPHVCGQACSKDGFGLDQADYFGCSCRCDTGGALGOS 840  
QY 841 CEPRTGVCRCPNTGPTCSEPARDHYLPDLHLRLLEBAATPEGHAVRFGNPLEFEN 900  
DB 841 CEPRTGVCRCPNTGPTCSEPARDHYLPDLHLRLLEBAATPEGHAVRFGNPLEFEN 900

QY 901 FSWRGYAQMVPQPRIVARLNLTSPDLFWLVFRYVNRGAMSVSGRVSVREGRSAACANC 960  
DB 901 FSWRGYAQMVPQPRIVARLNLTSPDLFWLVFRYVNRGAMSVSGRVSVREGRSAACANC 960  
QY 961 TAQSQPVAFPPSTPAPITVPORGFGSEFFVLPDCTWALRVEAGVLLDVVLLPSAYEA 1020  
DB 961 TAQSQPVAFPPSTPAPITVPORGFGSEFFVLPDCTWALRVEAGVLLDVVLLPSAYEA 1020  
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDINSLRPCTEQL 1080  
DB 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAAGLEALCRQDINSLRPCTEQL 1080  
QY 1081 SPSPHPLITCTGSDVDVQLOVAVPQGRYALVVEYANEDARQVGVAVHTPOAPQOGLL 1140  
DB 1081 SPSPHPLITCTGSDVDVQLOVAVPQGRYALVVEYANEDARQVGVAVHTPOAPQOGLL 1140  
QY 1141 SLHCLVSTLCRGRTARTQDHLAVFHLDSASVRLTAEOARFPLHGVTLVPIBEFSEFV 1200  
DB 1141 SLHCLVSTLCRGRTARTQDHLAVFHLDSASVRLTAEOARFPLHGVTLVPIBEFSEFV 1200  
QY 1201 EPRVSCISSHGAFGPNSAACLPGRFPKPPQPIILRDCQVPLPPLPLTHAQDLTATSP 1260  
DB 1201 EPRVSCISSHGAFGPNSAACLPGRFPKPPQPIILRDCQVPLPPLPLTHAQDLTATSP 1260  
QY 1261 AGPRPPTAVDDAETLLREPOATVVFTHVPTLGRYAFLLHGYQPAHPTPPVEVLIN 1320  
DB 1261 AGPRPPTAVDDAETLLREPOATVVFTHVPTLGRYAFLLHGYQPAHPTPPVEVLIN 1320  
QY 1321 AGRYVQGHANASFCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEGRWMLDYVLYVP 1380  
DB 1321 AGRYVQGHANASFCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEGRWMLDYVLYVP 1380  
QY 1381 ENVYSFGVLEEDLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLYNNGARPCOC 1440  
DB 1381 ENVYSFGVLEEDLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLYNNGARPCOC 1440  
QY 1441 HEVGATGPTCEPFGQCPCHAHVIGRDCRATGYMGFPCNCRPCDCGABLCDELGTQCIC 1500  
DB 1441 HEVGATGPTCEPFGQCPCHAHVIGRDCRATGYMGFPCNCRPCDCGABLCDELGTQCIC 1500  
QY 1501 PPRITPDCILLCOPTFGCHPLVGCBECSGPGIQLTDPCTDSDGCKCRPNVTGR 1560  
DB 1501 PPRITPDCILLCOPTFGCHPLVGCBECSGPGIQLTDPCTDSDGCKCRPNVTGR 1560  
QY 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCQSLGTFSLDAA 1620  
DB 1561 CDTCSPGFHGYPRCPCDCHEAGTAPGVCDPLTGQCYCKENVQGPCKDCQSLGTFSLDAA 1620  
QY 1621 NPKCTCFCFGATERCRRSSSYTRQEFVDMEGHWLLSTDRQVVPHERQGTENLRDLRH 1680  
DB 1621 NPKCTCFCFGATERCRRSSSYTRQEFVDMEGHWLLSTDRQVVPHERQGTENLRDLRH 1680  
QY 1681 VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLYELHSETQRGDVFPVPMESRPDVVLOGN 1740  
DB 1681 VPEAVPEAPPELYWQAPPSYLGDRVSSYGGTLYELHSETQRGDVFPVPMESRPDVVLOGN 1740  
QY 1741 QMSITPLEPAYPFGHVHRQQLQVGNFRHTETRTNVSREELMMVLASLEQLQIRALPS 1800  
DB 1741 QMSITPLEPAYPFGHVHRQQLQVGNFRHTETRTNVSREELMMVLASLEQLQIRALPS 1800  
QY 1801 QISSAVSLRVALEVASPAGQAGALANVELCLCPASVYRSDSCQECAPGFYRDKVGLGR 1860  
DB 1801 QISSAVSLRVALEVASPAGQAGALANVELCLCPASVYRSDSCQECAPGFYRDKVGLGR 1860  
QY 1861 CVPCQCHCHDRCLPGSGVCDQHNTEGANCERCOAGFMSRRDPSAPCVSCPPLSV 1920  
DB 1861 CVPCQCHCHDRCLPGSGVCDQHNTEGANCERCOAGFMSRRDPSAPCVSCPPLSV 1920  
QY 1921 SNNFAECVLRGGRTQCLCKPGYAGASCERCAPGFPFNPLVLGSSCQPCDCSNGDPLN 1980  
DB 1921 SNNFAECVLRGGRTQCLCKPGYAGASCERCAPGFPFNPLVLGSSCQPCDCSNGDPLN 1980



XX 22-JUN-2001; 2001WO-US019929.  
 XX PF  
 XX PR  
 XX PR 22-JUN-2000; 2000US-0213156P.  
 XX PR 22-JUN-2000; 2000US-0213161P.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM CORP.  
 XX PA (SMK ) SMITHKLINE BEECHAM PLC.  
 XX PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA,  
 XX PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX PR  
 XX WPI: 2002-139783/18.  
 XX DR N-PSDB; AAD27805.  
 XX  
 XX Novel secreted and membrane-associated polypeptides and polynucleotides  
 XX useful for preventing, ameliorating or correcting dysfunction or disease  
 XX including diabetes, cancer, hypertension and growth abnormalities.  
 XX  
 XX Claim 1; Page 115-122; 138pp; English.  
 XX  
 XX The invention relates to secreted and membrane-associated polypeptides  
 XX and polynucleotides. The sequences of the invention are useful in  
 XX diagnostic assays for detecting diseases associated with inappropriate  
 XX activity or levels of these polynucleotides, and in identifying their  
 XX agonists and antagonists that are potentially useful in therapy. The  
 XX sequences of the invention are useful as vaccines for inducing  
 XX immunological response. The sequences of the invention are useful for  
 XX treating cancers, infections, autoimmune disorders, haematopoietic  
 XX disorders, wound healing disorders, cholesterol ester storage disease,  
 XX inflammation, congenital muscular dystrophy, junctional epidermolysis  
 XX bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
 XX viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
 XX allergies, schizophrenia, sbq542445PROA-associated disorders,  
 XX septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
 XX graft versus host disease, ischaemia, stroke, acute respiratory disease  
 XX syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
 XX brain disorders including parasupranuclear palsy, myotonic dystrophy,  
 XX depression, anxiety disorders and sleep disorders, cardiovascular  
 XX diseases including congestive heart failure and myocardial infarction,  
 XX respiratory diseases including chronic obstructive pulmonary disease,  
 XX acute bronchitis and adult respiratory distress syndrome, liver disorders  
 XX including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
 XX and non-viral hepatitis, type II diabetes mellitus, renal disease  
 XX including acute and chronic renal failure, glomerulonephritis, Fanconi's  
 XX syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
 XX and tendinitis, gastrointestinal diseases including intestinal  
 XX obstruction and tropical sprue, spleen disorders including hypersplenism,  
 XX Hodgkin's disease and malignant lymphoma, testicular cancer, male  
 XX reproductive diseases including low testosterone and male infertility.  
 XX The present sequence is human laminin alpha protein  
 XX  
 XX Sequence 3696 AA;

Query Match 99.7%; Score 20060.5; DB 5; Length 3696;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3687; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 MAKRLCAGSALCVGRPGAPLLVGLALGAARAREEAGGFSLHPYFNLAEGARTAA 60  
 DB 1 MAKRLCAGSALCVGRPGAPLLVGLALGAARAREEAGGFSLHPYFNLAEGARTAA 60  
 QY 61 SATCGEAPARGSPRPTECLYKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 120  
 DB 61 SATCGEAPARGSPRPTECLYKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 120  
 QY 121 IDGTERWQSPPLSRGLSEYNEVNTLDLGOVHFVAVLKEFANSRPDLWLERSMDFGR 180  
 DB 121 IDGTERWQSPPLSRGLSEYNEVNTLDLGOVHFVAVLKEFANSRPDLWLERSMDFGR 180  
 QY 181 TYQPWFQFASKRDCLERFQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240  
 DB 181 TYQPWFQFASKRDCLERFQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240

DB 181 TYQPWFQFASKRDCLERFQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240  
 QY 241 AMNFSYSLREFTKATNVRLRFRNTLLGHLMGKALRDPVTRRYYSIKDISIGRRC 300  
 DB 241 AMNFSYSLREFTKATNVRLRFRNTLLGHLMGKALRDPVTRRYYSIKDISIGRRC 300  
 QY 301 VCHGHADACDAKDPDPFRLOCTCOHNTCCGTCPCPGFNOQPKPATANSANECQSCN 360  
 DB 301 VCHGHADACDAKDPDPFRLOCTCOHNTCCGTCPCPGFNOQPKPATANSANECQSCN 360  
 QY 361 CYGHATCYVDPEVDRRRASQSLDGTYYGGVYCIDQHHHTAGVNCERCLPGYRSPNHL 420  
 DB 361 CYGHATCYVDPEVDRRRASQSLDGTYYGGVYCIDQHHHTAGVNCERCLPGYRSPNHL 420  
 QY 421 DSPHVCRRNCESDFTDGTCELTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTSSND 480  
 DB 421 DSPHVCRRNCESDFTDGTCELTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTSSND 480  
 QY 481 TREOVLPAQOIVNCDSCAAGTQGNACRKPVRGRCLCKENFOGTHCELCAFGYGGCOP 540  
 DB 481 TREOVLPAQOIVNCDSCAAGTQGNACRKPVRGRCLCKENFOGTHCELCAFGYGGCOP 540  
 QY 541 CQSSPGVADRDCTPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600  
 DB 541 CQSSPGVADRDCTPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCD 600  
 QY 601 EAGRCLQCFEAGFHCDCRCPGYHGFNCOACTCDPRGALDOLCGAGGLCRCPGYTGA 660  
 DB 601 EAGRCLQCFEAGFHCDCRCPGYHGFNCOACTCDPRGALDOLCGAGGLCRCPGYTGA 660  
 QY 661 CQSCSPGFHGFPCVCFCHCSAEGSLHAACDPRSGGQCRPRVTGLRCDTVPGAYNFFYC 720  
 DB 661 CQSCSPGFHGFPCVCFCHCSAEGSLHAACDPRSGGQCRPRVTGLRCDTVPGAYNFFYC 720  
 QY 721 EAGSCHPAGLAPVDPAQVPCMCRAHVEGSDCRCKPGFWGLSPNPEGCTCSCDL 780  
 DB 721 EAGSCHPAGLAPVDPAQVPCMCRAHVEGSDCRCKPGFWGLSPNPEGCTCSCDL 780  
 QY 781 RGLTGGVAECQPGTGQCFCKPHVCGACSKDGGFFGLDQADYFCRCRCDIGGALQGS 840  
 DB 781 RGLTGGVAECQPGTGQCFCKPHVCGACSKDGGFFGLDQADYFCRCRCDIGGALQGS 840  
 QY 841 CEPRTGVCRCRPNTOGTCSEPARDHYLDLHLELEEAATPEGHAVRFGFNLEFEN 900  
 DB 841 CEPRTGVCRCRPNTOGTCSEPARDHYLDLHLELEEAATPEGHAVRFGFNLEFEN 900  
 QY 901 FSWRGYAQMAPVQPRIVARLNLTSPDLFWLVYVNRGAMSVSGRVSVREGRSAAACANC 960  
 DB 901 FSWRGYAQMAPVQPRIVARLNLTSPDLFWLVYVNRGAMSVSGRVSVREGRSAAACANC 960  
 QY 961 TAQSQPVAPPPSTEPAFITVPORGGEPEFVLPNGTWALRVEAGVLLDYVLLPSAYVEA 1020  
 DB 961 TAQSQPVAPPPSTEPAFITVPORGGEPEFVLPNGTWALRVEAGVLLDYVLLPSAYVEA 1020  
 QY 1021 ALLQLRVREACTYRPSAQSGDNCILYTHLPDGFPSAAGLEALCRDONSLEPRFCPTQL 1080  
 DB 1021 ALLQLRVREACTYRPSAQSGDNCILYTHLPDGFPSAAGLEALCRDONSLEPRFCPTQL 1080  
 QY 1081 SPSPHPLITCTGSDVDVQLQVAVPOPGRYALWEVANEDARQEVGVAVHTPQRAPOQGLL 1140  
 DB 1081 SPSPHPLITCTGSDVDVQLQVAVPOPGRYALWEVANEDARQEVGVAVHTPQRAPOQGLL 1140  
 QY 1141 SLHPLCYLSTLCRGRTADTODHLAVFHLDSASVRLTAEOARFFHLHGVTLPFIEBSPBEV 1200  
 DB 1141 SLHPLCYLSTLCRGRTADTODHLAVFHLDSASVRLTAEOARFFHLHGVTLPFIEBSPBEV 1200  
 QY 1201 EPRVSCISGHGAFGNASACLPSRFPKPPQPIILLDDCOVILPPCLPLTHAQDLTPATSP 1260  
 DB 1201 EPRVSCISGHGAFGNASACLPSRFPKPPQPIILLDDCOVILPPCLPLTHAQDLTPATSP 1260  
 QY 1261 AGPRPRPTAVDPDAEPTLLREPOATVVTTHVPTLGRYAFLLHGYQPAHPTFVEVLIN 1320  
 DB 1261 AGPRPRPTAVDPDAEPTLLREPOATVVTTHVPTLGRYAFLLHGYQPAHPTFVEVLIN 1320

QY 1321 AGRVMOGHANASFCPHGVGCRTHLVVCRGQALLDVTHSELTVTVRVPGRWMLDYLWVP 1380  
DB 1321 AGRVMOGHANASFCPHGVGCRTHLVVCRGQALLDVTHSELTVTVRVPGRWMLDYLWVP 1380  
QY 1381 ENVYSFGYLREPELDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGC 1440  
DB 1381 ENVYSFGYLREPELDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGC 1440  
QY 1441 HEVGATGTCPEPFGGOCPCAHVIGRDCSRCATGYWGFPCNCRPCDCGARLCCDELGTGCIC 1500  
DB 1441 HEVGATGTCPEPFGGOCPCAHVIGRDCSRCATGYWGFPCNCRPCDCGARLCCDELGTGCIC 1500  
QY 1501 PPRITPPDCLLCQPTFCGCHPLVGCCECNCSGPGIQELDTPTCDTDSGQCKRCRNVGTGR 1560  
DB 1501 PPRITPPDCLLCQPTFCGCHPLVGCCECNCSGPGIQELDTPTCDTDSGQCKRCRNVGTGR 1560  
QY 1561 CDTCSPGFHGYPGRPCDCHCEAGTAGVCDPLTGOCYCKENVQPKCDQCSLGTFSLDAA 1620  
DB 1561 CDTCSPGFHGYPGRPCDCHCEAGTAGVCDPLTGOCYCKENVQPKCDQCSLGTFSLDAA 1620  
QY 1621 NPKGCTRCFCGATERCRSSSYTROEFVDMEGWLLSTDROVPHRQPGTEMRLADLRH 1680  
DB 1621 NPKGCTRCFCGATERCRSSSYTROEFVDMEGWLLSTDROVPHRQPGTEMRLADLRH 1680  
QY 1681 VPEAVPEAPPYLYWQAPPSYLGDRVSSYGGTLRYELHSETORGVDVFPWESRPDVLQGN 1740  
DB 1681 VPEAVPEAPPYLYWQAPPSYLGDRVSSYGGTLRYELHSETORGVDVFPWESRPDVLQGN 1740  
QY 1741 QMSITFLPAPYTPGCHVHRGQLQVEGNFRHTETENTVSRREELMMVLASLQQLIRALFS 1800  
DB 1741 QMSITFLPAPYTPGCHVHRGQLQVEGNFRHTETENTVSRREELMMVLASLQQLIRALFS 1800  
QY 1801 QISSAVSLRRVALVAVSPAGQALASNVELCLCPASRYGSDCQBCAPGFYRDVXGLFLGR 1860  
DB 1801 QISSAVFLRRVALVAVSPAGQALASNVELCLCPASRYGSDCQBCAPGFYRDVXGLFLGR 1860  
QY 1861 CVPCCCHGSHDRCLPGSGVGVCDQNTGHAECRCQAGFMSRDDPSAPCVSCPCPLSVP 1920  
DB 1861 CVPCCCHGSHDRCLPGSGVGVCDQNTGHAECRCQAGFMSRDDPSAPCVSCPCPLSVP 1920  
QY 1921 SNNFAGCVLRRGTQCLCKPGYAGASERCAPFGFNPLVLGSSCQPCDCSGNGDPNLL 1980  
DB 1921 SNNFAGCVLRRGTQCLCKPGYAGASERCAPFGFNPLVLGSSCQPCDCSGNGDPNLL 1980  
QY 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNTRCDCTPCGTACDPSHSHC 2040  
DB 1981 FSDCDPLTGACRGCLRHHTTGPCEICAPGFYGNALLPGNTRCDCTPCGTACDPSHSHC 2040  
QY 2041 LCKAGVTGRRCDRCQBGHFGFNGCGGCRPCACGPAAGSECHPQSGQCHCRPGTWPQCR 2100  
DB 2041 LCKAGVTGRRCDRCQBGHFGFNGCGGCRPCACGPAAGSECHPQSGQCHCRPGTWPQCR 2100  
QY 2101 ECAPGWGLPEQCRRCQPCGRCDPHTGRNCNPPGLSGERCDCSCQHQVVPVGPVGH 2160  
DB 2101 ECAPGWGLPEQCRRCQPCGRCDPHTGRNCNPPGLSGERCDCSCQHQVVPVGPVGH 2160  
QY 2161 SHCEVCDHCWVLLDDLERAGALLPAIHEQLRGINASSMAMARHLRNASTADIQSOLR 2220  
DB 2161 SHCEVCDHCWVLLDDLERAGALLPAIHEQLRGINASSMAMARHLRNASTADIQSOLR 2220  
QY 2221 SPLGRPHETAQQLLEVLEQGSTSIGQDARLGGQ-AVGTFRDQASQLLAGTEATLGHAKTLL 2279  
DB 2221 SPLGRPHETAQQLLEVLEQGSTSIGQDARLGGQAVGTFRDQASQLLAGTEATLGHAKTLL 2280  
QY 2280 AATRAVDRTLSUMSOTGHLGLANASPSGEOLLRTLAVERLLWEMRARDLGAQAAAE 2339  
DB 2281 AATRAVDRTLSUMSOTGHLGLANASPSGEOLLRTLAVERLLWEMRARDLGAQAAAE 2340  
QY 2340 AELAAAOURLLARVOEQLSLWENQALATQTRDRLAQHEAGLMDLREALNRAVDATRAQ 2399  
DB 2341 AELAAAOURLLARVOEQLSLWENQALATQTRDRLAQHEAGLMDLREALNRAVDATRAQ 2400

QY 2400 ELNSNRQERLEBALQKQELSRDNATLOATLHAEDTLASVFRLLHSLDQAKEELERLAA 2459  
DB 2401 ELNSNRQERLEBALQKQELSRDNATLOATLHAEDTLASVFRLLHSLDQAKEELERLAA 2460  
QY 2460 SLDGARTPLLRQWQTFSPAGSKRLRVEAAEAHAQOLGOLALNLSSIILDVNODRITQRAI 2519  
DB 2461 SLDGARTPLLRQWQTFSPAGSKRLRVEAAEAHAQOLGOLALNLSSIILDVNODRITQRAI 2520  
QY 2520 EASNAYSRILOAVQAAEDAAQALQADHTWATVTVROGLVDBAQOLLANSTALEAMLOE 2579  
DB 2521 EASNAYSRILOAVQAAEDAAQALQADHTWATVTVROGLVDBAQOLLANSTALEAMLOE 2580  
QY 2580 QORLGLVMAALQARTQLRDVRAXKDOLEAHTQAAQAMLAMDTDETSSKIAHAKAAVAEA 2639  
DB 2581 QORLGLVMAALQARTQLRDVRAXKDOLEAHTQAAQAMLAMDTDETSSKIAHAKAAVAEA 2640  
QY 2640 QDTATRVQSOLQAMQNVNRWQGYEGLRGQDLGOAVLDAGHSVSTLEKTLIOLLAKLSI 2699  
DB 2641 QDTATRVQSOLQAMQNVNRWQGYEGLRGQDLGOAVLDAGHSVSTLEKTLIOLLAKLSI 2700  
QY 2700 LENRGVHNASLASISIGRVRELIQAARGAASKVKVPKMFNGRSGVOLRTPRDLADLAAY 2759  
DB 2701 LENRGVHNASLASISIGRVRELIQAARGAASKVKVPKMFNGRSGVOLRTPRDLADLAAY 2760  
QY 2760 TALKFYLQGPPEPGQGTEDRFVMYMGSRQATGDYMGVSLRDKKXVHWVYOLGEGAPVLS 2819  
DB 2761 TALKFYLQGPPEPGQGTEDRFVMYMGSRQATGDYMGVSLRDKKXVHWVYOLGEGAPVLS 2820  
QY 2820 IDDEDGEOPAAVSLDRTLOFGHMSVTVVERQMTQETKGTIVAPCAEGLLNLRPDDFVFFYVG 2879  
DB 2821 IDDEDGEOPAAVSLDRTLOFGHMSVTVVERQMTQETKGTIVAPCAEGLLNLRPDDFVFFYVG 2880  
QY 2880 GYPSSTTPPLRFPFGYRGCIEMDTLNEEVSVSYNPFRTFQDQTAVDPRCAKSKSTGDPW 2939  
DB 2881 GYPSSTTPPLRFPFGYRGCIEMDTLNEEVSVSYNPFRTFQDQTAVDPRCAKSKSTGDPW 2940  
QY 2940 LTDGSLDGTGFPARISFDSQISITTKRFBQELRLVSYSGVLFLKQOSQFLCLAVQSGSLV 2999  
DB 2941 LTDGSLDGTGFPARISFDSQISITTKRFBQELRLVSYSGVLFLKQOSQFLCLAVQSGSLV 3000  
QY 3000 LLYDFGAGLKKAVLPLOPPPLTSASKAIQVFLGGSRKXVLVRVERATVYVSEQNDLLE 3059  
DB 3001 LLYDFGAGLKKAVLPLOPPPLTSASKAIQVFLGGSRKXVLVRVERATVYVSEQNDLLE 3060  
QY 3060 ADAYYLGVPDQLPPLSRWLFTGSGVRGCVKGIKALGYVDLKRINTTVGSAGCTADL 3119  
DB 3061 ADAYYLGVPDQLPPLSRWLFTGSGVRGCVKGIKALGYVDLKRINTTVGSAGCTADL 3120  
QY 3120 LVGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOG 3179  
DB 3121 LVGRAMTFHGHGFLRLALSNVAPLTGNVYSGFGFHSQAQDSALLYRASPDGLCQVSLQOG 3180  
QY 3180 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGFPPELOPQE 3239  
DB 3181 RVSLQLLRTEVKTQAGFADGAPHYVAFYSNATGVWLYVDDQLQOMKPHRGFPPELOPQE 3240  
QY 3240 GPPRLLLGGLPESGTIYNFGCISNVFVQELLGPQVEDLQONLGSVNVTSTGCAPALQAO 3299  
DB 3241 GPPRLLLGGLPESGTIYNFGCISNVFVQELLGPQVEDLQONLGSVNVTSTGCAPALQAO 3300  
QY 3300 TPGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGILAR 3359  
DB 3301 TPGLGPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGILAR 3360  
QY 3360 HRNWPISUMHVLPRSSGGLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTLRAQSRQR 3419  
DB 3361 HRNWPISUMHVLPRSSGGLLFTARLRPGSPSLALFLSNGHFVAQMEGLGTLRAQSRQR 3420  
QY 3420 SRPGRWHKVSVRWEKXRIILLVTDGARAWSOEPPHROHQGAHPQPHTLFVGGGLPASSHSS 3479  
DB 3421 SRPGRWHKVSVRWEKXRIILLVTDGARAWSOEPPHROHQGAHPQPHTLFVGGGLPASSHSS 3480  
QY 3480 KLPVTYVFGSGCVKRLRHGRPLGAPTRMAGVTTCILQGLEAGLFFPGSGGVIITLIDPGAT 3539

Db 3481 KLPVTVFGGCVKRLRHLHGRPLGAPTRMAGVTTPCITLGPLEAGLFPFGSGGVTITLDPGAT 3540  
 QY 3540 LPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSV 3599  
 Db 3541 LPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGEFSTSVTRPSV 3600  
 QY 3600 LCGQWHLAVKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQWPP 3659  
 Db 3601 LCGQWHLAVKSGNVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQWPP 3660  
 QY 3660 AYCGCMRLAVNRSPVAMTRSVVEHVGAVGASGCPAA 3695  
 Db 3661 AYCGCMRLAVNRSPVAMTRSVVEHVGAVGASGCPAA 3696  
 RESULT 3  
 AAEL17309  
 ID AAE17309 standard; protein; 3705 AA.  
 XX  
 AC AAE17309;  
 DT 18-APR-2002 (first entry)  
 DE Human laminin alpha protein, sbg417005LAMININ\_ALPHA #1.  
 XX  
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;  
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;  
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;  
 KW depression; cardiovascular disease; myocardial infarction; renal failure;  
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;  
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;  
 KW hypoplasia; renal disease; hypoglycaemia; gastrointestinal disease;  
 KW neoplasia; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;  
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;  
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;  
 KW allergy; laminin alpha protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200198342-A1.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001-WO-019929.  
 XX  
 PR 22-JUN-2000; 2000US-0213156P.  
 PR 22-JUN-2000; 2000US-0213161P.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 PA (GLAX) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;  
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX  
 DR WPI; 2002-139783/18.  
 DR N-PSDB; AAD27804.  
 XX  
 PT Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT useful for preventing, ameliorating or correcting dysfunction or disease  
 PT including diabetes, cancer, hypertension and growth abnormalities.  
 XX  
 PS Claim 1; Page 107-114; 138pp; English.  
 XX  
 CC The invention relates to secreted and membrane-associated polypeptides  
 CC and polynucleotides. The sequences of the invention are useful in  
 CC diagnostic assays for detecting diseases associated with inappropriate  
 CC activity or levels of these polynucleotides, and in identifying their  
 CC agonists and antagonists that are potentially useful in therapy. The  
 CC sequences of the invention are useful as vaccines for inducing

CC immunological response. The sequences of the invention are useful for  
 CC treating cancers, infections, autoimmune disorders, haematopoietic  
 CC disorders, wound healing disorders, cholesteryl ester storage disease,  
 CC inflammation, congenital muscular dystrophy, functional epidermolysis  
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
 CC allergies, schizophrenia, sbg42445PROA-associated disorders,  
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease,  
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
 CC brain disorders including paraspranuclear palsy, myotonic dystrophy,  
 CC depression, anxiety disorders and sleep disorders, cardiovascular  
 CC diseases including congestive heart failure and myocardial infarction,  
 CC respiratory diseases including chronic obstructive pulmonary disease,  
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
 CC and tendinitis, gastrointestinal diseases including intestinal  
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
 CC reproductive diseases including low testosterone and male infertility.  
 CC The present sequence is human laminin alpha protein  
 XX  
 SQ Sequence 3705 AA;

Query Match 99.6%; Score 20030; DB 5; Length 3705;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 3683; Conservative 3; Mismatches 9; Indels 10; Gaps 1;

QY 1 MAKILCAGSALCVRGPRGAPAPLLVLLGALLGAAAREEAGGFSLHPPFNLAEGARIAA 60

Db 1 MAKILCAGSALCVRGPRGAPAPLLVLLGALLGAAAREEAGGFSLHPPFNLAEGARIAA 60

QY 61 SATCGEAPARGSPRPTEDELYCKLVGPGVAGGPNQITRGQYCDICTAANSNKAHPASNA 120

Db 61 SATCGEAPARGSPRPTEDELYCKLVGPGVAGGPNQITRGQYCDICTAANSNKAHPASNA 120

QY 121 IDGTERWQSPPLSRGLEYNEVNVTLDLGQVHVAVYLKFNANSPRDLVWLSRMDFOR 180

Db 121 IDGTERWQSPPLSRGLEYNEVNVTLDLGQVHVAVYLKFNANSPRDLVWLSRMDFOR 180

QY 181 TYQPWQPFASAKRDLERFQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240

Db 181 TYQPWQPFASAKRDLERFQPTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPG 240

QY 241 AMNFSYSPLLREFTKATNVLRLFTNTLLGHLMGKALRDPVTRYYYSIKDISIGREC 300

Db 241 AMNFSYSPLLREFTKATNVLRLFTNTLLGHLMGKALRDPVTRYYYSIKDISIGREC 300

QY 301 VCHGHADACDAKOPTDFRLQCTCOHNTCGTCDRCPCGPNQOPWKPATANSANECQSCN 360

Db 301 VCHGHADACDAKOPTDFRLQCTCOHNTCGTCDRCPCGPNQOPWKPATANSANECQSCN 360

QY 361 CYGHATCYVDPEVDRRRASQSLDGTVOGGVCIDCOHHTAGVNCERCLPGYRSNHPJ 420

Db 361 CYGHATCYVDPEVDRRRASQSLDGTVOGGVCIDCOHHTAGVNCERCLPGYRSNHPJ 420

QY 421 DSPHVCRCNCESDFTDGTCTEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTSSND 480

Db 421 DSPHVCRCNCESDFTDGTCTEDLTGRCYCRPNFSGERCDCVCAEGFTGFPSCYPTSSND 480

QY 481 TREQVLPAQIVNCDSCAAGTQGNACRDKPRVGRCLCKENFGTHCELCAPOFYGGQCP 540

Db 481 TREQVLPAQIVNCDSCAAGTQGNACRDKPRVGRCLCKENFGTHCELCAPOFYGGQCP 540

QY 541 CQCSSPGVADRDCTPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGGSPAGTLPFGCD 600

Db 541 CQCSSPGVADRDCTPDTGQCRVGFEGATCDRCAPGYFHFPLCQLCGGSPAGTLPFGCD 600

QY 601 EAGCLCPQFAGHCDRCBPGVHGPNCOACTCDPRGALDQICGAGGLCRCPGVGTGA 660

Db 601 EAGCLCPQFAGHCDRCBPGVHGPNCOACTCDPRGALDQICGAGGLCRCPGVGTGA 660

601 EAGRCLQPEFAGPHCDRCRPGVHGFPCNCACTCDPRGALDQLCGAGGLCLCRPGYTGA 660 Db  
661 QBCSPGFHGFPPSCVPCCHCAEAGSLHAAACDPRGQCSRCRPRVTGLRCDTCVPGAYNFPYC 720 Qy  
661 QBCSPGFHGFPPSCVPCCHCAEAGSLHAAACDPRGQCSRCRPRVTGLRCDTCVPGAYNFPYC 720 Db  
721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSCDRCKPFGWGLSPSPNPECTRCSDLL 780 Qy  
721 EAGSCHPAGLAPVDPALPEAQVPCMCRAHVEGSCDRCKPFGWGLSPSPNPECTRCSDLL 780 Db  
781 RGTGLGVAECOPGTGOCFCFKPHVCGACASCKDQFFGLDQADYFPGCRSCRCRDIGALGQS 840 Qy  
781 RGTGLGVAECOPGTGOCFCFKPHVCGACASCKDQFFGLDQADYFPGCRSCRCRDIGALGQS 840 Db  
841 CEPRTGVCRCRPNTOGTPTCEPARDHYLPLDHLRLLEBEAATPEGHAVRFGFNPLEFEN 900 Qy  
841 CEPRTGVCRCRPNTOGTPTCEPARDHYLPLDHLRLLEBEAATPEGHAVRFGFNPLEFEN 900 Db  
901 FSWRGYAQMAPVOPRIVARINLNTSPDLFWLVFRYVNRGAMSVGRVSVREGRSAAACANC 960 Qy  
901 FSWRGYAQMAPVOPRIVARINLNTSPDLFWLVFRYVNRGAMSVGRVSVREGRSAAACANC 960 Db  
961 TAQSQPVAFPPSTPEAFITVPORGFGEFVLPNGTVALRVEAGVLLDVVLLPSAYYEA 1020 Qy  
961 TAQSQPVAFPPSTPEAFITVPORGFGEFVLPNGTVALRVEAGVLLDVVLLPSAYYEA 1020 Db  
1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLBALCRQNSLPRPCPTBOL 1080 Qy  
1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLBALCRQNSLPRPCPTBOL 1080 Db  
1081 SPSPHPLITCTGSDVDVQLQVAVPOGRVALVVEYANEDARQEVAVVHTPORAPQOGLL 1140 Qy  
1081 SPSPHPLITCTGSDVDVQLQVAVPOGRVALVVEYANEDARQEVAVVHTPORAPQOGLL 1140 Db  
1141 SLHPCLYSTLCRTATDTHQHLAVFHLDSBASVRLTAEOARFHLGTVLPIIEEFPSEFV 1200 Qy  
1141 SLHPCLYSTLCRTATDTHQHLAVFHLDSBASVRLTAEOARFHLGTVLPIIEEFPSEFV 1200 Db  
1201 EPRVCSLSSHGAGPNSAACLPKSRFPKPPQPIILRDCQVILPPLGLPLTHAQDLTPATSP 1260 Qy  
1201 EPRVCSLSSHGAGPNSAACLPKSRFPKPPQPIILRDCQVILPPLGLPLTHAQDLTPATSP 1260 Db  
1261 AGPRPPPTAVDPAEFTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320 Qy  
1261 AGPRPPPTAVDPAEFTLLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPVEVLIN 1320 Db  
1321 AGRVWQHGANASCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEGRWLWLDVVLVVP 1380 Qy  
1321 AGRVWQHGANASCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEGRWLWLDVVLVVP 1380 Db  
1381 ENVYSFGYLREELDKSYDFISHCAAQGYHISFSSSSSIFCRNAAASLSLFYNNGARPCGC 1440 Qy  
1381 ENVYSFGYLREELDKSYDFISHCAAQGYHISFSSSSSIFCRNAAASLSLFYNNGARPCGC 1440 Db  
1441 HEVGATGPTCEPFGGQCPCHAVIGRDCSRCATGYWGNPCPCDCGARLDELITGQCIC 1500 Qy  
1441 HEVGATGPTCEPFGGQCPCHAVIGRDCSRCATGYWGNPCPCDCGARLDELITGQCIC 1500 Db  
1501 PPRTPIDCLLCOPTGCHPLVGCCECNCSGPGIQLDTPDCTDSDQCRPNVTGRR 1560 Qy  
1501 PPRTPIDCLLCOPTGCHPLVGCCECNCSGPGIQLDTPDCTDSDQCRPNVTGRR 1560 Db  
1561 CDTCSPGFEGYPCRPCDCHEAGTAGVCDPLTGOCYCKENVQGPCKDCQCSLGTFSLDA 1620 Qy  
1561 CDTCSPGFEGYPCRPCDCHEAGTAGVCDPLTGOCYCKENVQGPCKDCQCSLGTFSLDA 1620 Db  
1621 NPKGTRCFCFGATERCRSSSYTROBFVDMEGWLLSTDRQVVPHERQPGTEMLRADLRH 1680 Qy  
1621 NPKGTRCFCFGATERCRSSSYTROBFVDMEGWLLSTDRQVVPHERQPGTEMLRADLRH 1680 Db  
1681 VPEAVPEAPPELYWQAPPYSLGDRVSSYGGTLRYELHSETQGRGVFVPMESRPDVLQGN 1740 Qy  
1681 VPEAVPEAPPELYWQAPPYSLGDRVSSYGGTLRYELHSETQGRGVFVPMESRPDVLQGN 1740 Db

1741 QMSITFLEPAYTPPGHVHRGQLOLVEGNPRHTTETNTVSRBELMMVLASLEOLOIRALFS 1800 Qy  
1741 QMSITFLEPAYTPPGHVHRGQLOLVEGNPRHTTETNTVSRBELMMVLASLEOLOIRALFS 1800 Db  
1801 QISSAVSLRVALLEVASPAGQGALASNVLCCLCPASRYGDSQCECAPFYRDVKGLFLGR 1860 Qy  
1801 QISSAVSLRVALLEVASPAGQGALASNVLCCLCPASRYGDSQCECAPFYRDVKGLFLGR 1860 Db  
1861 CVPQCCHGSHDRCLPQSGVYCVDCOHNTEGAHCERCOAGFMSSRDDPSAPCVSCPCLVSP 1920 Qy  
1861 CVPQCCHGSHDRCLPQSGVYCVDCOHNTEGAHCERCOAGFMSSRDDPSAPCVSCPCLVSP 1920 Db  
1921 SNNFABGCVLGRGRTQCLCKPGYAGACERCAPGFGNPLVLGSSCQPCDCSGNGDPNLL 1980 Qy  
1921 SNNFABGCVLGRGRTQCLCKPGYAGACERCAPGFGNPLVLGSSCQPCDCSGNGDPNLL 1980 Db  
1981 FSDCDPLTGACRCLRHITTPRCETCAPGYGNALLPNCNTRCDCTPCGTACDPSHSHC 2040 Qy  
1981 FSDCDPLTGACRCLRHITTPRCETCAPGYGNALLPNCNTRCDCTPCGTACDPSHSHC 2040 Db  
2041 LCKAGVTGRRCDRCQBGHFGNGCGCRPCACGPAAGSECHPQSGQCHCRPGTGPQCR 2100 Qy  
2041 LCKAGVTGRRCDRCQBGHFGNGCGCRPCACGPAAGSECHPQSGQCHCRPGTGPQCR 2100 Db  
2101 ECAPGWGLPEOCRRRCQPCGRCDPHTGRQNCNCPGLSGERCDDTCSQHOHVPVPGGPVGH 2160 Qy  
2101 ECAPGWGLPEOCRRRCQPCGRCDPHTGRQNCNCPGLSGERCDDTCSQHOHVPVPGGPVGH 2160 Db  
2161 SHICEVCDHCVVLLDDLEAGALLPAIHEQLRGINASSMAWARLHRLNAGIADLQSOQLR 2220 Qy  
2161 SHICEVCDHCVVLLDDLEAGALLPAIHEQLRGINASSMAWARLHRLNAGIADLQSOQLR 2220 Db  
2221 SPGLPHETAOQLVLEEQSTSLGQDARRLLGQAVGTRD-----QASQLLAGTEA 2270 Qy  
2221 SPGLPHETAOQLVLEEQSTSLGQDARRLLGQAVGTRD-----QASQLLAGTEA 2270 Db  
2271 TLGHAKTLLAAIRAVDRTLSELMSOTGHLGANASAPSGEOLLRTLAEVERLLWEMARD 2330 Qy  
2271 TLGHAKTLLAAIRAVDRTLSELMSOTGHLGANASAPSGEOLLRTLAEVERLLWEMARD 2330 Db  
2281 TLGHAKTLLAAIRAVDRTLSELMSOTGHLGANASAPSGEOLLRTLAEVERLLWEMARD 2340 Qy  
2281 TLGHAKTLLAAIRAVDRTLSELMSOTGHLGANASAPSGEOLLRTLAEVERLLWEMARD 2340 Db  
2331 LGAPQAAAEEIAAQRILARVQBOQLSSWENQALATQTRDRLAQHAQGLMDREALNR 2390 Qy  
2331 LGAPQAAAEEIAAQRILARVQBOQLSSWENQALATQTRDRLAQHAQGLMDREALNR 2390 Db  
2341 LGAPQAAAEEIAAQRILARVQBOQLSSWENQALATQTRDRLAQHAQGLMDREALNR 2400 Qy  
2341 LGAPQAAAEEIAAQRILARVQBOQLSSWENQALATQTRDRLAQHAQGLMDREALNR 2400 Db  
2391 AVDTREAGELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVRELLHSLDQA 2450 Qy  
2391 AVDTREAGELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVRELLHSLDQA 2450 Db  
2401 AVDTREAGELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVRELLHSLDQA 2460 Qy  
2401 AVDTREAGELNSRQERLEALQKQELSRDNATLQATLHAARDTLASVRELLHSLDQA 2460 Db  
2451 KEELERLAASLDGARTPLLQRMOTFSPAGSKLRLVEAAEAHAQQLGOLALNLSIILDVN 2510 Qy  
2451 KEELERLAASLDGARTPLLQRMOTFSPAGSKLRLVEAAEAHAQQLGOLALNLSIILDVN 2510 Db  
2461 KEELERLAASLDGARTPLLQRMOTFSPAGSKLRLVEAAEAHAQQLGOLALNLSIILDVN 2520 Qy  
2461 KEELERLAASLDGARTPLLQRMOTFSPAGSKLRLVEAAEAHAQQLGOLALNLSIILDVN 2520 Db  
2511 QDRLTORATEASNAYSRILOAVQAAEDAAQALQOQADHTWATVVRQGLVDRQAQQLANST 2570 Qy  
2511 QDRLTORATEASNAYSRILOAVQAAEDAAQALQOQADHTWATVVRQGLVDRQAQQLANST 2570 Db  
2521 QDRLTORATEASNAYSRILOAVQAAEDAAQALQOQADHTWATVVRQGLVDRQAQQLANST 2580 Qy  
2521 QDRLTORATEASNAYSRILOAVQAAEDAAQALQOQADHTWATVVRQGLVDRQAQQLANST 2580 Db  
2571 ALEEAQMSQORGLVWAAALQARTQLDRVRAKDDQLEAHIQAAQAMLMAMDTDTSTKIA 2630 Qy  
2571 ALEEAQMSQORGLVWAAALQARTQLDRVRAKDDQLEAHIQAAQAMLMAMDTDTSTKIA 2630 Db  
2581 ALEEAQMSQORGLVWAAALQARTQLDRVRAKDDQLEAHIQAAQAMLMAMDTDTSTKIA 2640 Qy  
2581 ALEEAQMSQORGLVWAAALQARTQLDRVRAKDDQLEAHIQAAQAMLMAMDTDTSTKIA 2640 Db  
2631 HAKAABAADTATRVQSOLOAMQENVERWQOYEGRLGQDLGOAVLDAGHSVSTLEKTL 2690 Qy  
2631 HAKAABAADTATRVQSOLOAMQENVERWQOYEGRLGQDLGOAVLDAGHSVSTLEKTL 2690 Db  
2641 HAKAABAADTATRVQSOLOAMQENVERWQOYEGRLGQDLGOAVLDAGHSVSTLEKTL 2700 Qy  
2641 HAKAABAADTATRVQSOLOAMQENVERWQOYEGRLGQDLGOAVLDAGHSVSTLEKTL 2700 Db  
2691 POLLAKLSILENRGVHNASLASISIGRVRELIQAARGAASKVKVPMKFNRSQVQLRTP 2750 Qy  
2691 POLLAKLSILENRGVHNASLASISIGRVRELIQAARGAASKVKVPMKFNRSQVQLRTP 2750 Db  
2701 POLLAKLSILENRGVHNASLASISIGRVRELIQAARGAASKVKVPMKFNRSQVQLRTP 2760 Qy  
2701 POLLAKLSILENRGVHNASLASISIGRVRELIQAARGAASKVKVPMKFNRSQVQLRTP 2760 Db  
2751 RLADLAAVATALKFYLOQPEPEPGOGTDRFVWYMGSRQATGDYWGVSRLDKKVVHYQL 2810 Qy  
2751 RLADLAAVATALKFYLOQPEPEPGOGTDRFVWYMGSRQATGDYWGVSRLDKKVVHYQL 2810 Db  
2761 RLADLAAVATALKFYLOQPEPEPGOGTDRFVWYMGSRQATGDYWGVSRLDKKVVHYQL 2820 Qy  
2761 RLADLAAVATALKFYLOQPEPEPGOGTDRFVWYMGSRQATGDYWGVSRLDKKVVHYQL 2820 Db





atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NOVX nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which bind to a NOVX protein, and are also useful as targets for the identification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motility, cellular proliferation, haematopoiesis, wound healing and angiogenesis. NOVX nucleic acid sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NOVX homologues in other cell types. Cells comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents the laminin alpha-5-like protein NOV1a. The gene encoding NOV1a is located on chromosome 20

Sequence 3600 AA;

Query Match 90.7%; Score 18254.5; DB 5; Length 3600;

Best Local Similarity 91.8%; Pred. No. 0;

Matches 3433; Conservative 18; Mismatches 103; Indels 187; Gaps 23;

QY	1	MAKRLCAGSALCVRGPRGPAPILLVGLALLGAARAREAGGFSLHPPYFNLAEGARIAA	60
DB	1	MAKRLCAGSALCVRGPRGPAPILLVGLALLGAARAREAGGFSLHPPYFNLAEGARIAA	39
QY	61	SATCCEBAPAGSPPTEDLYCKLVGGVAGGDPNQTIRGOYCDICTAANSKAPASNA	120
DB	40	SATCCEBAPAGSPPTEDLYCKLVGGVAGGDPNQTIRGOYCDICTAANSKAPASNA	99
QY	121	IDGTERWQSPPLSRGLENEVNVTLDLGQVPHVAVLILKANSPPRDLWLERSMDFGR	180
DB	100	IDGTERWQSPPLSRGLENEVNVTLDLGQVPHVAVLILKANSPPRDLWLERSMDFGR	159
QY	181	TYQPOWPFASSKRDCLERFPOTLRIRTRDDAAICTTYSRIIVLENGEIVVSLVNGRPG	240
DB	160	TYQPOWPFASSKRDCLERFPOTLRIRTRDDAAICTTYSRIIVLENGEIVVSLVNGRPG	219
QY	241	ANMFYSPLLRFTKATNVRLFLATNTLLHLMGKALRDPATRRYYSIKDISIGRC	300
DB	220	ANMFYSPLLRFTKATNVRLFLATNTLLHLMGKALRDPATRRYYSIKDISIGRC	279
QY	301	VCHGHADACADKDPDTPRLQCTOHTCGTCDRCFCGFGNQPAPATANSANECQSCN	360
DB	280	VCHGHADACADKDPDTPRLQCTOHTCGTCDRCFCGFGNQPAPATANSANECQ-CE	338
QY	361	CYGHATDCYDEVDERRASQSLDGTGOGGVCIDQHTTAGVNCERCLPGFYSPNHL	420
DB	339	CYGHATDCYDEVDERRASQSLDGTGOGGVCIDQHTTAGVNCERCLPGFYSPNHL	398
QY	421	DSPHVCRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGPFPSSND	480
DB	399	DSPHVCRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGPFPSSND	458
QY	481	TREQVLPAQIVSCDCAAGTGNACRDPVGRCLCKPNFGTHCELCAFGYGGCP	540
DB	459	TREQVLPAQIVSCDCAAGTGNACRDPVGRCLCKPNFGTHCELCAFGYGGC-P	517
QY	541	CQCSS---PGVADRDCTDGTGCRVGPGEATCDRCAPGYF-----HFPLCQCGCSP	591
DB	518	ASVPALPEWMTAVTLTQASAG--AEWASRGPHVIAVPPATFTLSASHPLRSVAVCGCSP	574
QY	592	AGTLPEGCDEAGRLCQPFAGPHCDRCPCYGHGPNCOACTCDPRGALDOI-CGAGGLCR	651
DB	575	AGTLPEGCDEAGRLCQPFAGPHCDRCPCYGHGPNCOACTCDPRGALDOI-CGAGGLCR	634
QY	652	CRPGYGTACQECSPGFHGFPSVCPCHCSAEGSLHAAC-----DPRSGQCSCR-P	706
DB	635	CRPGYGTACQECSPGFHGFPSVCPCHCSAEGSLHAAC-----DPRSGQCSCR-P	689
QY	707	---CDTCVPGANPPYCEAGSCHPAGLAPVDPALPEAQVPCMAHVEGSPCDRCVPGFWG	764
DB	690	HVCVPVTTGPTAKPLTAGSCHPAGLAPVDPALPEAQVPCMAHVEGSPCDRCVPGFWG	749

QY	765	LSPSNPEGCTRCSDLRGLTGVAECQGTGQCFKPHVCGOACASCXKDGPFGLQADYF	824
DB	750	LSPSNPEGCTRCSDLRGLTGVAECQ-GTGQCFKPHVCGOACASCXKDGPFGLQADYF	808
QY	825	GCRSCRCIDIGGALGQSCPRGTCRPNNTQGTSEPARDHYLPDLHLRLLEZEAATP	884
DB	809	GCRSCRCIDIGGALGQSCPRGTCRPNNTQGTSEPARDHYLPDLHLRLLEZEAATP	868
QY	885	EGHAVRFGNPLEFENFNSWRGVAQMAPVQPRIVARLNTLSPDLFWLFRYVNRGAMVSG	944
DB	869	EGHAVRFGNPLEFENFNSWRGVAQMAPVQPRIVARLNTLSPDLFWLFRYVNRGAMVSG	928
QY	945	RVSUREEGSACANCTAOSQVAPPPSTEPAPITVQPGFGEPPFVLPNGTVALRVEABG	1004
DB	929	RVSUREEGSACANCTAOSQVAPPPSTEPAPITVQPGFGEPPFVLPNGTVALRVEABG	988
QY	1005	VLLDYVLLPSAYEAAQLQLRVTEACTYRPAQSGDNCLLYTHLPDGFPSAAGLEAL	1064
DB	989	VLLDYVLLPSAYEAAQLQLRVTEACTYRPAQSGDNCLLYTHLPDGFPSAAGLEAL	1048
QY	1065	CRODNLPRCPTEQLSPSHPLITCTGSDVDVQVAVPQGRVALVVEYANEDARQEV	1124
DB	1049	CRODNLPRCPTEQLSPSHPLITCTGSDVDVQVAVPQGRVALVVEYANEDARQEV	1108
QY	1125	GVAVHTPQAPQGLLSLHPCLYSTLCRGRTARDTQHLAVFHLDSASVRLTAEQARFEL	1184
DB	1109	GVAVHTPQAPQGLLSLHPCLYSTLCRGRTARDTQHLAVFHLDSASVRLTAEQARFEL	1168
QY	1185	HGVTLPVIEEFSEFVEPRVSCISSHGAGPNSAACLPKPFKPPQPIILRDCQVILPFP	1244
DB	1169	HGVTLPVIEEFSEFVEPRVSCISSHGAGPNSAACLPKPFKPPQPIILRDCQVILPFP	1228
QY	1245	GLPLTHAQDLTPATSPAGPRPPTAVDPDAFTLLREPOATVFTTHVTTLGRVAFLLH	1304
DB	1229	GLPLTHAQDLTPATSPAGPRPPTAVDPDAFTLLREPOATVFTTHVTTLGRVAFLLH	1288
QY	1305	GYOPAPHTPEVVLINAGRWQGHANASCPHGCGRTLVCEGQALLDVTHSELVTYR	1364
DB	1289	GYOPAPHTPEVVLINAGRWQGHANASCPHGCGRTLVCEGQALLDVTHSELVTYR	1348
QY	1365	VPGRWLMDYLVLVVENVYVSGYLREELDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1424
DB	1349	VPGRWLMDYLVLVVENVYVSGYLREELDKSYDFISHCAAQGYHISPSSSSLFCRNAA	1408
QY	1425	ASLSLFYNNGARPCGCHVEGATGTCPEPGGQCPCHAHVIGRDCSCATGYWGFNCRCP	1484
DB	1409	ASLSLFYNNGARPCGCHVEGATGTCPEPGGQCPCHAHVIGRDCSCATGYWGFNCRAC	1468
QY	1485	DCGARLDELGTGQICPPRTIPDCLLCPQTFPGCHPLVGCCECNCSGPGIQELTDPTCD	1544
DB	1469	DCGARLDELGTGQICPPRTIPDCLLCPQTFPGCHPLVGCCECNCSGPGIQELTDPTCD	1528
QY	1545	TDGQCKCRPNVTGRRCDTCSPGFHGYPRCPDCHAGTAPGVCDPLTGQCYCKENVQ	1604
DB	1529	TDGQCKCRPNVTGRRCDTCSPGFHGYPRCPDCHAGTAPGVCDPLTGQCYCKENVQ	1588
QY	1605	PKDCQSLGTSGLDANPKGCTCFGATERCSSSYTROBVDMEGWLLSTDQVVP	1664
DB	1589	PKDCQSLGTSGLDANPKGCTCFGATERCSSSYTROBVDMEGWLLSTDQVVP	1648
QY	1665	HERQPGTEMLRADLRHVPEAVPAFFELVQWAPPSYLGDRVSSYGGTLYELHSETQGD	1724
DB	1649	HERQPGTEMLRADLRHVPEAVPAFFELVQWAPPSYLGDRVSSYGGTLYELHSETQGD	1708
QY	1725	VFPVMSRPPVTLQGNQMSITFLPAYPTFGHVHRCQLOLVEGNFRHTTNTVSRBELM	1784
DB	1709	VFPVMSRPPVTLQGNQMSITFLPAYPTFGHVHRCQLOLVEGNFRHTTNTVSRBELM	1768
QY	1785	MVLASLEQLQIRALFSQISSAVSLRRAVLEVASPAGQALASNVCLCLCPASVYRGSCOE	1844
DB	1769	MVLASLEQLQIRALFSQISSAVSLRRAVLEVASPAGQALASNVCLCLCPASVYRGSCOE	1828

Qy	1845	CAPGFYRDVKGLGFLGRCPQCQCHGSHDRCLPGSGVCVDQHNTEGAHCRCQAGFMSGRD	1904
Db	1829	CAPGFYRDVKGLGFLGRCPQCQCHGSHDRCLPGSGVCV-COHNTEGAHCRCQAGFVSSRD	1887
Qy	1905	DPAPCVSCPCPLSVSRNNPABECVLRGGRTQCLCKPGYAGASCRCAPGPGNPLVLGS	1964
Db	1888	DPAPCVSCPCPLSVSPSN-----RCAPGFTGNPLVLGS	1920
Qy	1965	SCQPCDCSNGDNNLLFSDCDPLTGACRGCLRHTTGPCEIICAPGFGYNALLPGNCTRCD	2024
Db	1921	SCQPCDCSNGDNNLLFSDCDPLTGACRGCLRHTTGPCEIICAPGFGYNALLPGNCTRCD	1980
Qy	2025	CTFCGTEACDPHSGHCLCKAGVTRGRCDRCOEGHFGNGCGCRPCACGPAABEGSECHPQ	2084
Db	1981	CTFCGTEACDPHSGHCLCKAGVTRGRCDRCOEGHFGDGGCGCRPCACGPAABEGSECHPQ	2040
Qy	2085	SGOCHCRPGTMGQCRCAPGYWGLPEQGCRRQCQCPGRCDPHTGRCNCPGGLSBERCDT	2144
Db	2041	SGOCHCRPGTMGQCRCAPGYWGLPEQGCRCRCQCPGRCDPHTGRCNCPGGLSBERCDT	2100
Qy	2145	CSQOHOVPVPGGPVGHSHICEVCDHCVCVLLDDLEFAGALLPAIHQELRGINASSWAWAR	2204
Db	2101	CSQOHOVPVPGGPVGHSHICEVCDHCVCVLLDDLEFAGALLPAIHQELRGINASSWAWAR	2160
Qy	2205	LHRLNASIADL-----QSOLRSPGLPRHETHAQQLVELEQQST	2241
Db	2161	LHRLNASIADLOVLSVLAPPQCPQVAFTRLPQSQLRSPGLPRHETHAQQLVELEQQST	2220
Qy	2242	SLGQDARRLGQAVGTDRQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSTQCHLGL	2301
Db	2221	SLPP-----QAVGTDRQASQLLAGTEATLGHAKTLLAAIRAVDRTLSELMSTQCHLGL	2273
Qy	2302	ANASAPSGEQLLRTLAEVERLLMEMRARDLGAPOAAAEALAAQORLLARVOQLSSLWE	2361
Db	2274	ANASAPSGEQLLRTLAEVERLLMEMRARDLGAPOAAAEALAAQORVILARVQQLSSLWE	2333
Qy	2362	ENQALATQTRDLRAQHEAGLMDLEARNRAVDATREAEQLNSNRQERLEALQOKELSR	2421
Db	2334	ENQALATQTRDLRAQHEAGLMDLEARNRAVDATREAEQLNSNRQERLEALQOKELSR	2393
Qy	2422	DNATLOATLHAARTLTASVFLLSHSDQAK-ELERLAASLDGARTPLQORMOTTFSPAGS	2480
Db	2394	DNATLOATLHAARTLTASVFLLSHSDGFLSKFQELERLAAASLDGARTPLQORMOTTFSPAGS	2453
Qy	2481	KLRIVERAAEHAQQLGOLALNLSSIILVDNQDLRTORAIENASNAYSRILQAVQAAEDDAG	2540
Db	2454	KLRIVERAAEHAQQLGOLALNL-SIIILVDNQDLRTORAIENASNAYSRILQAVQAAEDDAG	2512
Qy	2541	QALQOQADHTWATVYRQGLVDRBAQOLLANSTALEAMLQEOORLGL-VMA--ALQOART	2595
Db	2513	QALQOQADHTWATVYRQGLVDRBAQOLLANSTALEEMLQEOORLGLGECWAPMGALRPAGT	2572
Qy	2596	QLRDVRACKQDQLEAHIQAAQAMLAMDITDTSKKTIAHAKAVAAEQDTATRVQSQLOAMQE	2655
Db	2573	QLRDVRACKQDQLEAHIQAAQAMLAMDITGTSKKTIAHAKAVAAEQDTATRVQSQLOAMQE	2632
Qy	2656	NVERWQGYEGILRGODLQOAVLDAGHSVSTLEKTLPOLLAKLSTILENRGVHNASLALSAS	2715
Db	2633	NVERWQGYEGILRGODLQOAVLDAGSVSTLEKTLPOLLAKLSTILENRGVHNASLALSAS	2692
Qy	2716	IGRVRELTAAQARGAASK-VKVPKMFNGRSGVQLTRPDLADLAAYTALKFYLQGPPEPG	2774
Db	2693	IGRVRELTAAQARGAASKVKVPKMFNGRSGVQLTRPDLADLAAYTALKFYLQGPPEPG	2752
Qy	2775	QGTEDRFVYMGSRQATGDYMGVSLRDKKXHWVYQLGEAGPAVLUSDIDEDGEOFAAVSLD	2834
Db	2753	QGTEDRFVYMGSRQATGDYMGVSLRDKKXHWVYQLGEAGPAVLUSDIDEDGEOFAAVSLD	2812
Qy	2835	RTLQFGHMSVTVVERQWIGETKGDTPVPAEGLLNLRPDDFVYVGGYPSFTPTPPLLRFP	2894
Db	2813	RTLQFGHMSVTVVERQWIGETKGDTPVPAEGLLNLRPDDFVYVGGYPSFTPTPPLLRFP	2872
Qy	2895	GYRGCIEMDTLNEEVSVLYNFERTFQDTPAVDRPCARKSKSTGDDPWLTDGSMVDTGTGARI	2954

Db	2873	GYRGCIMDTLANEVVSLYNFERTFQLDVAVDRPCARSASTGDPWLTDSYLDGTGFARI	2933
Qy	2955	SFDSQISTTKRFEQELRLVSYSGVLFFLKQSQFLCLAVQEGSLVLLYDFGAGLKAPEL	3014
Db	2933	SFDSQISTTKRFEQELRLVSYSGVLFFLKQSQFLCLAVQEGSLVLLYDFGAGLKAPEL	2992
Qy	3015	QPPPPITSASKAIQVFLLLGGSKRVLVRVERATVTVSVEQNDLEADAYLGGVPPDQLP	3074
Db	2993	QPPPPITSASKAIQVFLLLGGSKRVLVRVERATVTVSVEQNDLEADAYLGGVPPDQLP	3051
Qy	3075	PSRLWLPPTGGSGVRGCVKGIKALGKTVYDLKRLNTTGVSGAGTADLLVGRAMTFHGHGFLR	3134
Db	3052	PSRLWLPPTGGSGVRGCVKGIKALGKTVYDLKRLNTTGVSGAGTADLLVGRAMTFHGHGFLR	3111
Qy	3135	LALSNVAPITGNVYSGFGFHSQAQDSALLYRASPDGLCOVSLQQGRVSLQLLARTVKTQA	3194
Db	3112	LALSNVAPITGNVYSGFGFHSQAQDSALLYRASPDGLCOVSLQQGRVSLQLLARTVKTQA	3171
Qy	3195	GFADGAPHYVAFYSNATGVMWLYVDQLQOMKPHRGPPPELQPOEGEPRLLLGGLPESGT	3254
Db	3172	GFADGAPHYVAFYSNATGVMWLYVDQLQOMKPHRGPPPELQPOEGEPRLLLGGLPESGT	3231
Qy	3255	IYNSFGCISNVFQRIILGQRPVFDLQONLGSVNVSTGCAPALQAQTPGLGPRGLQATARK	3314
Db	3232	IYNSFGCISNVFQRIILGQRPVFDLQONLGSVNVSTGCAPALQAQTPGLGPRGLQATARK	3284
Qy	3315	ASRSQPAPAHPCAMLPPLHRTTRDSYQFGGSLSSHLEFVGIARHNWPSLSMHLVLRPS	3374
Db	3285	ASRSQPAPAHPCAMLPPLHRTTRDSYQFGGSLSSHLEFVGIARHNWPSLSMHLVLRPS	3332
Qy	3375	SRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQSRQRSPGRWHKVSVRWEK	3434
Db	3333	SRGLLFTARLRPGSPSLALFLSNHGFVAQMEGLGTRLRQAQSRQRSPGRWHKVSVRWEK	3339
Qy	3435	NRILLVTDGARANSQEGPHROHOGASHPOPHITLVGGLPASSHSSKLPVTVGFSGCVKRL	3494
Db	3340	NRILLVTDGARANSQEGPHROHOGASHPOPHITLVGGLPASSHSSKLPVTVGFSGCVKRL	3399
Qy	3495	RLHGRPLGAPTRMAGVTPCITGLPLEAGLFPFGSGGVITLDLPQATLPDVGLELEVRPLAV	3554
Db	3400	RLHGRPLGAPTRMAGVTPCITGLPLEAGLFPFGSGGVITLDLPQATLPDVGLELEVRPLAV	3459
Qy	3555	TGLIFHLGQARTPPYLOQLQVTEKOVLLRADDGAGEFSTSVTRPSVLCGQWHLRAVWKSG	3614
Db	3460	TGLIFHLGQARTPPYLOQLQVTEKOVLLRADDGAGEFSTSVTRPSVLCGQWHLRAVWKSG	3519
Qy	3615	NVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAYQPPHPPAYCGCMRRLAVNRSP	3674
Db	3520	NVLRLVDAQSNHTVGPLLAAAGAPAPLYLGLPEPMAYQPPHPPAYCGCMRRLAVNRSP	3579
Qy	3675	VAMTRSVFHVGVAGSCCPAA	3695
Db	3580	VAMTRSVFHVGVAGSCCPAA	3600
RESULT 5			
ABB09503			
ID	ABB09503 standard; protein; 3597 AA.		
XX			
AC	ABB09503;		
XX			
DT	01-NOV-2003 (first entry)		
XX			
DE	Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.		
XX			
KW	Human; NOV1c; neurological disorder; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; pain; behavioural disorder;		
KW	addiction; tuberculous mycobacteriosis; cancer; immune disorder; allergy;		
KW	autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;		
KW	thyroiditis; cardiovascular disease; hypertension; reproductive disorder;		
KW	endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;		
KW	pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;		

RESULT 5  
ABB09503  
ID ABB09503 standard: protein: 3597 AA.

AA ABB09503;  
AC

XX DT 01-NOV-2002 (first entry)

XX DE human laminin alpha-5-like NOV1c protein. SEQ ID NO:6.

XX Human; NOVX; neurological disorder; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;  
KW addiction; tubercle sclerosis; cancer; immune disorder; allergy;  
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;  
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;  
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; tinea;  
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy; atherosclerosis; cell signal processing-related disorder; metabolic pathway regulation disorder; cytostatic; neuroprotective; antiinflammatory; immunosuppressive; analgesic; antithrombotic; dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis; differentiation; proliferation; motility; haematopoiesis; wound healing; angiogenesis; forensic biology; transgenic animal; drug screening; gene therapy; NOV1c; laminin alpha-5-like; chromosome 20.

OS Homo sapiens.  
XX Key Location/Qualifiers  
XX Key 1. 14  
XX Peptide /label= Signal\_peptide  
XX Protein 15. 3597  
XX /note= "Mature NOV1c protein"  
WO200253742-A2.  
XX 11-JUL-2002.  
XX 07-JAN-2002; 2002WO-US000375.  
XX 05-JAN-2001; 2001US-0260018P.  
XX 08-JAN-2001; 2001US-0260360P.  
XX 28-FEB-2001; 2001US-0272411P.  
XX 02-MAR-2001; 2001US-0272817P.  
XX 05-JUL-2001; 2001US-0303231P.  
XX 12-JUL-2001; 2001US-0305060P.  
XX 10-SEP-2001; 2001US-0318405P.  
XX 12-SEP-2001; 2001US-0318700P.  
XX 04-JAN-2002; 2002US-00037417.  
(CURA-) CURAGEN CORP.  
XX Kekuda R, Alsbrook JP, Tetherer VT, Liu X, Spytek KA;  
XX Patturajan M, Grosse WM, Lapeley DM, Burgess CE, Vernet CAM, Li L;  
XX Gorman L, Edinger S, Sciorio P, Ellerman K, Malyankar U;  
XX Rothenberg M, Stone D, Boldos F, Guo X, Shenoy S, Anderson D;  
XX Padigaru M, Taupier RJ, Miller CE, Eisen A;  
WPI: 2002-583619/62.  
XX N-PSDB; ABQ93881.  
XX Novel polypeptides and nucleic acids homologous to transmembrane  
XX receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
XX treating cancer, atherosclerosis, neurological, skin and autoimmune  
XX disorders.  
XX Claim 1c; Page 20-21; 323pp; English.  
XX The invention relates to 24 novel human proteins designated NOV1-NOV14  
XX (AB09501-AB09524), collectively referred to as NOVX proteins, and  
XX nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and  
XX nucleotides are useful in the treatment, diagnosis or prevention of NOVX-  
XX associated disorders or in the manufacture of a medicament for treating  
XX such disorders, with specific applications described for each of the 24  
XX NOVX proteins, based on their homology to known proteins. Various  
XX disorders are associated with NOVX proteins including neurological  
XX disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
XX pain, behavioural disorders, addiction, tuberculous sclerosis, cancers  
XX (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
XX (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
XX various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
XX (e.g., hypertension), reproductive disorders, endometriosis,  
XX incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
XX cirrhosis, glomerular endonephrosis, polycystic kidney disease, endocrine  
XX disorders, obesity, bacterial infections and particularly cardiomyopathy,  
XX atherosclerosis, cell signal processing-related disorders and disorders  
XX of metabolic pathway regulation. NOVX nucleic acids and polypeptides may  
XX be used to identify cellular receptors or downstream effectors which  
XX binds to a NOVX protein, and are also useful as targets for the  
XX identification of small molecules that modulate or inhibit processes such

CC as neurogenesis, cell differentiation, cell motility, cellular  
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX  
CC nucleic acid sequences can be used to identify a cell or tissue type and  
CC are useful as a source of primers or probes for forensic biology and for  
CC identifying and cloning NOVX homologues in other cell types. Cells  
CC comprising NOVX nucleic acids are useful for producing non-human  
CC transgenic animals which are useful for studying the function and  
CC activity of NOVX proteins and for identifying and evaluating modulators  
CC of NOVX activity. The present sequence represents the laminin alpha-5-  
CC like protein NOV1c. The gene encoding NOV1c is located on chromosome 20  
XX  
XX  
SQ Sequence 3597 AA;  
Query Match 90.6%; Score 18231; DB 5; Length 3597;  
Best Local Similarity 91.7%; Pred. NO. 0;  
Matches 3428; Conservative 18; Mismatches 108; Indels 184; Gaps 21;  
QY 1 MAKELCAGSALCVGRGPRGAPILLVGLALLGAARAREAGGGSFSLHPPYFNLAEGARIAA 60  
DB 1 MAKELCAGSALCVGRGPRGAPILLVGLALLGAARAREAGGGSFSLHPPYFNLAEGARIAA 39  
QY 61 SATCGEEAPARGSPRETDLYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 120  
DB 40 SATCGEEAPARGSPRETDLYCKLVGGPVAGGDPNQTIRGQYCDICTAANSNKAHPASNA 99  
QY 121 IDGTERWQSPPLSRGLEYNVNVTLDLGOVHVAVYLKKEANSRPRDLWVLESMDFGR 180  
DB 100 IDGTERWQSPPLSRGLEYNVNVTLDLGOVHVAVYLKKEANSRPRDLWVLESMDFGR 159  
QY 181 TYQPMOFFFASKRDCLERFGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRFG 240  
DB 160 TYQPMOFFFASKRDCLERFGPOTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRFG 219  
QY 241 AMNFSYPLIREFTKATNRLRLPLRNTLLHLMKALRDPVTRYYYSIKDISIGRC 300  
DB 220 AMNFSYPLIREFTKATNRLRLPLRNTLLHLMKALRDPVTRYYYSIKDISIGRC 279  
QY 301 VCHGHADACDAKDPDTPFRLOCTCOHNTCGTCRCPCGFCNQPKPATAANSANEQSCN 360  
DB 280 VCHGHADACDAKDPDTPFRLOCTCOHNTCGTCRCPCGFCNQPKPATAANSANEQ-CE 338  
QY 361 CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVCIDQCHHTAGVNCBRCCLPGYRSNHL 420  
DB 339 CYGHATDCYYDPEVDRRRASQSLDGTYYGGGVCIDQCHHTAGVNCBRCCLPGYRSNHL 398  
QY 421 DSHVRCRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGFPSCTPTSSND 480  
DB 399 DSHVRCRNCESDFTDGTCEDLTGRCYCRPNFSGERCDCVCAEGTGFPSCTPTSSND 458  
QY 481 TREQVLPAGQIVNCDSCSAAGTQGNACRDKPRVGRCLCKENFOGTHCELCAFGYFGCQP 540  
DB 459 TREQVLPAGQIVNCDSCSAAGTQGNACRDKPRVGRCLCKENFOGTHCELCAFGYFGCQP 517  
QY 541 CQSS---PGVADDRCDPTGQCRVGEATCDRCAPQVF-----HFPLCQLGCSGP 591  
DB 518 ASVPALWPMPTAVTLTQASAG---AEWASGRPHVIAVPATFTSLASHPLSAVCGCSP 574  
QY 592 AGTLPEGCDEAGRCCLQCPBFAGPHCDRCRPGVHGFENCOACTCDPRGALDQLCGAGLGR 651  
DB 575 AGTLPEGCDEAGRCCLQCPBFAGPHCDRCRPGVHGFENCOACTCDPRGALDQLCGAGLGR 634  
QY 652 CRPGYGTACQECSPGFHGFPPSPVCPCHCSAAGSLHAC-----DPRSGQSCRPVTVGLRC 707  
DB 635 CRPGYGTACQECSPGFHGFPPSPVCPCHCSAAGSLHAC-----DPRSGQSCRPVTVGLRC 698  
QY 708 DTCVPGYNYFFCYEAGSCHPAGLAPVDLPALPAQVPCMCRAHVGEPSCDRCRPGFWGLSP 767  
DB 689 TRVCVPTTSTAKLALATLPVWPPVDPALPAQVPCMCRAHVGEPSCDRCRPGFWGLSP 748  
QY 768 SNPEGTRCSCDLRGTLGGVABEQPQTGQCFCKPHVCGQACASCKDGFFGLDQADYFGCR 827  
DB 749 SNPEGTRCSCDLRGTLGGVABEQPQTGQCFCKPHVCGQACASCKDGFFGLDQADYFGCR 808

QY 828 SRCIDIGGALGSCBPTGVCRCRNTQPTCSBPARDHYLPDLHHLLELEEAATPEGH 887  
DB 809 SRCIDIGGALGSCBPTGVCRCRNTQPTCSBPARDHYLPDLHHLLELEEAATPEGH 868  
QY 888 AYRFGNPLEFFENFNRGQAQAPVOPRIVARLNLTSPLDFWLVRVYNRGAMSYSGRVS 947  
DB 869 AYRFGNPLEFFENFNRGQAQAPVOPRIVARLNLTSPLDFWLVRVYNRGAMSYSGRVS 928  
QY 948 VREGRSAACANTAQSOQVAPPPSTEPAFITVPOQFGPBPVLPNGWALRVEAGVLL 1007  
DB 929 VREGRSAACANTAQSOQVAPPPSTEPAFITVPOQFGPBPVLPNGWALRVEAGVLL 988  
QY 1008 DYVLLPSAYYEAALLQALVTEACTVYRPSAQSGDNCLLYTHPLDGPSPSAGLEALCRQ 1067  
DB 989 DYVLLPSAYYEAALLQALVTEACTVYRPSAQSPSPCLLYTHPLDGPSPSAGLEALCRQ 1048  
QY 1068 DNSLPRCPTEQSPSPHPLITCTGSDVDVQVQVAPQPGRYALVVEYANEDARQEVGVA 1127  
DB 1049 DNSLPRCPTEQSPSPHPLITCTGSDVDVQVQVAPQPGRYALVVEYANEDARQEVGVA 1108  
QY 1128 VHTPORAPOGLLSLHPCLYSTLCRTATDQDHLAVFHLDSASVRLTAEQARTFLHGV 1187  
DB 1109 VHTPORAPOGLLSLHPCLYSTLCRTATDQDHLAVFHLDSASVRLTAEQARTFLHGV 1168  
QY 1188 TLVPIBEFSEFVEPRVSCISSHGAFGPNASACLPSRFPKPPQPIILRDCQVPIPPGLP 1247  
DB 1169 TLVPIBEFSEFVEPRVSCISSHGAFGPNASACLPSRFPKPPQPIILRDCQVPIPPGLP 1228  
QY 1248 LTHAQDLTPATSPAGPRPPTAVDPDABPTLLREPOATVFTVHTVPTLGRVAFLLHGVO 1307  
DB 1229 LTHAQDLTPATSPAGPRPPTAVDPDABPTLLREPOATVFTVHTVPTLGRVAFLLHGVO 1288  
QY 1308 PAHPTPPVEVLINAGRWQGHANASCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEP 1367  
DB 1289 PAHPTPPVEVLINAGRWQGHANASCPHGYGCRITLVCEGQALLDVTHSELTVTVRVEP 1348  
QY 1368 GRWLMDYLVVDPENYVGYLREELDKSYDFISHCAACQVHI SPSSSSLFCRNAASL 1427  
DB 1349 GRWLMDYLVVDPENYVGYLREELDKSYDFISHCAACQVHI SPSSSSLFCRNAASL 1408  
QY 1428 SLFYNGARPCGHEVGATGPTCEPFGGQCPCHAVIGRDCSCATGYGFGFNCPCDCG 1487  
DB 1409 SLFYNGARPCGHEVGATGPTCEPFGGQCPCHAVIGRDCSCATGYGFGFNCPCDCG 1468  
QY 1488 ARLCDELTGQICPPRTIPDCLLQOPQTFGCHPLVGCRCNCGSGPIQELTDPCTDTS 1547  
DB 1469 ARLCDELTGQICPPRTIPDCLLQOPQTFGCHPLVGCRCNCGSGPIQELTDPCTDTS 1528  
QY 1548 GQCKCRPNVTGRCDTCSPGHGYPRCPDCEAGTAPGVCDPAGQCVCKENVGPKC 1607  
DB 1529 GQCKCRPNVTGRCDTCSPGHGYPRCPDCEAGTAPGVCDPAGQCVCKENVGPKC 1588  
QY 1608 DQCSLGTFSLDAAANPKGCTRCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVPHER 1667  
DB 1589 DQCSLGTFSLDAAANPKGCTRCFCGATERCRSSSYTRQEFVDMEGWVLLSTDRQVPHER 1648  
QY 1668 QPTEMLRADLRHVPEAVPAFELVWQAPPVYLGRVSSYGTLRYELHSETQRGDVV 1727  
DB 1649 QPTEMLRADLRHVPEAVPAFELVWQAPPVYLGRVSSYGTLRYELHSETQRGDVV 1708  
QY 1728 PMSRDPVWLQGNMSITFLEPAYTPGHVHRGQLQVEGNFRHTETRNVSREELMMVL 1787  
DB 1709 PMSRDPVWLQGNMSITFLEPAYTPGHVHRGQLQVEGNFRHTETRNVSREELMMVL 1768  
QY 1788 ASLEQLQIRALFQSISSAVALRRVALEVASPAGGALASVELCLCPASVYRGDSQCECAP 1847  
DB 1769 ASLEQLQIRALFQSISSAVALRRVALEVASPAGGALASVELCLCPASVYRGDSQCECAP 1828  
QY 1848 GFYEDVKGLFLGRVCPCQCHGSHDRCLPSPGVCVDCOHNTEGAHCRCAQGFVSSRDPDS 1907  
DB 1829 GFYEDVKGLFLGRVCPCQCHGSHDRCLPSPGVCVDCOHNTEGAHCRCAQGFVSSRDPDS 1887  
QY 1908 APCVSCPCLSVSPNNFAEGVLRGRTQCLCKPGVAGASCERCAPGFGNPLVLGSSCQ 1967

DB 1888 APCVSCPCLSVSPNNFAEGVLRGRTQCLCKPGVAGASCERCAPGFGNPLVLGSSCQ 1920  
QY 1968 PCDCSNGDNPLLFSDCDPLTGACRGLRHTTTPRCCEICAPGYGNALLPCNCTRCDCCTP 2027  
DB 1921 PCDCSNGDNPLLFSDCDPLTGACRGLRHTTTPRCCEICAPGYGNALLPCNCTRCDCCTP 1980  
QY 2028 CGTEACDPHSGHCLCKAGVTGRCDCRQEGHFGNGCGCRPCACGPAABEGSCHPQSGQ 2087  
DB 1981 CGTEACDPHSGHCLCKAGVTGRCDCRQEGHFGNGCGCRPCACGPAABEGSCHPQSGQ 2040  
QY 2088 CHCRPGTMGPQCRPCAPGYWGLPEQGCRCRQCQPGGCDPHTGRCNCPPLGSLGRCDCCTCSQ 2147  
DB 2041 CHCRPGTMGPQCRPCAPGYWGLPEQGCRCRQCQPGGCDPHTGRCNCPPLGSLGRCDCCTCSQ 2100  
QY 2148 QHQPVPAGVPVGHSHICHCEVCDHCVLLDDLELAGALLPAIHQRLRGINASSWAWARLHR 2207  
DB 2101 QHQPVPAGVPVGHSHICHCEVCDHCVLLDDLELAGALLPAIHQRLRGINASSWAWARLHR 2160  
QY 2208 LNASIADL-----QSLSRPLGPRHETAOQLVLSQOSTSLG 2244  
DB 2161 LNASIADLQVLSVLPFPQPVQAFTRFLPQSLASPLGPRHETAOQLVLSQOSTSLP 2220  
QY 2245 QDARRLGGQAVGTEDQASOLLAGTEATLGHAKTLAAIRAVDRITLSLMSQTHLGLANA 2304  
DB 2221 P-----QAVGTRDQASOLLAGTEATLGHAKTLAAIRAVDRITLSLMSQTHLGLANA 2273  
QY 2305 SAPSGEQLLRTLAEBVERLLWEMRARDLGAPOAAAEAEELAAQRLARVQSLSLWBEHQ 2364  
DB 2274 SAPSGEQLLRTLAEBVERLLWEMRARDLGAPOAAAEAEELAAQRLARVQSLSLWBEHQ 2333  
QY 2365 ALATQTRDRLAQHAGLMDLREALNBAVDATRAEOLNSRQERLEALOKKOLSRDNA 2424  
DB 2334 ALATQTRDRLAQHAGLMDLREALNBAVDATRAEOLNSRQERLEALOKKOLSRDNA 2393  
QY 2425 TLOATLHAARDTLASVRELLHSLDOAK-BELERLAAALDQARTPLLMQRTFSPAGSKLR 2483  
DB 2394 TLOATLHAARDTLASVRELLHSLDOAK-BELERLAAALDQARTPLLMQRTFSPAGSKLR 2453  
QY 2484 LVEAAEAHAQOLGOLALNLSIILDVNQDLRTQBAIEASNAYSRILQAVQAAEDAAQAL 2543  
DB 2454 LVEAAEAHAQOLGOLALNLSIILDVNQDLRTQBAIEASNAYSRILQAVQAAEDAAQAL 2512  
QY 2544 QOAHWTATVVRQGLVDRQAQOLLANSTALBEAMLOEQRLGL--VMA---ALQARTQLR 2598  
DB 2513 QOAHWTATVVRQGLVDRQAQOLLANSTALBEAMLOEQRLGLGECWAPMGALRPAQTQLR 2572  
QY 2599 DVRAKDKQLEAHIQAAQAMLANDTDETSKKIAHAKAVAAEAQDTATRVQSOLOMQENVE 2658  
DB 2573 DVRAKDKQLEAHIQAAQAMLANDTDETSKKIAHAKAVAAEAQDTATRVQSOLOMQENVE 2632  
QY 2659 RWQOYEGRLGODLGOAVLDAGHSVSTLEKTLPOLLAKLSTLENRGVHNASLALSASIGR 2718  
DB 2633 RWQOYEGRLGODLGOAVLDAGHSVSTLEKTLPOLLAKLSTLENRGVHNASLALSASIGR 2692  
QY 2719 VRELIQAARGAASK-VKVPKMGKRSVQLRTPRDLADLAAYTALKFYLGQPEPEPGQT 2777  
DB 2693 VRELIQAARGAASKVVKVPKMGKRSVQLRTPRDLADLAAYTALKFYLGQPEPEPGQT 2752  
QY 2778 EDRFVYMGSRQATGDYMGVSLRDKKVVHVVYQGEAGPAVLSDIDEGEOPAAVSLDRTL 2837  
DB 2753 EDRFVYMGSRQATGDYMGVSLRDKKVVHVVYQGEAGPAVLSDIDEGEOPAAVSLDRTL 2812  
QY 2838 QFGHMSVTVVERQMTQETKGDTPVAPGAGLLNLRPDDFVYVGGYFSTFTTTPPLLRFPYGR 2897  
DB 2813 QFGHMSVTVVERQMTQETKGDTPVAPGAGLLNLRPDDFVYVGGYFSTFTTTPPLLRFPYGR 2872  
QY 2898 GCIEMDTLNEBVSILYNFERTFQDITAVDRPCARSKSTGDPMLTDSGLDGTGPARISFD 2957  
DB 2873 GCIEMDTLNEBVSILYNFERTFQDITAVDRPCARSKSTGDPMLTDSGLDGTGPARISFD 2932  
QY 2958 SOISTTKRFECELRILVSYGVLFFLKQOSQFCLAVQEGSLVLLYDFCAGLKKAIVPQPP 3017

2933 SQISTTKRFEQLRLNSVSGVLFELKQSQFLCLAVQEGSLVLLYDFGAGLKKAVLPQPP 2992  
3018 PPLTSASKAIOVELLGGSRKRLVRVERATVYSVEQNDLELADAYLGGVPPDQLPPSL 3077  
2993 PPLTSASKAIOVELLGGSRKRLVRVERATVYSVEQNDLELADAYLGGVPPDQL-PSL 3051  
3078 RMLFPPTGSGVRGCVKGIKALGKYVDLKRLLNTTGVSACTADLLVGRAMTFPHGHGFLRLAL 3137  
3052 RMLFPPTGSGVRGCVKGIKALGKYVDLKRLLNTTGVSACTADLLVGRAMTFPHGHGFLRLAL 3111  
3138 SNVAPLTGNYSGFGFHSADQSALLYVRASPDGLQCUSLQGRVSLQLLLETKVTOGFA 3197  
3112 SNVAPLTGNYSGFGFHSADQSALLYVRASPDGLQCUSLQGRVSLQLLLETKVTOGFA 3171  
3198 DGAPHYVAFYSNATGVLYYDDQLQOMKPHRPPPELQPOPEPPRLLLGLPESGTIYN 3257  
3172 DGAPHYVAFYSNATGVLYYDDQLQOMKPHRPPPELQPOPEPPRLLLGLPESGTIYN 3231  
3258 FSGCISNVFORLLGPORVFDLQNLGSVNVSTGCAPALQATPGLGPRGLQATARKASR 3317  
3232 FSGCISNVFORLLGPORVFDLQNLGSVNVSTGCAPALQATPGLGPRGLQATARKASR 3284  
3318 RSROPASHPACMLPHLRTTRDSYQFGSLSSHLEFVIGILARHNWPSLSMHVLPSSRG 3377  
3285 RSROPASHPACMLPHLRTTRDSYQFGSLSSHLEFVIGILARHNWPSLSMHVLPSSRG 3329  
3378 LLLFTARLRPGSPSLALFSLNGHFVAQMEGLTELRAQSRQSRPRGHWKHVVRWEKNRI 3437  
3330 -----VSRWEKNRI 3339  
3438 LLVTDGARANSQEGPHRQHGAEHPQHTLVGGLPASSHSSKLPTVTGFGSGVKRLRLH 3497  
3340 LLVTDGARANSQEGPHRQHGAEHPQHTLVGGLPASSHSSKLPTVTGFGSGVKRLRLH 3399  
3498 GRPLCAPTRMAGVTPCILGLEAGLFFPGSGGVITLPLGATLPDVGLELEVRPLAVTGL 3557  
3400 GRPLCAPTRMAGVTPCILGLEAGLFFPGSGGVITLPLGATLPDVGLELEVRPLAVTGL 3459  
3558 IFHLQOARTPPYLOLVTEKQVLLRADDDGAGEFSTSTPSPVLCGOWHRLAVNKSQNVL 3617  
3460 IFHLQOARTPPYLOLVTEKQVLLRADDDGAGEFSTSTPSPVLCGOWHRLAVNKSQNVL 3519  
3618 RLEVDAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQPPAYCGCVRRLAVNRSFVAM 3677  
3520 RLEVDAQSNHTVGPLLAAAAGAPAPLYLGLPEPMAVQPPAYCGCVRRLAVNRSFVAM 3579  
3678 TRSVEVHGAVGASGCPAA 3695  
3580 TRSVEVHGAVGASGCPAA 3597

RESULT 6  
ABB81589  
ID ABB81589 standard; protein; 3635 AA.  
XX ABB81589;  
AC ABB81589;  
XX  
DT 19-SEP-2002. (first entry)  
DE Mouse laminin alpha 5 amino acid sequence SEQ ID NO:4.  
XX Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;  
KW tissue repair development; laminin; healing; vascular tissue;  
KW re-endothelialisation; vascular injury; cell attachment; cell stasis;  
KW proliferation; migration.  
XX Mus musculus.  
XX WO200250111-A2.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
PF

XX 21-DEC-2000; 2000US-0257449P.  
PR 28-MAR-2001; 2001US-0279282P.  
PR 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOTRATUM INC.  
PA Trygsvason K, Doi M, Thyboll J;  
PI WPI; 2002-557650/59.  
XX N-PSDB; ABQ72907.  
DR New human laminin-10 proteins, useful for accelerating the healing of  
PT vascular tissue, improving the biocompatibility of grafts, or for  
PT promoting re-endothelialization at the site of vascular injuries.  
XX Claim 9; Page 94-105; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
CC an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are  
CC useful in maintaining cell/tissue phenotype as well as promoting cell  
CC growth and differentiation in tissue repair development. Specifically,  
CC laminin 10 can be used for accelerating the healing injuries of vascular  
CC tissue, improving the biocompatibility of grafts useful for treating such  
CC injuries, for promoting re-endothelialisation at the site of vascular  
CC injuries, for promote cell attachment and subsequent cell stasis,  
CC proliferation, differentiation, and/or migration. The present sequence  
CC represents mouse laminin alpha 5 which is used in the exemplification of  
CC the present invention  
XX Sequence 3635 AA;  
SQ Query Match 78.7%; Score 15839; DB 5; Length 3635;  
Best Local Similarity 79.4%; Pred. No. 0;  
Matches 2874; Conservative 277; Mismatches 452; Indels 18; Gaps 8;  
QY 79 DLYCKLVGPGVAGGDPNQTIRQYCDICTAANSKHAHPASNAIDGTERWQSPPLSRGLE 138  
Db 1 DLYCKLVGPGVAGGDPNQTIRQYCDICTAANSKHAHPASNAIDGTERWQSPPLSRGLE 60  
QY 139 YNEVNTLGLQGVHVAVYLIKFANSPRDLWLSRMDFGRTYQWQFASSKRDCLER 198  
Db 61 YNEVNTLGLQGVHVAVYLIKFANSPRDLWLSRMDFGRTYQWQFASSKRDCLER 120  
QY 199 FGPQTLERITRDAATCTTEYSRIVPLENGEIVSLVNGRPGAMFSPPLREFTKATN 258  
Db 121 FGPQTLERITRDAATCTTEYSRIVPLENGEIVSLVNGRPGAMFSPPLREFTKATN 180  
QY 259 VRLRFLRTNTLLHLMKALRDPVTTRYYYSKDTSIGRCVCHGHADCAKDPDFF 318  
Db 181 IRLRFLRTNTLLHLMKALRDPVTTRYYYSKDTSIGRCVCHGHADCAKDPDFF 240  
QY 319 RLQCTQHNTCGGTCDRCPCGFGNQPKPATANSANECQSCNCHGHAYDYDPEVDRE 378  
Db 241 RLQCTQHNTCGGTCDRCPCGFGNQPKPATANSANECQSCNCHGHAYDYDPEVDRE 300  
QY 379 ASQSLDGTGGVGVICDQHTAGVNCERCLGFRYSPNHPLDSPHVCRNCNCSDFDGG 438  
Db 301 ASQSLDGTGGVGVICDQHTAGVNCERCLGFRYSPNHPLDSPHVCRNCNCSDFDGG 360  
QY 439 TCEDLGRVCYRPNFSGERCDVCAEQFTGFPSCYPTPS-SSNDTREQVLPAGQVNCDCS 497  
Db 361 TCEDLGRVCYRPNFSGERCDVCAEQFTGFPSCYPTPS-SSNDTREQVLPAGQVNCDCS 420  
QY 498 AAGTQGNACRKPDRVGRCLCKNFQTHCELAPGYGCGQPCQCSSPGVADRCDDPT 557  
Db 421 AAGTQGNACRKPDRVGRCLCKNFQTHCELAPGYGCGQPCQCSSPGVADRCDDPT 480  
QY 558 GQCRVRGEGATCDRCAPGYRHHPLCQLCGGSPAGTLPPEGCDACRCLCQPEFAGPHCD 617  
Db 481 GQCMRTGFEGRDCHCALGYHFFPLCQLCGGSPAGTLPPEGCDACRCLCQPEFAGPHCD 540  
QY 618 RCRPGVHGFPNQACTCDPRGALDQLCGAGGLRCRPGYTGTAQCQCSGFGHFFPSVCVC 677



541 RCLPGVHGYFDCACACDPGRALDOOCVGGCHCRPONTGATCQESPGFYFPSPCIPC 600  
678 HCSAGSLSHAACDPSGQSCSRPRVTGLRCDTCVPGAYNFPYCBAGSCHPAGLAPVDPAL 737  
601 HCSAGSLSHTCDPTTGGCRPRVTGLHCDMCPVPGAYNFPYCBAGSCHPAGLAPANPAL 660  
738 PEAQVPCMCRAHVEGSCDRCKPQFWGLSPNPGCTRCSCDLRGLTGGVAECQPGTGQC 797  
661 PETQAPCMCRAHVEGSCDRCKPQFWGLSASNPBGCTRCSDPRGTLGGVTECQ-GNGQC 719  
798 FCKPHVCQAACASCKDGFGLDADYFGCRSCRCDDIGGALGQSCBPTGVCRCRPNTOGP 857  
720 FCKAHVCCKTCAACKDGFGLDADYFGCRSCRCDDVGGLGQSCBPTGACRCRPNTOGP 779  
858 TCSEPARDHYLPDLHHLLELEEAATPEGHAVRFGFNPFLBFENFWSRGAQMAVQPRIV 917  
780 TCSEPAKDHLPDLHHLLELEEAATPEGHAVRFGFNPFLBFENFWSRGAHMAVQPRIV 839  
918 ARLNLTSPDLFWLFRYVNRGAMSVGRVSVREGRSAACACTAQSQPVAFPPSTEPAP 977  
840 ARLNLTSPDLFWLFRYVNRGAMSVGRVSVREGRSAACACTAQSQPVAFPPSTEPAP 899  
978 ITVPQGFGEFVLPNPGTMAWRAEAGVLLDYVLLPSAYEALLQLRVTEACTYRPSA 1037  
900 VTVPQGFGEFVLPNPGTMAWRAEAGVLLDYVLLPSAYEALLQLRVTEACTYRPSA 959  
1038 QOSGDNCLLYTHLPDGFPSAAGLEALCRQNSLPRCPTEQLSPSHPLITTCGSDVDV 1097  
960 LHSTENCLVYAHLPDGFPSAAGTEALCRHNSLPRCPTEQLSPSHPLITTCGSDVDV 1019  
1098 QLOVAPQGFGRYALVVEANEDARQEVGVAHTPQAPQOGLLSLPHSTYLCRGATARD 1157  
1020 QLENAVPOQGYVLVVEVGEDSHQEMGVAVHTPQAPQOGLLSLPHSTYLCRGATARD 1157  
1158 TODHLAVHLSSEASVRLTABOARFLHGVTLPIEBFSEFVEPRVSVCSHSGAGPNS 1217  
1080 TOHHLAIFHLDSSEASIRLTAEQAEFFLHSTVLPVEEFSTEFVEPRVSVCSHSGAGPNS 1139  
1218 AACLPSPRPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSPAGRPPTTAVDPDABP 1277  
1140 AACLPSPRPKPPQPIILRDCQVILPPLPGLPLTHAQDLTPATSPAGRPPTTAVDPDABP 1199  
1278 TLLRBPQATVFTTHVTLGRYALHGVTLPIEBFSEFVEPRVSVCSHSGAGPNS 1337  
1200 TLLRBPQATVFTTHVTLGRYALHGVTLPIEBFSEFVEPRVSVCSHSGAGPNS 1259  
1338 YGCRVLVCEGOALLDVTHSELTVTVRVEGRWMLDYVLVWPNVSVFYLREELDKS 1397  
1260 YGCRVLVCEGOALLDVTHSELTVTVRVEGRWMLDYVLVWPNVSVFYLREELDKS 1319  
1398 YDFISHCAQGYHISPSSSSLFCNAAASLSLFYNNGARPCGCHGVGATGTCBPFGQC 1457  
1320 YDFISHCAQGYHISPSSSSLFCNAAASLSLFYNNGARPCGCHGVGATGTCBPFGQC 1379  
1458 PCHAHVIGRDCSRCATGYWGFPCNCRPCDGCARLDELGTGQCICPPRTTIPPCDCLQPOTF 1517  
1380 PCHAHVIGRDCSRCATGYWGFPCNCRPCDGCARLDELGTGQCICPPRTTIPPCDCLQPOTF 1439  
1518 GCHPLVGCCECNCSPGQIBLTDPTDTSQCKRPNVTGRRCDTCSGFGHYRRCRCP 1577  
1440 GCHPLVGCCECNCSPGQIBLTDPTDTSQCKRPNVTGRRCDTCSGFGHYRRCRCP 1499  
1578 DCHBAGTAPGVCDPLTGQYCKENVQPKDCQSLGTFSLDAANPKGTCRCFCGATERC 1637  
1500 DCHBAGTAPGVCDPLTGQYCKENVQPKDCQSLGTFSLDAANPKGTCRCFCGATERC 1559  
1638 RSSSYTROQFVDMGCVLLSTDRQVPHRQPGTEMRLADLRHVPBAVPEAPPELYWQAP 1697  
1560 GNSNLARHEFVDMGCVLLSTDRQVPHRQPGTEMRLADLRHVPBAVPEAPPELYWQAP 1615  
1698 PSYLGDRVSSYGGTLRYELHSETQGRGVFVPMESRPDVLVQGNQMSITFLEPAYTTPGHV 1757

1616 PSYLGDRVSSYGGTLRYELHSETQGRGVFVPMESRPDVLVQGNQMSITFLEPAYTTPGHV 1675  
1758 HRGQLQVVEGNFRHTRTNTVSEELMMVLASLEQLQIRALFSQISSAYSLLRVALEVAS 1817  
1676 HRGQLQVVEGNFRHTRTNTVSEELMMVLASLEQLQIRALFSQISSAYSLLRVALEVAS 1735  
1818 PAGQALASNVVELCLCPASVYRGSQCBAPGFYRDKVGLFLGRVCPQCHGSHDRCLPGS 1877  
1736 EAGSGPPASNVVELCMCPANVYRGSQCBAPGFYRDKVGLFLGRVCPQCHGSHDRCLPGS 1795  
1878 GVCVDCQHNTEGAHCRCQAGMSS--RDDPSAPCVSCPPLSVPSNNFAEGCVLRGRTO 1936  
1796 GICVGCQHNTEGAHCRCQAGMSS--RDDPSAPCVSCPPLSVPSNNFAEGCVLRGRTO 1855  
1937 CLCPKPGYAGASCRCAPGFYRDKVGLFLGRVCPQCHGSHDRCLPGS 1996  
1856 CLCPKPGYAGASCRCAPGFYRDKVGLFLGRVCPQCHGSHDRCLPGS 1915  
1997 HTTGPRCEICAPQYGNALLPGNCTRCDDTTCOTEAADPHSGHCLCKAGVTRGRDRCOE 2056  
1916 HTTGPRCEICAPQYGNALLPGNCTRCDDTTCOTEAADPHSGHCLCKAGVTRGRDRCOE 1975  
2057 GHFGFNGCGCRPCACGPAAGSECHPQSGQCHCRPTGMPQCRCAPOGVMGLPEGCRR 2116  
1976 GHFGFNGCGCRPCACGPAAGSECHPQSGQCHCRPTGMPQCRCAPOGVMGLPEGCRR 2035  
2117 CQCPGRCDDPHTGRCNCPGLSGERCDTCSQHQVVPVPGPVGHSIHCEVCHCVVLLLD 2176  
2036 CQCPGRCDDPHTGRCNCPGLSGERCDTCSQHQVVPVPGPVGHSIHCEVCHCVVLLLD 2095  
2177 DLRAGALLPAIHEQRLGINASSMAWHLRLNASTADIQSLRSLPLGRPHRTAQOLEVL 2236  
2096 DLRAGALLPAIHEQRLGINASSMAWHLRLNASTADIQSLRSLPLGRPHRTAQOLEVL 2155  
2237 EQQSTSLGQDARLGGQAVGTRDQASQLLAGTEATLGHAKTLAALRAVDRTLSELMQOT 2296  
2156 EQQSTSLGQDARLGGQAVGTRDQASQLLAGTEATLGHAKTLAALRAVDRTLSELMQOT 2215  
2297 GHGLANASAPSGEQLLRLARVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQ 2356  
2216 GOSPGDALVPSGEQLRWALAEVERLLWEMRARDLGAPOAAAEALAAQRLARVQEQ 2275  
2357 SSWERNQALATOTDRLOHEAGLMDREALNRAVDATREAOELNSRQEBLEALQK 2416  
2276 TSFWEENQSLATHIRDLQAQYESGLMDREALNRAVDATREAOELNSRQEBLEALQK 2335  
2417 QELSRDNLATLHAARDTLASVFLHSLDQAEELERLAASLDGARTPLQRMQTPS 2476  
2336 QELSRDNLATLHAARDTLASVFLHSLDQAEELERLAASLDGARTPLQRMQTPS 2395  
2477 PASKRLRLEBAABAHAQOGLALNLSIILVNDQDLTORAIBASNAYSRILQAVQAAE 2536  
2396 PASKRLRLEBAABAHAQOGLALNLSIILVNDQDLTORAIBASNAYSRILQAVQAAE 2455  
2537 DAAGQALQADHTWATVVRQGLVDRAQQLANSTALEAMLQEQORLGLVMAALQGARTQ 2596  
2456 DAAGQALQADHTWATVVRQGLVDRAQQLANSTALEAMLQEQORLGLVMAALQGARTQ 2515  
2597 LRDYRAKQOOLEHIAHQAQAMLDMDTSETSKIAHAKAVAAQAQDTATRVQSOLOAMQEN 2656  
2516 LHNWARKQOALEHIAHQAQAMLDMDTSETSKIAHAKAVAAQAQDTATRVQSOLOAMQEN 2575  
2657 VERWQOQYEGRLQDGLQAVLDAGHSVSTLEKTLPLQALKLILNENRGVHNASALSASI 2716  
2576 VERWQOQYEGRLQDGLQAVLDAGHSVSTLEKTLPLQALKLILNENRGVHNASALSASI 2635  
2717 GRVRELLAQARGNASKVKPKFNGRSGVOLTRPDRLADLAAYTALKFYLOG--PEPSPG 2774  
2636 GRVRELLAQARGNASKVKPKFNGRSGVOLTRPDRLADLAAYTALKFYLOG--PEPSPG 2695  
2775 QGTEDRFVWYMSRQATGDYNGVSLRDKKVVHVVYQLGAGPAVLSDIDEDIEQFAAVSLD 2834  
2696 KNTGDHFLVYMSRQATGDYNGVSLRDKKVVHVVYQLGAGPAVLSDIDEDIEQFAAVSLD 2755





Db 241 RLQCAQHNTCCGSDRCPCPGFNQCPWKPATTDSANECQSCNCHGHAYDCYYDEVDERN 300  
QY 379 ASQSJGTVGGGVICIDOHHTAGVNCBRLPGFYRSPNHPLDSDHVCRCNCSDFTDG 438  
Db 301 ASQNDNVYGGGVCLDCOHHTTGNCERCLPGFFRAPDQPLDSDHVCRCNCSDFTDG 360  
QY 439 TCEDLTGRCYCRPNFSGBERCDVCAEGFTGFPSCYTPS - SSNDTREQVLPAGQVNCDCS 497  
Db 361 TCEDLTGRCYCRPNFSGBERCDVCAEGFTGFPSCYTPS - SSNDTREQVLPAGQVNCDCN 420  
QY 498 AAGTQGNACRKPVRGRCLCKNFQTHCELCAPOFYGPGOCOCSSPGVADRCDDPT 557  
Db 421 AAGTQGNACRKPRLGRCKENFNGAHCELCAPOFGHPSCHPCQCSSPGVANSICDPES 480  
QY 558 GOCRCEVREGATCDRCAPGYEHP2LQJCGSPAGTLPEGCDABGRCLCOPEFAGPHCD 617  
Db 481 GQCMCKTGEBDRCHCALGYHFFLQJCGSPAGTLPEGCDABGRCCQCPGPDGPHCD 540  
QY 618 RCRPGYHGPNCQACTCDPRGALDQJCGAGGCLRCRPGYGTGTACQCSGPHGFPSCVPC 677  
Db 541 RCLPGYHGYDCHACACDPRGALDQJCGAGGCLRCRPGYGTGTACQCSGPHGFPSCVPC 600  
QY 678 HCSAOSLHAA CDPRSQCSCRPVTLGLCDTCVPGAYNFPYCEAGSCHPAGLAPDPA 737  
Db 601 HCSADGSLHTTCDPTTGQCRCPRTVTLGLCDTCVPGAYNFPYCEAGSCHPAGLAPDPA 660  
QY 738 PBAOVPCMAHVBGSCDRCKPFGWGLSPNPEGCTRCSDLRGTGLGAVACQPGTQC 797  
Db 661 PETQAFOMCRHVBGSCDRCKPFGWGLSPNPEGCTRCSDLRGTGLGAVACQPGTQC 719  
QY 798 FCKPHVCGQACSKDGFGLDQADYFGCRSCRDIGGALGOCSPRTGVCRCRNTQGP 857  
Db 720 FCKAHVCGTKCAACKDGFGLDQADYFGCRSCRDIGGALGOCSPRTGVCRCRNTQGP 779  
QY 858 TCSEPARDHYLPDLHLRLLEBAATPEGHAVRFGNPLEFENFNGWRYAQAQMAPVQPRIV 917  
Db 780 TCSEPARDHYLPDLHLRLLEBAATPEGHAVRFGNPLEFENFNGWRYAQAQMAPVQPRIV 839  
QY 918 ARNLATSPLFLWLVRYVARGMSVRSVREBGSAA CANCTAQSQVAPVPPSTEPAF 977  
Db 840 ARNLATSPLFLWLVRYVARGMSVRSVREBGSAA CANCTAQSQVAPVPPSTEPAF 899  
QY 978 ITVPQRFGEFPVNLPGTVALRVEAGVLLDYVLLPSAYEAALLQLRVTEACTYRPSA 1037  
Db 900 ITVPQRFGEFPVNLPGTVALRVEAGVLLDYVLLPSAYEAALLQLRVTEACTYRPSA 959  
QY 1038 QQSGDNCLLYTHLPDGFPSAAGLEALCRQDNLPRPCPTQELSPSHPLITCTGSDVDV 1097  
Db 960 LHSTENCLVYHLPLDGFPSAAGLEALCRQDNLPRPCPTQELSPSHPLITCTGSDVDV 1019  
QY 1098 QLQVAVPQORYALVVEYANEDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCGTARD 1157  
Db 1020 QLEMAVPPQCYLVVVEYGEDSHQEMGVAVHTPQAPQOGLLSLHPCLYSTLCGTARD 1079  
QY 1158 TODHLAVFLHDSBASVRLTAEQARFFLHGVTLPVIEEFSPFVPRVSCISSHGAFGPN 1217  
Db 1080 TOHHLAIFHLHDSBASVRLTAEQARFFLHGVTLPVIEEFSPFVPRVSCISSHGAFGPN 1139  
QY 1218 AACLPSPRFPXPOPIILRDQVTLPLPGLPLTHAQDLTPATSPAGPRPPPTAVDPDAP 1277  
Db 1140 AACLPSPRFPXPOPIILRDQVTLPLPGLPLTHAQDLTPATSPAGPRPPPTAVDPDAP 1199  
QY 1278 TLREPOATVFTTHVPTLGRYAFLLHGYQPAHPTFPFVEVLINAGRVWQGHANASFCPHG 1337  
Db 1200 TLLHHPGTVFTTQVPTLGRYAFLLHGYQPAHPTFPFVEVLINAGRVWQGHANASFCPHG 1259  
QY 1338 YGCRTLVVCBQGLLDVTHSELTVTVRVPGRWMLDYLVDENVYVSGYLBREPLDKS 1397  
Db 1260 YGCRTLVLCBQGLLDVTHSELTVTVRVPGRWMLDYLVDENVYVSGYLBREPLDKS 1319  
QY 1398 YDFTSHCAAQGYHTSPSSSILFCRANAASLFFYNGARPCGCHVEGATGPTCEPFGGQC 1457

Db 1320 YDFISHCATQGYHISFSSSSSPFCRANAATSLSLFYNNALPGCGCHEVGAVSPCTCEPFGGQC 1379  
QY 1458 PCHAHVIGRDCSCATGYWGFNCRPCDCGALCDBELTGQCICPPRTTIPDCCLLCQOPQT 1517  
Db 1380 PCKGHVIGRDCSCATGYWGFNCRPCDCGALCDBELTGQCICPPRTTIPDCCLLCQOPQS 1439  
QY 1518 GCHPLVCEBSCNCGSGPIQELTDPTCOTDSGQCKCRPNVTGRCDTCSGFGHGYPCRC 1577  
Db 1440 GCHPLVCEBSCNCGSGPIQELTDPTCOTDSGQCKCRPNVTGRCDTCSGFGHGYPCRC 1499  
QY 1578 DCHAGTAPGVCDPLTGQCYCKENVGPKDCQSLGTFSLDAAANPKGCTRCFCFGATERC 1637  
Db 1500 DCHAGTAPGVCDPLTGQCYCKENVGPKDCQSLGTFSLDAAANPKGCTRCFCFGATERC 1559  
QY 1638 RSSSYTRQEFVDMGVLLSTDRQVYVHERHQPOTEMLRADLRHVPAVPAEPAPLWQAP 1697  
Db 1560 GNSNLAHREHVEFDMGVLLSTDRQVYVHERHQPOTEMLRADLRHVPAVPAEPAPLWQAP 1615  
QY 1698 PSYLGDRVSSYGGTLYVELHSETQGRGVFVPMSSRPDVLQGNOMITTELEPAYPPGHV 1757  
Db 1616 PSYLGDRVSSYGGTLYVELHSETQGRGVFVPMSSRPDVLQGNOMITTELEPAYPPGHV 1675  
QY 1758 HRGOLQVLEGNFRHTETRTNVSREELMMVLASLEQIQIRALFSQTSSSSLRRLVLEAS 1817  
Db 1676 HRGOLQVLEGNFRHTETRTNVSREELMMVLASLEQIQIRALFSQTSSSSLRRLVLEAS 1735  
QY 1818 PAGOGALANVELCLCPASVYRGDSCECAPGVYDVYKGLFLGRVCPQCHGHSDRCLPGS 1877  
Db 1736 EAGRPASVVELCWPANVYRGDSCECAPGVYDVYKGLFLGRVCPQCHGHSDRCLPGS 1795  
QY 1878 GVCVDCQHNTEGAHRCERCAQAGMSS - RDDPSAPCVSCPCPLSVPSNNFAGBVCVLRGRTQ 1936  
Db 1796 GVCVDCQHNTEGAHRCERCAQAGMSS - RDDPSAPCVSCPCPLSVPSNNFAGBVCVLRGRTQ 1855  
QY 1937 CLKVPYAGASCERCAPGFGNPLVGLSSCORDCSGNGDPLNLLFSDCDPLTGACRGCLR 1996  
Db 1856 CLKVPYAGASCERCAPGFGNPLVGLSSCORDCSGNGDPLNLLFSDCDPLTGACRGCLR 1915  
QY 1997 HTTCPRCEICAPGYGNALLPGNCTRCCTPCGTAEADPHSGHCLCKAGVTGRRCDRCQE 2056  
Db 1916 HTTCPRCEICAPGYGNALLPGNCTRCCTPCGTAEADPHSGHCLCKAGVTGRRCDRCQE 1975  
QY 2057 GHFNGCGGRCPCACPAAGSECHQSCQCHCRPCTMTGPOCEBAGPYWGLPEQGCRR 2116  
Db 1976 GHFNGCGGRCPCACPAAGSECHQSCQCHCRPCTMTGPOCEBAGPYWGLPEQGCRR 2035  
QY 2117 CQCPGRCDPHTGRCNCPGCLSGERCDCSQOQVVPVGGPVGHSIHCEVCDHCVLLLD 2176  
Db 2036 CQCPGRCDPHTGRCNCPGCLSGERCDCSQOQVVPVGGPVGHSIHCEVCDHCVLLLD 2095  
QY 2177 DLERAGALLPAIHQPLRGINASSMAWHLRLNASIADLOSRLSPGLPHEHTAQOQLEVL 2236  
Db 2096 DLERAGALLPAIHQPLRGINASSMAWHLRLNASIADLOSRLSPGLPHEHTAQOQLEVL 2155  
QY 2237 EQQSTSLQDARLLGGQAVGTDCQASOLLAGTATLGHAKTLLAAIRAVDRTLSLMSQT 2296  
Db 2156 EQQSTSLQDARLLGGQAVGTDCQASOLLAGTATLGHAKTLLAAIRAVDRTLSLMSQT 2215  
QY 2297 GHLGLANASAPSGQLLRTLAELVRLLEWEMARLDGAPQAAAAEALAAQRLARVQEQ 2356  
Db 2216 GHLGLANASAPSGQLLRTLAELVRLLEWEMARLDGAPQAAAAEALAAQRLARVQEQ 2275  
QY 2357 SSLWEENALATQFDRLAQHEAGLMDLREALNAVDAEAOELNERNORLEALQK 2416  
Db 2276 TSFWEENQSLATHRDQLAQYESGLMDLREALNAVDAEAOELNERNORLEALQK 2335  
QY 2417 QELSRDNATQATLHAARDTLASVFRLLHSIDQAKEELERLASLDGARTPLLMQTFPS 2476  
Db 2336 QELSRDNATQATLHAARDTLASVFRLLHSIDQAKEELERLASLDGARTPLLMQTFPS 2395  
QY 2477 PAGSKRLVUEAAHAQOLGOLALNLSIILVDNODLTQPAIENASVAYSILOAVAAE 2536  
Db 2396 PASSKVDLVEAAHAQOLGOLALNLSIILVDNODLTQPAIENASVAYSILOAVAAE 2455

QY 2537 DAAGALQADHTWATVROGLVDRAOILLANSTALEEAMLOEQOQLGLVWALQAGTQ 2596  
DB 2456 DAAGALQARSRWVWVQVGLAAGRAOLLANSALSETILLQOGLQAGLQAGTQ 2515  
QY 2597 LRDRVAKKDOLEAHIOAAQAMLANDTDETSKIAHAKAVAAEAQDTATRVQSOLOQAMQEN 2656  
DB 2516 LHNWAKENQLAAQIOEAQAMLANDTSETSEKIAHAKAVAAEAALSTATHVQSOLOQAMQXN 2575  
QY 2657 VERQGOYEGLRQODLQOAVLDAGHSVSTLEKTLQOLLAKLSILENGVHNASIALSASI 2716  
DB 2576 VERMQSQLGQLQOQLSVERDASSVSTLEKTLQOLLAKLSILENGVHNASIALSANI 2635  
QY 2717 GRVRELLAQAAGKASKVKPKNGRSGVOLRTPRODLADLAAYTALKFYLQG--PPEPG 2774  
DB 2636 GRVKLLIAQAESAASKVKVSKNGRSGVRLRPRDLADLAAYTALKFHIQSPVPAPEP 2695  
QY 2775 QGTEDRFVMYMGSAQAGDYNGVSLRKKVHVYVOLGEAGPAVLISIDEDIGEOFAAVSLD 2834  
DB 2696 KNTGDHFVLYNGSAQAGDYNGVSLRKKVHVYVOLGEAGPAVLISIDEDIGEOFAAVSID 2755  
QY 2835 RTLOFGHMSVTVEMOIBQKGTDPVAPGAELNLNRPDDFVYVGGVPSFTTTPPLRFP 2894  
DB 2756 RTLOFGHMSVTVEMOIBQKGTDPVAPGAELNLNRPDDFVYVGGVPSFTTTPPEPLRFP 2815  
QY 2895 CYRGCIEMDTLNEEVSILNFERFOLDTAVDRPCARSKSTGDPWLTGDSYLDGTGARI 2954  
DB 2816 GYLGCIEMETLNEEVSILNFERFOLDTAVDRPCARSKATGDPWLTGDSYLDGSGFARI 2875  
QY 2955 SFDQSIITTKRPEBELRVSGVLFKQOSQFLCLAVQEGSLVLLYDFGAGLKKAVPL 3014  
DB 2876 SFEKQFNSTKFPDQELRVSYNGIIFELKQOSQFLCLAVQEGSLVLLYDFGAGLKKADPL 2935  
QY 3015 QPPPLTSASKAIQVFLGGSRKRVLRVERATVYVSEQNDLEADAYLGGVPPDQLP 3074  
DB 2936 QPPQALTAASKAIQVFLAGNKRKRVLRVERATVYVSDQNDLEADAYLGGVPPDQLP 2995  
QY 3075 PSLRWLFTGSGVSGVGIKALQKVDLKLNTTWSAGCTADLLVGRAMTFHGHFLR 3134  
DB 2996 LSLRLQFPSSGSGVSGVGIKALQKVDLKLNTTWSAGCTADLLVGRAMTFHGHFLP 3055  
QY 3135 LALSNAVPLTGNVSGVGFHSAQDSALLYRASPDGLQVSLQOGRVSLQLLRTEVKTQA 3194  
DB 3056 LALPDVAPITEVTVSGVGFRTQDNNLLYVTSFDPGPYQVSRHGVTLRFMNOEVETOR 3115  
QY 3195 GFADGAPHYAFYNATGWLYVDQLOOMKPHRGPPPELOQOPEGPRLLLGLPESGT 3254  
DB 3116 VFADGAPHYAFYNATGWLYVDQLOQVKSHERITPMLQLOPEPRLLLGLPVSQT 3175  
QY 3255 IYNSGCIISNVFVQVORLLGQVDFDLOQNLGVNVYSTGCAPALQATPOLGPRGQATARK 3314  
DB 3176 FHNFSGCCSNVFNQRLRPQVDFDLQNMGSVNVSVGCTPAQLIETS-----RATAQK 3228  
QY 3315 ASRRSQPARHPACMLPPLHRTTRDSYQFGGSLSHLEFVGILARHNPWLSMHVLPRL- 3373  
DB 3229 VSRRSRQPSQDLACTTPWLPGTIQDAYQFGGLPSPYQFVIGSPSHRNLHLSMLVRPHA 3288  
QY 3374 SSRGILLTARIPQSPSLALFLNNGHVAVQMEGLTRFLAQSRQSRPGRGHWKSVYRWE 3433  
DB 3289 ASQGLLLTAPMSGRSPSLVFLNNGHVAVQMEGLTRFLAQSRQSRGAGOWHVRVWVG 3348  
QY 3434 KNRILLVTDGARAWQEGFHRHQCAEHPQHTLTVFGGLPASHSSKLPVTVGFSGCVXR 3493  
DB 3349 MQQIQLVVDGSGQVWSQKALHHRVPAERPPQYTLVSGGLPASSYSSKLPVSVGFGCLKK 3408  
QY 3494 LRLHGRPLGAPTRMAGVTPCILGPLEAGLFPFGSGGVITLDLPGATLPDVGLELEVERPLA 3553  
DB 3409 LQLDKQPLRTETQMVGVPFCVSGPDLGLFPFGSEGVVTLPLPKAKMPYVSLELEMRPLA 3468  
QY 3554 VTGLLFHILGOARTPPYLOLQVTEKOVLLRADGAGEFSTSVTRPSVLCDGOWHRLAYMKS 3613  
DB 3469 AAGLIFHLQOALATPYMQLVKLTQEVLLQANDGAGEFSTWTYTK-LCDGWHRAVIMG 3527

QY 3614 GNVLEFYDAQSNHTVGPFLAAAGAPAPLYVLGGLPSPMAVQVPPPPAYCGCRRLAUNRS 3673  
DB 3528 RDTLRELVDTQSNHTTGRLPESLAGSPALLHGLSPKSTARPPELPAYRGCLRLKLLINGA 3587  
QY 3674 PVMTSRSEVHCAYCASCAPA 3694  
DB 3588 PNVVTASVQIOGAVGMRGCPSS 3608  
RESULT 8  
ABB81598  
ID ABB81598 standard; protein; 2743 AA.  
XX ABB81598;  
AC AC  
XX 19-SEP-2002 (first entry)  
XX Human laminin alpha 5 2743 N-terminal amino acid sequence SEQ ID NO:36.  
XX Laminin alpha 5; laminin 10; vulnary; cell growth; differentiation;  
XX tissue repair development; laminin; healing; vascular tissue;  
XX re-endothelialisation; vascular injury; cell attachment; cell stasis;  
XX proliferation; migration.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1..35  
FT Peptide /label= signal  
FT Protein 36..2743  
FT /label= laminin\_alpha\_5  
XX WO200250111-A2.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-US051035.  
XX 21-DEC-2000; 2000US-0257449P. ✓  
XX 28-MAR-2001; 2001US-0279282P.  
XX 13-NOV-2001; 2001US-00279282.  
XX (BIOS-) BIOSTRATUM INC.  
XX Tryggvason K, Doi M, Thyboll J;  
XX WPI; 2002-557650/59.  
XX N-PSDB; ABQ72930.  
XX New human laminin-10 proteins, useful for accelerating the healing of  
XX vascular tissue, improving the biocompatibility of grafts, or for  
XX promoting re-endothelialization at the site of vascular injuries.  
XX Disclosure; Page 223-231; 231pp; English.  
XX The present invention describes human laminin alpha 5. Also described is  
XX an isolated laminin 10. Laminin 10 has vulnary activity. Laminins are  
XX useful in maintaining cell/tissue phenotype as well as promoting cell  
XX growth and differentiation in tissue repair development. Specifically,  
XX laminin 10 can be used for accelerating the healing injuries of vascular  
XX tissue, improving the biocompatibility of grafts useful for treating such  
XX injuries, for promoting re-endothelialisation at the site of vascular  
XX injuries, and promote cell attachment and subsequent cell stasis.  
XX proliferation, differentiation, and/or migration. The present sequence  
XX represents the 2743 N-terminal amino acid sequence of human laminin alpha  
XX 5, which is used in the exemplification of the present invention  
XX Sequence 2743 AA;  
Query Match 75.2%; Score 15120; DB 5; Length 2743;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKRLCAGSALCVRGPRGAPALLVGLGALLGAABAREAGGSLHPYPENLAEGARIAA 60  
DB 1 MAKRLCAGSALCVRGPRGAPALLVGLGALLGAABAREAGGSLHPYPENLAEGARIAA 60  
QY 61 SATCEEAPAGSPRPTEDLYCKLVGGPVAGGDPNQTIRQYCDICTAANSNKAHPASNA 120  
DB 61 SATCEEAPAGSPRPTEDLYCKLVGGPVAGGDPNQTIRQYCDICTAANSNKAHPASNA 120  
QY 121 IDGTERWQSPPLSGLEYNVNTLDDLGQVHVAVYVLIKFANSPRDPLWVLEERSMDGFR 180  
DB 121 IDGTERWQSPPLSGLEYNVNTLDDLGQVHVAVYVLIKFANSPRDPLWVLEERSMDGFR 180  
QY 181 TYQWQFPASSKRCLOLERFPGQTLERITRDDAAICTTEYSRIVPLENGEIVWSLVNVRPG 240  
DB 181 TYQWQFPASSKRCLOLERFPGQTLERITRDDAAICTTEYSRIVPLENGEIVWSLVNVRPG 240  
QY 241 AMNYSYSLLEEFKATNVRLEFRTWTLHGLMGKALRDPVTTRYVYSIKDISIGSRC 300  
DB 241 AMNYSYSLLEEFKATNVRLEFRTWTLHGLMGKALRDPVTTRYVYSIKDISIGSRC 300  
QY 301 VCHGHADACDAKDPDTPFRLOCTCOHNTCGTCDRCPCGFNQKPWKPATANSANECQSCN 360  
DB 301 VCHGHADACDAKDPDTPFRLOCTCOHNTCGTCDRCPCGFNQKPWKPATANSANECQSCN 360  
QY 361 CVGHATCYVDEVDRRASOSLDTYGGGVCICDQHTTAGVNCERCLPGFVRSNHP 420  
DB 361 CVGHATCYVDEVDRRASOSLDTYGGGVCICDQHTTAGVNCERCLPGFVRSNHP 420  
QY 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSSSND 480  
DB 421 DSPHVCRRNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSSSND 480  
QY 481 TREQVLPAGQVNCDCSAAGTQGNACKDRVGRCLCKNFQTHCELCAFGYFGGCP 540  
DB 481 TREQVLPAGQVNCDCSAAGTQGNACKDRVGRCLCKNFQTHCELCAFGYFGGCP 540  
QY 541 CQCSSPGVADDRCDPTDQCRVRFEGATCDRCAPGYHFFPLCQLCGSPAGTLPEGCD 600  
DB 541 CQCSSPGVADDRCDPTDQCRVRFEGATCDRCAPGYHFFPLCQLCGSPAGTLPEGCD 600  
QY 601 EAGCLCOPEPAGHCDRCRPGVHGFNCOACTCDPRGALDOLCGAGGLCRCPGVTGTA 660  
DB 601 EAGCLCOPEPAGHCDRCRPGVHGFNCOACTCDPRGALDOLCGAGGLCRCPGVTGTA 660  
QY 661 CQECSPGFHGPSPVCHCSAAGSLHAACDPRSGQCSRCPRVTGLRCDTCVPGAYNFPYC 720  
DB 661 CQECSPGFHGPSPVCHCSAAGSLHAACDPRSGQCSRCPRVTGLRCDTCVPGAYNFPYC 720  
QY 721 EAGSCHPAGLAPVDPALPEAQVPCMAHVEGSPCDCKEFGWGLSPSNPEGCTRCSD 780  
DB 721 EAGSCHPAGLAPVDPALPEAQVPCMAHVEGSPCDCKEFGWGLSPSNPEGCTRCSD 780  
QY 781 RGLTGGVAECOPGTGCFKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDGALGQS 840  
DB 781 RGLTGGVAECOPGTGCFKPHVCGQACASCKDGFGLDQADYFGCRSCRCIDGALGQS 840  
QY 841 CEPRTGVCRCRPNTOGTGTCSEPARDHYLPDLHLRLELEBAATPEGHAVRFGFNPLEFEN 900  
DB 841 CEPRTGVCRCRPNTOGTGTCSEPARDHYLPDLHLRLELEBAATPEGHAVRFGFNPLEFEN 900  
QY 901 FSWRGYAQMAPVQPRIVARLNLTSPOLFVLIYFVNRGAMSVGRVSVREGRSAACANC 960  
DB 901 FSWRGYAQMAPVQPRIVARLNLTSPOLFVLIYFVNRGAMSVGRVSVREGRSAACANC 960  
QY 961 TAQSQPVAFPPSTEPAFITVPOKGFEPFVLPNGTVALRVEAGVLLDYVLLPSAYYEA 1020  
DB 961 TAQSQPVAFPPSTEPAFITVPOKGFEPFVLPNGTVALRVEAGVLLDYVLLPSAYYEA 1020  
QY 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQNSLPRPCTEQL 1080  
DB 1021 ALLQLRVTEACTYRPSAQSGDNCLLYTHPLDGFPSAAGLEALCRQNSLPRPCTEQL 1080  
QY 1081 SPSHPPLITCTGSDVDVQLQVAPQGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL 1140

DB 1081 SPSHPPLITCTGSDVDVQLQVAPQGRYALVVEYANEDARQEVGVAVHTPQRAPOQGLL 1140  
QY 1141 SLHPCLYSTLCRGRTARDTQDLAVFHLDSASVRLTAEQARFELHGVTLVPIEERSPFV 1200  
DB 1141 SLHPCLYSTLCRGRTARDTQDLAVFHLDSASVRLTAEQARFELHGVTLVPIEERSPFV 1200  
QY 1201 EPRVSCISSHAGAGPNSAACLPSPFPKPOPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260  
DB 1201 EPRVSCISSHAGAGPNSAACLPSPFPKPOPIILRDCQVILPPLPGLPLTHAQDLTPATSP 1260  
QY 1261 AGPRPRPTAVDPAEBPTLLREPAQTVVFTTHVPTLGRVAFLLHGYQPAHPTFPFVEVLIN 1320  
DB 1261 AGPRPRPTAVDPAEBPTLLREPAQTVVFTTHVPTLGRVAFLLHGYQPAHPTFPFVEVLIN 1320  
QY 1321 AGRVWQGHANASCPHGYGORTLVWCEQALLDVTHSELTVTVRVPBGRWLMDYVLP 1380  
DB 1321 AGRVWQGHANASCPHGYGORTLVWCEQALLDVTHSELTVTVRVPBGRWLMDYVLP 1380  
QY 1381 ENVYSFGLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGC 1440  
DB 1381 ENVYSFGLREEPLDKSYDFISHCAAQGYHISPSSSSLFCRNAASLSLFYNNGARPCGC 1440  
QY 1441 HEVGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFNCRPCDCGABLCDELTGQCIC 1500  
DB 1441 HEVGATGPTCEPFGGQPCCHAHVIGRDCSRCATGYWGFNCRPCDCGABLCDELTGQCIC 1500  
QY 1501 PPRTIPDCLLCQFQFGCHPLVGCCECNCSPGFIQELTDPCTDSDGCKCRPNVTGR 1560  
DB 1501 PPRTIPDCLLCQFQFGCHPLVGCCECNCSPGFIQELTDPCTDSDGCKCRPNVTGR 1560  
QY 1561 CDTCSGPHGYPRCRRCDCHAGTAPGVCDPLTGOCYCKENVGKPCQCSLGTSLDAA 1620  
DB 1561 CDTCSGPHGYPRCRRCDCHAGTAPGVCDPLTGOCYCKENVGKPCQCSLGTSLDAA 1620  
QY 1621 NPKGTRCFGATERCRSSSYTROBFVDMEGWLLSTDRQVPHEROFGTEMLRADLRH 1680  
DB 1621 NPKGTRCFGATERCRSSSYTROBFVDMEGWLLSTDRQVPHEROFGTEMLRADLRH 1680  
QY 1681 VPBAVPEAPPELYWAPPYSLGDRVSSYGGTLYELHSETQBGDVVPMESRPDVVLGN 1740  
DB 1681 VPBAVPEAPPELYWAPPYSLGDRVSSYGGTLYELHSETQBGDVVPMESRPDVVLGN 1740  
QY 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTVSRREELMMVLASLEQLQIRALFS 1800  
DB 1741 QMSITFLEPAYTPGHVHRGQLQVVEGNFRHTETRTVSRREELMMVLASLEQLQIRALFS 1800  
QY 1801 QISSAVSLRVALEVASPAGQALASNTVELCLCPASVYRSDSCOECAQFYRDKLFLGR 1860  
DB 1801 QISSAVSLRVALEVASPAGQALASNTVELCLCPASVYRSDSCOECAQFYRDKLFLGR 1860  
QY 1861 CVPCHGSHSDRLPGSGVCDVCOHNTGHAHCERCAQGFMSRSDPSPAPVSCPCLSV 1920  
DB 1861 CVPCHGSHSDRLPGSGVCDVCOHNTGHAHCERCAQGFMSRSDPSPAPVSCPCLSV 1920  
QY 1921 SNNFASGCVLRGORTQCLCKPGVAGASCERCAQGFNPLVIGSSCQPCDCSNGDPNLL 1980  
DB 1921 SNNFASGCVLRGORTQCLCKPGVAGASCERCAQGFNPLVIGSSCQPCDCSNGDPNLL 1980  
QY 1981 FSDCDPLTGACRGLRHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTACDPHSGHC 2040  
DB 1981 FSDCDPLTGACRGLRHTTGPCEICAPGFYGNALLPGNCTRCDCCTPCGTACDPHSGHC 2040  
QY 2041 LCKAGVTGRCDRCRCEGHFGNGCGRCPACGPAEGSECHPOSGOCHCRPGTWGPCCR 2100  
DB 2041 LCKAGVTGRCDRCRCEGHFGNGCGRCPACGPAEGSECHPOSGOCHCRPGTWGPCCR 2100  
QY 2101 ECAPGWGLPEQGCRCRCQPCGRCDPHTGRNCNPPGLSGERCDCSCQOQVVPFGPVGH 2160  
DB 2101 ECAPGWGLPEQGCRCRCQPCGRCDPHTGRNCNPPGLSGERCDCSCQOQVVPFGPVGH 2160  
QY 2161 SHCEVCDHCVVLLDLEAGALLPAIHEOLRGINASSMAWALHRLNASIADLQSLR 2220

Db	2161	SIHCEVCDHCVVLLDDLLERAGALLPAIHEQRLGINASSAWARLHRLNASIADLQSLR	2220
Qy	2221	SPLGPRHETAQOLEVLEEQQTSLSGDARRLGQAVGTRDQASQLLAGTEATLGHAKTLLA	2280
Db	2221	SPLGPRHETAQOLEVLEEQQTSLSGDARRLGQAVGTRDQASQLLAGTEATLGHAKTLLA	2280
Qy	2281	AIRAVDRTLSELMQTHGLGNASAPSGEOLLRTLAVERLLWEMARDLGAPOAAEA	2340
Db	2281	AIRAVDRTLSELMQTHGLGNASAPSGEOLLRTLAVERLLWEMARDLGAPOAAEA	2340
Qy	2341	ELAAQRLLARVQEQSLSSLEENQALATQTRDRLAQHEAGLMDLREALNRAVDATRAQE	2400
Db	2341	ELAAQRLLARVQEQSLSSLEENQALATQTRDRLAQHEAGLMDLREALNRAVDATRAQE	2400
Qy	2401	INSRQERLEALQKQELSDNATLQATLHAARDTLASVRLAHSDDQAKEELERLAAS	2460
Db	2401	INSRQERLEALQKQELSDNATLQATLHAARDTLASVRLAHSDDQAKEELERLAAS	2460
Qy	2461	LDGARTPLQRMQTFSPAGSKLRLVEAAEAHAQQLGQALNLSSIIILDVNDRLTORAIE	2520
Db	2461	LDGARTPLQRMQTFSPAGSKLRLVEAAEAHAQQLGQALNLSSIIILDVNDRLTORAIE	2520
Qy	2521	ASNAYSRIQVQAEDDAAGALQADHTWATVVRQGLVDRAQQLANSTALEEAMLOEQ	2580
Db	2521	ASNAYSRIQVQAEDDAAGALQADHTWATVVRQGLVDRAQQLANSTALEEAMLOEQ	2580
Qy	2581	QELGLVMAALQARTQLRDVRAKDKOLEAHQIAQAQMLAMTDTSKKIAHAKAVAAEAQ	2640
Db	2581	QELGLVMAALQARTQLRDVRAKDKOLEAHQIAQAQMLAMTDTSKKIAHAKAVAAEAQ	2640
Qy	2641	DTATRVQSLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSIL	2700
Db	2641	DTATRVQSLQAMQENVERWQGYEGLRGQDLGQAVLDAGHSVSTLEKTLPLLAKLSIL	2700
Qy	2701	ENRGVHNASLALSASIGRVRELIQAARGAASKVKVPMKFNRS	2743
Db	2701	ENRGVHNASLALSASIGRVRELIQAARGAASKVKVPMKFNRS	2743
OS	RESULT 9		
ID	ABB09504		
XX	ABB09504 standard; protein; 1640 AA.		
AC	ABB09504;		
DT	01-NOV-2002 (first entry)		
DE	Human laminin alpha-5-like NOV1d protein, SEQ ID NO:8.		
XX	Human; NOVX; neurological disorder; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; pain; behavioural disorder;		
KW	addiction; tuberculous sclerosis; cancer; immune disorder; allergy;		
KW	autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;		
KW	thyroiditis; cardiovascular disease; hypertension; reproductive disorder;		
KW	endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;		
KW	pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;		
KW	polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;		
KW	atherosclerosis; cell signal processing-related disorder;		
KW	metabolic pathway regulation disorder; cytostatic; neuroprotective;		
KW	antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;		
KW	dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;		
KW	differentiation; proliferation; motility; haematopoiesis; wound healing;		
KW	angiogenesis; forensic biology; transgenic animal; drug screening;		
KW	Gene therapy; NOV1d; laminin alpha-5-like; chromosome 20.		
OS	Homo sapiens.		
XX	WO200253742-A2.		
PN	11-JUL-2002.		
PD	07-JAN-2002; 2002WO-US0000375.		
XX			

PR	05-JAN-2001;	2001US-0260018P.	
PR	08-JAN-2001;	2001US-0260360P.	
PR	28-FEB-2001;	2001US-0272411P.	
PR	02-MAR-2001;	2001US-0272817P.	
PR	05-JUL-2001;	2001US-0303231P.	
PR	12-JUL-2001;	2001US-0305060P.	
PR	10-SEP-2001;	2001US-0318405P.	
PR	12-SEP-2001;	2001US-0318700P.	
XX	04-JAN-2002;	2002US-00037417.	
PA	(CURA-) CURASEN CORP.		
XX	Kekuda R, Alsbrook JP, Tchernev VT, Liu X, Spytek KA;		
PI	Pattarajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;		
PI	Gorman L, Edinger S, Sciore P, Ellerman K, Malyanar U;		
PI	Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;		
PI	Padigaru M, Taupier RJ, Miller CE, Eisen A;		
XX	WPI; 2002-593619/62.		
DR	N-PSDB; ABQ93882.		
XX	Novel polypeptides and nucleic acids homologous to transmembrane		
PT	receptor, thymosin, neuromodulin-like family of proteins for diagnosing,		
PT	treating cancer, atherosclerosis, neurological, skin and autoimmune		
PT	disorders.		
XX	Claim 1c; Page 23; 323pp; English.		
PS	The invention relates to 24 novel human proteins designated NOV1-NOV14		
CC	(ABB09501-ABB09524), collectively referred to as NOVX proteins, and		
CC	nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and		
CC	nucleotides are useful in the treatment, diagnosis or prevention of NOVX-		
CC	associated disorders or in the manufacture of a medicament for treating		
CC	such disorders, with specific applications described for each of the 24		
CC	NOVX proteins, based on their homology to known proteins. Various		
CC	disorders are associated with NOVX proteins including neurological		
CC	disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),		
CC	pain, behavioural disorders, addition, tuberculous sclerosis, cancers		
CC	(e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders		
CC	various forms of arthritis, diabetes, thyroiditis, cardiovascular disease		
CC	(e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,		
CC	(e.g., hypertension), reproductive disorders, endometriosis,		
CC	cirrhosis, glomerular endotheliosis, scleroderma, alopecia, ulcers, pancreatitis,		
CC	disorders, obesity, bacterial infections, polycystic kidney disease, endocrine		
CC	atherosclerosis, cell signal processing-related disorders and disorders		
CC	of metabolic pathway regulation. NOVX nucleic acids and polypeptides may		
CC	be used to identify cellular receptors or downstream effectors which		
CC	binds to a NOVX protein, and are also useful as targets for the		
CC	identification of small molecules that modulate or inhibit processes such		
CC	as neurogenesis, cell differentiation, cell motility, cellular		
CC	proliferation, haematopoiesis, wound healing and angiogenesis. NOVX		
CC	nucleic acid sequences can be used to identify a cell or tissue type and		
CC	are useful as a source of primers or probes for forensic biology and for		
CC	identifying and cloning NOVX homologues in other cell types. Cells		
CC	comprising NOVX nucleic acids are useful for producing non-human		
CC	transgenic animals which are useful for studying the function and of NOVX		
CC	activity. The present sequence represents the laminin alpha-5-like		
CC	protein NOV1d. The gene encoding NOV1d is located on chromosome 20		
XX	Sequence 1640 AA;		
Qy	Query Match		
Db	Best Local Similarity 42.2%; Score 8499.5; DB 5; Length 1640;		
XX	Matches 1640; Conservative 99.7%; Pred. No. 0;		
XX	Mismatches 0; Indels 5; Gaps 1;		
Qy	2051	CDRCQEGHFGNCGGCRFCACGPAAGSGECPQSGCHCRPCTMGPCQECAPGYWGLP	2110
Db	1	CDRCQEGHFGNCGGCRFCACGPAAGSGECPQSGCHCRPCTMGPCQECAPGYWGLP	60
Qy	2111	EQGCRQCQCPGGRCDPHTGRCNCPGLSGRCDTCSQHQHVPVPGGVGHSIHCEVCDHC	2170
Db	61	EQGCRQCQCPGGRCDPHTGRCNCPGLSGRCDTCSQHQHVPVPGGVGHSIHCEVCDHC	120

QY 2171 VVLLDDLERAGALLPAHEQLRGINASSMAWARLHRLNASTADIQSOLRSLPLGRHETA 2230  
Db 121 VVLLDDLERAGALLPAHEQLRGINASSMAWARLHRLNASTADIQSOLRSLPLGRHETA 180  
QY 2231 QQLVLEBOOSTSLGQDARRLGGCAVGTDRDQASOLLAGTEATLGHAKTLLAIRAIVDRTLS 2290  
Db 181 QQLVLEBOOSTSLGQDARRLGGCAVGTDRDQASOLLAGTEATLGHAKTLLAIRAIVDRTLS 240  
QY 2291 ELMSOTGHILGANASAPSGEQLRLTAEVERLLWEMRARDIGAPOAAAEALAAQRLLA 2350  
Db 241 ELMSOTGHILGANASAPSGEQLRLTAEVERLLWEMRARDIGAPOAAAEALAAQRLLA 300  
QY 2351 RYQEOQLSSLWENQALATQDRDLACHEAGLMDLREALNRAVDATREAOELNSNRQERLE 2410  
Db 301 RYQEOQLSSLWENQALATQDRDLACHEAGLMDLREALNRAVDATREAOELNSNRQERLE 360  
QY 2411 EALORQELSRNATLQATLHAARTLASVFRLLHSLOAKEELERLAASLDGARTPLQ 2470  
Db 361 EALORQELSRNATLQATLHAARTLASVFRLLHSLOAKEELERLAASLDGARTPLQ 420  
QY 2471 RMOTFSPAGSKLRLVERABAHACQLGQLALNLSIIIDVNDRLTORAIBASNAYSRILQ 2530  
Db 421 RMOTFSPAGSKLRLVERABAHACQLGQLALNLSIIIDVNDRLTORAIBASNAYSRILQ 480  
QY 2531 AVQAAEDAAQALQOQADHTWATVVRQGLVDRACQLLANSTALEEAMLOEQQLGLVMAAL 2590  
Db 481 AVQAAEDAAQALQOQADHTWATVVRQGLVDRACQLLANSTALEEAMLOEQQLGLVMAAL 540  
QY 2591 QGARTQLDRVRAKQOQLEAHIQAAQAMLANDTETSKEIAHAKAVAAEAQDTRATVQSOL 2650  
Db 541 QGARTQLDRVRAKQOQLEAHIQAAQAMLANDTETSKEIAHAKAVAAEAQDTRATVQSOL 600  
QY 2651 QAMQENVRWQGYEGRLGQDQAVLDAGHSVSTLEKTLPOLLAKLSILENRGVHNASL 2710  
Db 601 QAMQENVRWQGYEGRLGQDQAVLDAGHSVSTLEKTLPOLLAKLSILENRGVHNASL 660  
QY 2711 ALSASTGRVRELLAQARGAASKVKVPKFNKSGVQLRTPRDLADLAAYTALKFYLGQPE 2770  
Db 661 ALSASTGRVRELLAQARGAASKVKVPKFNKSGVQLRTPRDLADLAAYTALKFYLGQPE 720  
QY 2771 PEPGQGTEDRFVYMGSQATGDYMGVSLRDKKXHVYQLGEAGPAVLSIDEDIGEQPAA 2830  
Db 721 PEPGQGTEDRFVYMGSQATGDYMGVSLRDKKXHVYQLGEAGPAVLSIDEDIGEQPAA 780  
QY 2831 VSLDRTLQFGHMSVTVVERQMIQETKGTDTVAPRAEGLNLNRPDFFVYGVGYSTTTPPL 2890  
Db 781 VSLDRTLQFGHMSVTVVERQMIQETKGTDTVAPRAEGLNLNRPDFFVYGVGYSTTTPPL 840  
QY 2891 LRFPFGYRGCIEMDTLNEEVVSLNFRFTFQDTPADRPCARSKSTGDPMLTDCSYLDGTG 2950  
Db 841 LRFPFGYRGCIEMDTLNEEVVSLNFRFTFQDTPADRPCARSKSTGDPMLTDCSYLDGTG 900  
QY 2951 FARISFDSQISTTKRFEQELRLVYSGVLFLLKQSQQLAVQEGSLVLLYDFGAGLKK 3010  
Db 901 FARISFDSQISTTKRFEQELRLVYSGVLFLLKQSQQLAVQEGSLVLLYDFGAGLKK 960  
QY 3011 AVPLQPPPLTSAKAIQVFLGGSKRVLVRVERATVYSVQNDNLEADAYILGGVPP 3070  
Db 961 AVPLQPPPLTSAKAIQVFLGGSKRVLVRVERATVYSVQNDNLEADAYILGGVPP 1020  
QY 3071 DQLPPSLRWLPPTGGSVRGCVKGIKALGVKVDLKRNLTTGVSAGCAADLLVGRAMTFHGH 3130  
Db 1021 DQLPPSLRWLPPTGGSVRGCVKGIKALGVKVDLKRNLTTGVSAGCAADLLVGRAMTFHGH 1080  
QY 3131 GFRLRLASNAPLNTGNTVSGFGHSAQDSALLYYRASPDGLCOVSLQCGVSLQLLRTEV 3190  
Db 1081 GFRLRLASNAPLNTGNTVSGFGHSAQDSALLYYRASPDGLCOVSLQCGVSLQLLRTEV 1140  
QY 3191 KTOAGFADGAPHYVAFYSNATGVWLYYDDQLQWKPHRGPPPELOQPGPPPLILGGPL 3250  
Db 1141 KTOAGFADGAPHYVAFYSNATGVWLYYDDQLQWKPHRGPPPELOQPGPPPLILGGPL 1200

QY 3251 ESTTIYNFGSCISNVFVQRLQFORVFDLQQLNGSVNVSTGCAPALQAOPTGLGPRGLOA 3310  
Db 1201 ESTTIYNFGSCISNVFVQRLQFORVFDLQQLNGSVNVSTGCAPALQAOPTGLGPRGLOA 1260  
QY 3311 TARKASRRSQPARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVGLIARHNWPSLSMHV 3370  
Db 1261 TARKASRRSQPARHPACMLPPLHRTTRDSYQFGGSLSSHLEFVGLIARHNWPSLSMHV 1320  
QY 3371 LPSSRGLLLFTARLRPSPSIALFLSNHGFVAQMEGLGTRLRQAQRORSRPGRWHKVS 3430  
Db 1321 LPSSRGLLLFTARLRPSPSIALFLSNHGFVAQMEGLGTRLRQAQRORSRPGRWHKVS 1380  
QY 3431 RWEKNRILAVTDCARAWSOEGPHRQGAEPHPOPHTLFVGGLPASSHSSKLPVTVGFSGC 3490  
Db 1381 RWEKNRILAVTDCARAWSOEGPHRQGAEPHPOPHTLFVGGLPASSHSSKLPVTVGFSGC 1440  
QY 3491 VKRLRHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 3550  
Db 1441 VKRLRHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVR 1500  
QY 3551 PLAVTGLIFHLGQARTPPYLQAOVTEKQVLLRADDGAGFSTSVTRPSVLCDCQWHRLAV 3610  
Db 1501 PLAVTGLIFHLGQARTPPYLQAOVTEKQVLLRADDGAGFSTSVTRPSVLCDCQWHRLAV 1555  
QY 3611 MKSGNVLRLEVDQAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQPPWPAYCGCMRRLLAV 3670  
Db 1556 MKSGNVLRLEVDQAQSNHTVGPLLAAAGAPAPLYLGLPEPMAVQPPWPAYCGCMRRLLAV 1615  
QY 3671 NRSPVAMTRSVFVHGVAGSGCPAA 3695  
Db 1616 NRSPVAMTRSVFVHGVAGSGCPAA 1640

## RESULT 10

AAM33009  
ID AAM39009 standard; protein; 1601 AA.

XX AAM39009;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2154.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
XX Wang J, Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang J, Zhao QA;  
XX Zhou P, Goodrich R, Drmanac R;

XX WPI: 2001-442253/47.  
DR N-PGDB; AA158165.  
XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2154; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AM38642-AM42213) with neotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
XX Sequence 1601 AA;  
XX  
XX Query Match 41.0%; Score 8255; DB 4; Length 1601;  
XX Best Local Similarity 100.0%; Pred. NO. 0;  
XX Matches 1601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2095 MGPOCECAGYMGAEQCCRCRCOCPCGRCDCPHTGRCNCPGLGRCDCSCQOQVVPV 2154  
DB 1 MGPOCECAGYMGAEQCCRCRCOCPCGRCDCPHTGRCNCPGLGRCDCSCQOQVVPV 60  
QY 2155 GGPVGHSHICEVCHDCVLLDDLEAGALLPAIHEQLRGINASSMWARHLNASIAD 2214  
DB 61 GGPVGHSHICEVCHDCVLLDDLEAGALLPAIHEQLRGINASSMWARHLNASIAD 120  
QY 2215 LQSLRSPGPRHETACQLEVEEQSTSLGQDARRLGQAVGTROASQALLAGTATLGH 2274  
DB 121 LQSLRSPGPRHETACQLEVEEQSTSLGQDARRLGQAVGTROASQALLAGTATLGH 180  
QY 2275 AKTLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQQLRTLAVERLLWENRARDLGAP 2334  
DB 181 AKTLAAIRAVDRTLSELMSQTHGLGLANASAPSGEQQLRTLAVERLLWENRARDLGAP 240  
QY 2335 QAAAEAEALAAQRLARVQEQSLWEENQALATQTRDLRAHEAGLMDLREALNRAVDA 2394  
DB 241 QAAAEAEALAAQRLARVQEQSLWEENQALATQTRDLRAHEAGLMDLREALNRAVDA 300  
QY 2395 TREAQELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEL 2454  
DB 301 TREAQELNSRNOERLEALQKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKEL 360  
QY 2455 ERLAASLDGARTPLORMOTFSPAGSKIRLVEAAEAHAQOLGOLANLSSIILDVNQRL 2514  
DB 361 ERLAASLDGARTPLORMOTFSPAGSKIRLVEAAEAHAQOLGOLANLSSIILDVNQRL 420  
QY 2515 TORAEASNAYSRILQAVQAEADAGCALQADHTWATVVRQGLVDRAQOALLANSTALEE 2574  
DB 421 TORAEASNAYSRILQAVQAEADAGCALQADHTWATVVRQGLVDRAQOALLANSTALEE 480  
QY 2575 AMLQEQORLGLVWAAQLQAGARTLQDRVAKKQDLERHQAQAAMLAMDTTETSKIAHAKA 2634  
DB 481 AMLQEQORLGLVWAAQLQAGARTLQDRVAKKQDLERHQAQAAMLAMDTTETSKIAHAKA 540  
QY 2635 VAAEQDTRVQSQIQAMQENVERVQYEGELRGODLQOAVLDAGHSVSTLEKTLPLL 2694  
DB 541 VAAEQDTRVQSQIQAMQENVERVQYEGELRGODLQOAVLDAGHSVSTLEKTLPLL 600  
QY 2695 AKLSILENRGVHNASIALSASIGRVRELIAQARGAASKVKVPMKFNRSRGVQLTRPDIA 2754

DB 601 AKLSILENRGVHNASIALSASIGRVRELIAQARGAASKVKVPMKFNRSRGVQLTRPDIA 660  
QY 2755 DLAAATALKFYLOQPEPEQCGTDEDFVMYMGSRQATGDMYGSRLDKKVVHMYQLGEAG 2814  
DB 661 DLAAATALKFYLOQPEPEQCGTDEDFVMYMGSRQATGDMYGSRLDKKVVHMYQLGEAG 720  
QY 2815 PAVLSIDEDIGEOFAAVSLDRTLOFGHMSVTVVEROMIOETKGTDTAPGABGLANLRPDDF 2874  
DB 721 PAVLSIDEDIGEOFAAVSLDRTLOFGHMSVTVVEROMIOETKGTDTAPGABGLANLRPDDF 780  
QY 2875 VFYVGGYPSFTFTPPPLLRFPFGYGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKS 2934  
DB 781 VFYVGGYPSFTFTPPPLLRFPFGYGCIEMDTLNEEVVSLYNFERTFQDITAVDRPCARSKS 840  
QY 2935 TGDPLWTDGSLYLOQGTGPARISFDSQISTTKRFEQELRLSVSGVLPFLKQOOSFCLCLAVQ 2994  
DB 841 TGDPLWTDGSLYLOQGTGPARISFDSQISTTKRFEQELRLSVSGVLPFLKQOOSFCLCLAVQ 900  
QY 2995 EGSILVLLYDFGAGIKKAVIQQPPPLTSASKAIVFLLGGSRKRLVVRERATVYSVEQD 3054  
DB 901 EGSILVLLYDFGAGIKKAVIQQPPPLTSASKAIVFLLGGSRKRLVVRERATVYSVEQD 960  
QY 3055 NDLELADAYILGGVPPDQLPPLSRWLFPPTGGSVRGCVKGIKALGKYVDLKRLLNTTGVASG 3114  
DB 961 NDLELADAYILGGVPPDQLPPLSRWLFPPTGGSVRGCVKGIKALGKYVDLKRLLNTTGVASG 1020  
QY 3115 CTADLLVGRAMTHGCHGFLRLALSNVAPLTGNVYSGFPHSAODSALLYRAAPDGLCQV 3174  
DB 1021 CTADLLVGRAMTHGCHGFLRLALSNVAPLTGNVYSGFPHSAODSALLYRAAPDGLCQV 1080  
QY 3175 SLQGRVSLQLLRTTEVTKQAGFADGAPHYVAFYSNATGWMLYVDDQLQOKMHRGPPPEL 3234  
DB 1081 SLQGRVSLQLLRTTEVTKQAGFADGAPHYVAFYSNATGWMLYVDDQLQOKMHRGPPPEL 1140  
QY 3235 QPOEGEPRLILGLPESGTYINFGCISNVFORLLGQORVFDLQONLGSVNVSTGAP 3294  
DB 1141 QPOEGEPRLILGLPESGTYINFGCISNVFORLLGQORVFDLQONLGSVNVSTGAP 1200  
QY 3295 ALQAOQTPGLGPEGLQATARKASRRSQARHPACMLPPLHRTTRDSYQFGSLSHLEFV 3354  
DB 1201 ALQAOQTPGLGPEGLQATARKASRRSQARHPACMLPPLHRTTRDSYQFGSLSHLEFV 1260  
QY 3355 GILARHNRWPSLSNHTLPRSRGILLFTARLRPGSPSLALFLNSGHFVAQWEGIGTLRLA 3414  
DB 1261 GILARHNRWPSLSNHTLPRSRGILLFTARLRPGSPSLALFLNSGHFVAQWEGIGTLRLA 1320  
QY 3415 QSRORSRPRGHWKVSVEWEKRIILLVTDGARAWSQEGPHRQHQGAEPHQPHTLFFVGLPA 3474  
DB 1321 QSRORSRPRGHWKVSVEWEKRIILLVTDGARAWSQEGPHRQHQGAEPHQPHTLFFVGLPA 1380  
QY 3475 SSHSKLPVTVVFGSGCVKRLRHGRPLGAPTRVAGVTTCILGPLEAGLFFPGSGGVITLD 3534  
DB 1381 SSHSKLPVTVVFGSGCVKRLRHGRPLGAPTRVAGVTTCILGPLEAGLFFPGSGGVITLD 1440  
QY 3535 LPGAATLDPVGLLEVRPLAVTGLIFHLGOARTPPYLOQVTEKQVLLRADDGAGEFSTSV 3594  
DB 1441 LPGAATLDPVGLLEVRPLAVTGLIFHLGOARTPPYLOQVTEKQVLLRADDGAGEFSTSV 1500  
QY 3595 TRPSVLCDCGWHRILAVNMKSGNVLEVDASQNTHTVGPLAAAAAGAPAPLYLGLPEPMVAV 3654  
DB 1501 TRPSVLCDCGWHRILAVNMKSGNVLEVDASQNTHTVGPLAAAAAGAPAPLYLGLPEPMVAV 1560  
QY 3655 QPWPAYCGCRRRLAVNRSVPVMTSRVSVVEHGVAGASCAPAA 3695  
DB 1561 QPWPAYCGCRRRLAVNRSVPVMTSRVSVVEHGVAGASCAPAA 1601

RESULT 11  
ADE08094  
ID ADE08094 standard; protein; 3332 AA.  
XX  
AC ADE08094;  
XX



DT	29-JAN-2004	(first entry)
DE	XX	Novel protein (useful for identifying genetic disorders) #249.
DE	XX	novel gene; novel protein; tissue marker; molecular weight marker;
XX	XX	chromosome marker; genetic disorder.
XX	XX	Unidentified.
OS	WO2003054152-A2.	
XX	XX	03-JUL-2003.
XX	XX	10-DEC-2002; 2002WO-US039555.
XX	XX	10-DEC-2001; 2001US-0339739P.
PR	11-DEC-2001; 2001US-0339453P.	
PR	14-MAR-2002; 2002US-0365091P.	
PR	14-MAR-2002; 2002US-0365384P.	
PR	12-APR-2002; 2002US-0372381P.	
PR	12-APR-2002; 2002US-0372615P.	
PR	22-APR-2002; 2002US-00128558.	
PR	24-APR-2002; 2002US-0376045P.	
XX	XX	(HYSE-) HYSEQ INC.
XX	XX	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI	PI	Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Drmanac RT, Wang Z;
PI	PI	Ma Y, Wang D, Chen R, Xu C, Boyle SJ;
XX	XX	WPI; 2003-569235/53.
DR	XX	N-PSDB; ADE07183.
DR	XX	New polynucleotides, useful for expressing recombinant proteins for
PT	PT	analysis, characterization or therapeutic use, or as markers for tissues
PT	PT	in which the corresponding protein is preferentially expressed.
XX	XX	Claim 20; SEQ ID NO 1160; 1177pp; English.
XX	XX	The invention comprises the amino acid and coding sequences of novel
XX	XX	proteins. The DNA and protein sequences of the invention are useful as:
CC	CC	markers for tissues in which the corresponding protein is preferentially
CC	CC	expressed; as molecular weight markers on gels; as chromosome markers or
CC	CC	tags; to identify chromosomes or to map related gene positions; and to
CC	CC	compare with endogenous DNA sequences in patients to identify potential
CC	CC	genetic disorders. The present amino acid sequence represents a protein
CC	CC	of the invention.
XX	XX	Sequence 3332 AA;
XX	XX	Query Match 34.4%; Score 6916; DB 7; Length 3332;
XX	XX	Best Local Similarity 39.3%; Pred. NO. 0;
XX	XX	Matches 1478; Conservative 541; Mismatches 1225; Indels 514; Gaps 68
Qy	16	PRG-----PAPILLVGLALLGA--ARAREE-AGGGSIRPPYFNLAEGARIAASATC 64
Db	7	PRGRALGPLVPTPTLLLVLRPACGATARDPGAAAGLSLHPTPTNLAEARIMATATC 66
Qy	65	GEAAPARGSPRTEDLYCKLVGGPVAGDPMOTIRGOVCDICTAANSNRHAPASNAIDGT 124
Db	67	GERGPEGEPQP--ELYCKLVGGPTAPGS--GHTTQGFCDYCNSDPRKAHPTTALDGS 123
Qy	125	ERWQSPPLSRGLEYNVNTLDLQGFHVAYVLIKFANGSPRDLWLWERSMDFGRTQIP 184
Db	124	ERWQSPPLSSGTQYNRVNLTLDLQGFHVAYVLIKFANGSPRDLWLWERSVDFGSTYSP 183
Qy	185	WQFASKEDCLERGPQTLERITDDAAICTTYSRIVPLENGEIVWSLVNRPQAMNF 244
Db	184	WQYFAHSKYDCLKFEGREANMAVTRDDVLVCTYSRIVPLENGEIVWSLVNRPQAKNF 243
Qy	245	SVSPLLREFTKATNVRLRLRNTNLLHMGKALREDPTVTRYYYSIKOISIGRCVCHG 304
Db	244	TSEHTLPETKATNIPRLRNTNLLHISKAORDPTVTRYYYSIKOISIGQCVCHG 303

QY 1379 VPENYVFGYREEPLDKSYDFISHCAAGYHISPSGSLFCRNASLSIFYNNGARPC 1438  
Db 1206 VPAENYDYLKHKSGMKSLEFITHCGKNSFYLDQTAARFCNARSALVAFYHKGALPC 1265  
QY 1439 GCHVEGATGFTCEPFGGQCPCHAHVGRDCSCATGYMGFPNCRPCDGCARLCEBLTQC 1498  
Db 1266 ECHPTGATGPHCSPEGQCPQPNVIGROCTRCATGHYGFPRCKFCSCGRRLCEBMTQC 1325  
QY 1499 ICPRTIPDCLLQCPQTEGCHPLVGCBCNCSGPGIOELTDPTCDTDSGQCKCPNVTG 1558  
Db 1326 RCPRTVRVQCEVETHSFSFHPMAGCECNSRGTTEAMPEDCRDSGQCRKFRITG 1385  
QY 1559 RRCDCSPGFHYGRPCDCHCEAGTAPGVCDPLTGQCYCKENVGPKDCQCSLGTFSLD 1618  
Db 1386 RQDRCASGFYRPECPVPCNCRDGTGPGVCDGTGACLCKENVGTECNVCREGPHLD 1445  
QY 1619 ANPXCCTCFGATERCSSSYTQEFVDMEGWLLSTDROVPHERQPCTEMLRADL 1678  
Db 1446 PANLKCTSCFCFGVNNQCHSHKRTKFDMLGMLHLETDADRVDPVSPNPGSNWADL 1505  
QY 1679 RHVPEAVPEAFPELYWQAPPSYLGDRVSSYGGTLRYELHSETQRGDFVFPMBESRDPVVLQ 1738  
Db 1506 QELPATIHGA---SWAFTSYLGDVSSYGGVITYQAKSFGLPDM-VLLEKKPDVOLT 1560  
QY 1739 GNMSTIFLEPAPVPTCHVHRGOLQLVEGNFRHTETRTNTVSRBELMVLASLEQIIRAL 1798  
Db 1561 GQMSIYIETNTPRDLRHGVRHYVEGNFRHASSRAPVSREELMTVLSRLADVRIQGL 1620  
QY 1799 FSQISSAVSLRRVALVAPAGGALASNVLCPLCPASVYRGSOCBAPGFYRDKGLFL 1858  
Db 1621 YFTETQRLTILSEVLEASDTSGRALAVEICACPPAVAGSDCCGCSFGYRDKGLYT 1680  
QY 1859 GRCVPCOCHGHSRCLPGSGVVDVCOHNTGAHCERCOAGFMSRDDPAPCVSCBPLS 1918  
Db 1681 GRCVPCNCHSNQCDGSGICVNCOHNTAGHCERCQEGYGNVHGS--CRACFCP-- 1736  
QY 1919 VPSNNAEGCVLGGRTQCLCKPGYAGASCERCAPGFCGNPLVLGSSCOPCSCNGNDN 1978  
Db 1737 -HTNSFATGCVNMGDVRSCKAGYGTQCCARCAPGFQNFQKFGSCCPCSCNSNGQ-- 1793  
QY 1979 LLFSDCDPLTGACRGCLRHHTGTPRCBICAPGFYGNALLPNCNTRCDCTPCGTEACDPHSG 2038  
Db 1794 --LGSCPLTGDGIN----- 1806  
QY 2039 HCLCKAGVTRCRRCDQEGHGFNGCGGCRPCACGPAAGSECHPGSGCHCRPGTMGPQ 2098  
Db 1807 -----PKDSSPAEB----- 1817  
QY 2099 CRECAPYWLGLPGQCRRCQCPGCRCDPHTGRNCPPGLSGERCDTCSQHQVVPVGGPV 2158  
Db 1818 ----- 1817  
QY 2159 GHSIHCEVCHCVULLDDLERAGALLPAIHEOLRGINASSMAWARHLNLSIADLQSO 2218  
Db 1818 -----CDDCSCVMTLLNDATWGEOLRLVKSQGLSASAGLLEGRHMETQAKDLRQ 1872  
QY 2219 LRSPGLPRHETAOLEVLEQQSTSLGODARRLGQAVGTRDQASQ-LAGTEATLGHAKTL 2278  
Db 1873 LLNYSRASNHGSKIEGLEBELDLNQEFTELQEKAVNSRKAQTLNNVNRATQSAKEL 1932  
QY 2279 LAAIRAVDRTLSEMSQ-TGHLGLANASAPSGEQLLRTLAEBERLLWEHWARDLGPQAA 2337  
Db 1933 DVKIKNVRNVHILLKQISGTDEGN-NVPSGD-FGREWAEAQRMRELRNFRNGKHLRE 1990  
QY 2338 AEELAAQORLLARVQQLSSLEENQALATQTRDLACHAEGMLDLREALNRAVDATRE 2397  
Db 1991 AEAQRESQULLNRTWQKHOGENGLANSRDSINEYAKLSDLRLAQEAAAQAKQ 2050  
QY 2398 AQELNSNQRLEBEALQRK-QEILSRDNATLQATLHAARDTLASVFKLLSLDQAKBELR 2456  
Db 2051 ANGLNQEN-ERALGAIQROVKEINSLOSDFTKYLTADSSLLQTNIALQLMKESQKEYEK 2109  
QY 2457 LAASLDGARTPLQRMQTPFPAGSKLRLVEAAEAHAQQLQALNLSIILVDNQRLTQ 2516

Db 2110 LAASLEARQELSDKRVRELSRSAGKTSLEBEEAKHARSLOELAKQLEEKRNAGSDBLVR 2169  
QY 2517 RATEASNAVSRILQAVQAAEDAAQALQOQADHTWATVVRQGLVDRQAQQLIANS-TALEEA 2575  
Db 2170 CAVDAATAYENILNAIKAEADAANRAASASESALQIVIKEDLPKAKTLSSNDKLLNEA 2229  
QY 2576 MLOEQOQRLGVMAALQOARTQLDRVAKQDLBAHQAAQ-AMLANDTDETSKIAHAKA 2634  
Db 2230 KMTQKLLQKQESPALNNLOQTINIVTVQKEVIDTNLTTRDGLHGIQORGIDAMISAKS 2289  
QY 2635 VABEAQOTATRVQSQQAQOENVERWQOYEGURGGDLGOAVLDAGHSVTELEKTLPOL 2694  
Db 2290 MVRKANDITDEVLDGLNPIQTDVERIKDTYGRQNEDEFKALTADNSVNKLTKLPDLW 2349  
QY 2695 AKLSILENRGRVHNASLA-----LSASIGRVELIAQARGAASKVKVPMKFNKRGSRVQLRTP 2750  
Db 2350 RKIESI-----NQQLPLGNI SDNMDRIELIQAARDAASKVAVPMRFRNGKSGVEVRLP 2403  
QY 2751 RDLADLAATALKFYLOGPEPECGQGTEDRFVVMGSRQATGYVMGVSRLDKKXHWYQL 2810  
Db 2404 NLEEDLKGYTSLSLFLQRPNSRENGGFENFVWYLGKNDASRDYIGNAVVDGQLTVCYNL 2463  
QY 2811 GEAGPAVLSIDEDIGEO-----FAAVSLDRITLQFGHMSVTVRQMTQ-ETKG--DRVAP 2861  
Db 2464 GDR-EAELQVDQILTKSETKEAVMDRVKFORIYQFARLNTKGTATSSKPTPGVYMDGR 2522  
QY 2862 GAEGLMLRDDDFFVYGGYPSFTPPPLLRFPYRCGCIEMDTLNEERWSLYNFERFQL 2921  
Db 2523 NSNTLLNLDPENVVYVGGYPPDFKLPRLSFPPYKGCIEDDDNENVLNLYNFKTFLNL 2582  
QY 2922 DTAVDPRCASKSGTDPWLTDGSLDGTGPARISFDSQISTTKRFEQELRLVSYGVLFF 2981  
Db 2583 NTEVECCRKEE-----SDKNYFECTGYARVTPQPH-APIPTFGQTIQTVDRLGLFF 2636  
QY 2982 LKQSQFLCLAVQSGSLVLYDFGAGLKK-----AVLPQPPPLTSASXAIQVFLGGS 3035  
Db 2637 AENGDRFTSLNIEDGLMVRKYNSELKPERGVGDALN-----NGRDSHIQI-KIGKL 2688  
QY 3036 RKRVLVVRATVYVSCDNDLELADAYLGGVPPDQLPPLSLRMLFF-TGGSVRGCVKGI 3094  
Db 2699 QKRWINVD---VONTIIDGEVDFSTYLLGI-----PIAIRERFNISIPAFRCMKNL 2740  
QY 3095 KALGKYVDLKEIN-TTGVSAQCTADLLVGRAMTPHGHFLRLALSNVA-PLTGNVYSGFG 3152  
Db 2741 K---KTSQVRLNDTVGVTKKCEDWKLVRASASFRGG--QLSFTDLGLPPTDLQASFG 2795  
QY 3153 PHSQDSNALLYRASPDGLQVSLQCGRVSLQLLRTB---VKTQAGFADGAPHYVAVYSN 3209  
Db 2796 FQTFQSGILLDHQHTWTRNLQVTLLEDGTYIELSTSDSGGPIFKSPQTYMDGLLHVSVISD 2855  
QY 3210 ATGVMLYVDDOLQOMKPHRGPPPELOPQEPGPPRLLLGGLPESGTIYNFGCISNVFQR 3269  
Db 2856 NSGLRLDIDQLLNS-----KRLKHISRSQSLRGG-----SNFEGCISNVFQR 2902  
QY 3270 LLGQRFVFDLQONLGSNNVST-GCA-----PALQATQCLG 3304  
Db 2903 LSLSPFVLDLTSNLSKSDVSLGSGSLNKPFLMLLKSTFRNKTTPRINQLLOQDTPVS 2962  
QY 3305 PRGLQATARKASRSRQPARHPACWLPPLRLTRTDSYQFGSSLSHLEF--VGILARHN 3362  
Db 2963 PRSVKVV-----QDACSPLPKQANHGALQFGDIPTSHLLFKLPQELLKPS 3009  
QY 3363 WPSLSMVLVPRSSGLLLFTARLRPGSPSLALFSLNGHFVAQMEGLGTRLBAQRQRSRP 3422  
Db 3010 QPAVDMQT--TSSRGLVPHTG---TKNSFMALYLSKGLRFALGTDGKLRKIKKEKND 3064  
QY 3423 GRWKVSVRWKRNILLVTDGARAWSOBGRHOGAEHPQPHTLFVG-----GLPASH 3477  
Db 3065 GKWHVTVFGHGEKRLVVDGLRA--REG-----SLPGNSIISIPAPYLSPSGK 3114  
QY 3478 SSKLPVTYVFGSCVKRLRHLGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGVTLTDLPG 3537

Db 3115 PKSLP-TNSFVGCLKNFOLDKSLYTPSSSFGVSSCLGGPLEKSGYFSEGGHVVLAHSV 3173  
 QY 3538 ATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLOVTEKQVLLRADDGAGFSTVTRP 3597  
 Db 3174 LLGPEFKLVSIRPSLSITGLIHIG-SQPKHLVYLEAGKVTASNDGAGTSTSVTPK 3232  
 QY 3598 SVLDCDQGWHLAYKSGNVLRLEVDQSNHTVGPLLAAAGAPAPLYLGGPEPMAVQPM 3657  
 Db 3233 QSLCDQGWHSVATIIKQHLHLELDDSSYTAGQIPFPFPASTQEBLHGGAPANTTURI 3292  
 QY 3658 P--PVCYGCWRRRLAVNRSPVAMTRSVVEHGAAGSCP 3693  
 Db 3293 FVMKSPFGCLRNTHVNHIPVFVTEALEVQGPVSLNGCP 3330

## RESULT 12

ID ABB64954 standard; protein; 3712 AA.

AC ABB64954;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 21654.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li FWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL09057.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

PS Disclosure; SEQ ID NO 21654; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABBS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX Sequence 3712 AA;

Query Match 25.3%; Score 5093; DB 4; Length 3712;  
 Best Local Similarity 31.6%; Pred. No. 1.6e-280;  
 Matches 1245; Conservative 611; Mismatches 1542; Indels 540; Gaps 121;

QY 45 LHPPYFNLAEGARIAASATCGEAPARGSPRTEDLYCKLVGGPVGAGDPM-QTRIGQYC 103  
 Db 24 LTFFPYFNLAETGKVIYATATCGQDTG-----PELYCKLVGANTGHDHIDYSVIQGVQC 76

QY 104 DICTAANSKAKHPASNAIDGTERMWQSPPLSRGLSEYNEVNTLDLQGVFHVAYVLKIFAN 163  
 Db 77 DYCDPTVPERNPPENAIDGTEAMWQSPPLSRGKMFNEVNLINTEQSFHVAYLIFIRGN 136  
 QY 164 SRPDLWLERSWDFGRITVQPMQFFASSKRCLEBFQGTLETRDDAACTTEYSRIV 223  
 Db 137 SRPGLWLTLEKTDIGKWTWPMQHEFSDPACETVFGKDTYKPIITRDDDDVCTTEYSKIV 196  
 QY 224 PIENGIVVSLVNGRPGAMNFSYPLBFTKATNVRLRFLRTNTLLHGLMGLARDPVT 283  
 Db 197 PLENGEIPVMLNRPSSSTNYFNSTVLOEWTRATNVIRLLRTKNLLHGLMSVARQDPTV 256  
 QY 284 TRRYYSIKDISIGRCVCHGHADACADKDPDTPPR-LOCTCOHNTCGGTCDCRCPGNG 342  
 Db 257 TRRYYSIKDISIGRCMCHGADTCVKDPKSPVRIILACQCHHTCGIQNECCPGFEQ 316  
 QY 343 QPWKATANSANECOSCNCHYHATCYDDPVDERRASQSLDGTYYGGGVCIDCOHHTAG 402  
 Db 317 KKWQNTNARPNPCFPCNCHGSHNECKYDEEVNRKGLSLDIGHYDGGGVCCQCHNTVG 376  
 QY 403 VNCERCLPGFYRSPNHPLDSPHVCRRCNCESDFTDGTCTEDLTGRCYCRPNFSGERCDVCA 462  
 Db 377 INCNKCKPKYRPGKHKWNETDVCSPCQCDYFFSTGHCEBETGNCECRAAFPPSCDCA 436  
 QY 463 EGFTPPPSCYPTPSSNDTRQVLPAGQIVNCDASAAGTQGNACKRDPVRGCLCKENFQ 522  
 Db 437 YGYGYGPN-----RE-----CECNLANGTNGYHCEASEG-QCCCKINFA 475  
 QY 523 GTHCELQAPGYG-PCOPCQCSSPGVADRDCTDPTDQCRCRVGFEGATCDRCAPGYFHF 581  
 Db 476 GAYCKQAEYGYGPECKACBCKNKGTSITDNCVTTGCKCLTNFGDNCERCKHGYFN 535  
 QY 582 FLCQLCGSPAGTLPBGCD-BAGRCLQPEFAGHCDRCRPGYHGFNQCQACTDPRGAL 640  
 Db 536 PTCYSYCDNQGTESEICNKGSGQICREGGGPRCQCLPGFYNYPDCKPCNCSSTGSS 595  
 QY 641 DQLCGAGGLCRCPGYTGTACQECSPGFHGPSPVCHCSAEGSLHAACDPRSSQCSGRP 700  
 Db 596 AITCDNTKCNCLNNAFAGKQCTLTAGYYSYDCLPCHCDSHGSGQVSCN-SDQCLCQP 654  
 QY 701 RVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAPVDPALPEAQVP-----CMCRAHVGSBCD 756  
 Db 655 NFDGRQCDCKEFGFYNFSCDCNCDPAGV--IDKFAGCGSVFVGLCKCKERVTGICN 712  
 QY 757 RCKPGFWGLSPSNPEGCTRCSCDLRGLTGGVABEQPGTGCFCXPHVCGACASCKDGF 816  
 Db 713 ECKPLYWNLINISNTEGCEICDCWTDGTISALDCTSKSGQCPCKPHTQRRCCRDGT 772  
 QY 817 GLDQADYGCRCRCDIGCALGQSCBPTGVCRCPNTQGTCTSEBARDHYLPDLHLRL 876  
 Db 773 DLDSASLFGCKDCSCDVGGSGQSVCDKISGQCKCHPRITGLACTQPLTTHFFFTLHQFY 832  
 QY 877 ELEEAATPEGHAVRFGFNLEFENFSWRGYAQMAPVQPRIVARLNLTSPLFLVFRYVN 936  
 Db 833 EYEDGSLPSGTQVRYDYDEAAFPGFSSKGYVFNVAIQNDVRNEVNFKSLYRVLRYVN 892  
 QY 937 RGAMSVGRSVRBEGRSAACACTAQSQVPAPPPSTEPAFITV--PQRFGBFPVLPNG 994  
 Db 893 PNAENVATISVTSNPLE-----VDQHRVLLQPTSEPOFVTVVAGPLGVKPSAIVLDGP 947  
 QY 995 TWALRVER-EGVLLDYVLLPSAYEALLQLRVTEACTYRPSAQSGDNCLLYTHLPDL 1053  
 Db 948 RVVFTTKANKVMLDYFVLLPAAVYEAAGILTRHISNPCL-----GNMELCRHYKVASVE 1002  
 QY 1054 GFPSMAGLEALCRQDNLSLPRECPTEQLSPSPPLIT-----CTGSDVDVQVAVPQP 1106  
 Db 1003 VESPA--TPFVIGENSKPTNFTVETYPDHELQVLSHVGDIPVLUSGQSNELHYIVDPVS 1060  
 QY 1107 GRVALVVEY-ANEDARQEVGVAVHTPQRAFPQGLLSLHPLCLYSTLCRGRTARDTQDLAVF 1165  
 Db 1061 GRVIFVIDYSDRNPDSYIYNLKLKNDPSETSVLLYPCLYSTICR-TSVNEDGMEKSF 1119  
 QY 1166 HUDSE--ASVRLTA---EQARFFLHGVTLPIDEEFSEFVEPRVSCISSHGAGFQNSAAC 1220

2144	FTTSQKLYNYDQ	LADELEBPKVLLDPNSVDLSPSKANSELES	DAKSYAKOVNOTLANAF	2203		
2234	EVLEQOSTISG	DARRLGQAVGTRDQASOLLAGTEATLGHAKTL	LAARAVDRTISEL	2292		
2204	DIERESTILG	NITVAYDEAVKSADQAEIASVEAL	SKNLEAASTKIDAALEQA	2259		
2293	MSOTGHGLAN	ASPEGOELLRTLAEBVRLLEWEMRARDLGA	POPAAEAEELAAAOQLLARV	2352		
2260	QHILGOINGTS	IELTNEQVL	EKARKLYE	EVNTLVLP	PIKAQNKSLNALKNVDIGEF	2314
2353	QEOLSSWEEN	QALATQTRDRLAHEAGLMDUREALN	RAVDATREACELASNRQERLEE	2411		
2315	SDHLEDFUN	WEASEQAKSAD	VERNVANQAFD	NSKPDVTVEQ	2357	
2412	ALORKOEL	SRDNATLOATLHAARDTLASVFLHLSLDOAKEELERLAASLDGARTPLLQ	2470			
2358	KJQAEKNIK	DAGNFINGDL	TLNQINKDLNLRDALNELNFSFNKYD	BELPYRE	2411	
2471	RMQTFSPAG	SKLPLVEAAEAHAQOLQALNLSIILDVNDRLTORAIEASNAYSRILQ	2530			
2412	DQHKEADA	LTQOABQKAAELAIKAQDLAAQYDTMTAS	NEPAIKATAYSGIVE	2464		
2531	AVQAAEDAA	QOALQQADHTWATVVRQGLVDRAQOILLANSTALEAMLEBQQ	2581			
2465	AVEAAQKLS	QDAISAGN	ATDKTDCIEERAHADTGTSTDLLOAROSLOKVQDDLEPR	2522		
2582	FLGLVMAAL	QAGARTOLRDVPAKDKOLEAHQ	AQAMLAMDITDETSK	2628		
2523	LNASAGVQ	KISAVNNATBEHLQDKINKLIDQLPASQORDMMKNKSNANASDALEILKNVLE	2582			
2629	IAHAKAVAAE	Q	DTATRVQSOLOQAMQENVERWQOQYEGLEGRQDLQGLQAVLDAGHSVSTLE	2687		
2583	ILEPVSVQ	TPKELEKAHGINRDLDLTKDVSQANKQLDDVEG	SVSKLS	2630		
2688	KTLPLLAKI	SILNENGVNASLALSASIGRVRELIQAARGAASKVKVPMKFNKESGVOL	2747			
2631	E	LAEDIEEQORHVQSQSLQOEIENLKAQVEAARQALANSIKVGNFKPSTIL	2685			
2748	RTPRDLAD	LAAYTALFYLOGPEPEPGQGTEDRFVVMYG	SRQATGYDMGVSLRDKK	2803		
2686	KTPKTKL	ATRLTNLSYFTTEP	SGFLLYLGNDNKTAQKNDFVAIVEVNGY	2738		
2804	VHVVYQEL	GAQPAVLSDIEDI	GEQFAAVSLDRILQFGHMSVTVVERQMIQETKQDTV	2859		
2739	PILTIDLGN	GPERRITSDKYVADGRWYQAV	VDR	MGPNAKLTIREEL	PNGDVVEH	2791
2860	ACAEGLNL	RDDDFVYVGVYP	STFTPPILLRFPYRGCIEMDTLNEEVVSL	2912		
2792	SKSGVLSG	QNILHVDKNRSLF	VGGYGLISDENAPDITTNFSFGSDIEDLKIGESVGL	2850		
2913	YNF	ERTFQD	TAVDRPCARSKSTGDPMLTDSGYLDGTGFAFARISFDSQIS	2961		
2851	WNFVYGD	NDQARERDVLLEKKKPVTLGRFKNGYVQLNATSNLKRSSIOFSFKADK	2910			
2962	TKRFEQEL	RLVSVSGVLPFLKQSQSOFCLAVQEGSLVLLYDFGAGLKKAVLPQPPPLT	3021			
2911	TS	NGLLFFYGRDKHYMAIEMIDGAIFFNISLIGEG	2944			
3022	SASKAIQV	FLLGSRKRV	LVYRVER	ATVVSVEQNDLELA	3060	
2945	GGVQ	SGSODRYNDNOMHKVQAEERENRGLLKVDIVISRTNAPLEADLEPKL	2997			
3061	DAYILGGV	PPDOLPPSLRWLPFTGSGVRGVKGIKALGVYDLKRLNT	TGVSAGCTADL	3119		
2998	RRLYFGG	HFERLNTSIS	LQP	NPDGIDNVINQGVDDLTXYVTOGGVEGCSAKF	3052	
3120	LVGRAMTF	PHGFGFLRLALSNAVPLTGNVYSGGFHSQAQDSALLYRASPD	GLQVQSLQ	3177		
3053	STTVSYAP	HEYGFLR	MNNVSS	DNNLHVLFHFKTQPNQVLFVAAHNHQDSSTIGLSIQ	3109	
3178	QGRVSLQ	LLRTE	VKTQAGFADQAPHYAFYSNATGVMLYVDDQLQOMKPHRGPPELOP	3236		
3110	DGLKXNSMG	QVLDIRINDGEDHVVTVQHTQGSRLTVDDVDNRUG	3161			

QY 3237 QP---EGPRLLLGLLPES-----GTIYNFSGCISNVFQRLGQPVFDL----QQ 3281  
Db 3162 QPILLEGSD-IFAGLPDPRTRNALASLAYFVGCISDVTN-----EIIINFANGAEK 3215  
QY 3282 NLGSVNVSTGCAPALCAQTFGLGP----- 3305  
Db 3216 KXGNZIN---GCPFHVLAYEPLVSPSYSGDNVEPWSNADTLPPLKPDIESTLPTTP 3272  
QY 3306 -----RGLQATARKASRRSQPAR-----HPA 3327  
Db 3273 TTTTITTTTSTTTTSTTTTSTTTTSPDIVDEKEIEAKTKOKILTTRPPAKUNLPDSR 3332  
QY 3328 CMLPPH---LRTTRDSYQFQGSLSHLEFVGILARHNWPSLSMHLPRSSRGLLFTA 3383  
Db 3333 CKLPEQPNFDVDFTEAGYRFYGLRQRLQINSLPVKVRHHDIGISPRTERPNGLLIY-A 3391  
QY 3384 RLKPGSPSLALFSLNGHFVAQMEGLGTRLRQ--SRQSRPRWHKYSVRWEKNRIILLVT 3441  
Db 3392 GSKRDDFIAYVLLDGRVYIEIR-VQAOLQAKITTEAELNDGTWHTVEVTRQKVSLLI 3450  
QY 3442 DGARWSQSGPHRQGHAEHPQ-----HTLFFVGL-----PASSHSSKLPVTVGF 3487  
Db 3451 D-----KLQPGSVDLNABERSAPVLAVELPIYLGCVNKFLESEVKNLTDFKTEVPY---F 3502  
QY 3488 SGCVKRLRHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDPGATLPDVGLEL 3547  
Db 3503 NGCLKNIKEDAMDLETPEEFQVWC-SEQVERGLFFNNQAFVKI-----FDHFDVGTET 3557  
QY 3548 EV---RPLAVTGLIFHLQARTPYLQLOQYTEKQVLLRADDDGAGFSTSVTRPS--VLC 3601  
Db 3558 KISFOPRDPDNGLLFSVHGKNSYAILLEL-VDNLTLYFTVKTDLKNIVSTNYKLPNBSFC 3616  
QY 3602 DQGMHRLAYMKSNGVLRLEVD-AQSNHTVGPPLAAAGAPAPLYLGLPEPMAVQWPW-- 3658  
Db 3617 DKTRNVQAIKFKVINIAVDPISSNPGVNGEGSVITRNPFLFG---HVAFQAPGI 3673  
QY 3659 ---PAYCGMRRLAVNRSPVAMTRSEVHGAVGASGCP 3693  
Db 3674 KTKSGFKGICISVEVQNRMINITPNMV-GDIWQGYCP 3710

RESULT 13

AAM50358  
ID AAM50358 standard; protein; 953 AA.  
XX AC AAM50358;  
XX DT 18-FEB-2002 (first entry)  
XX DE Human laminin-15 alpha 5 chain.  
XX KW Laminin-15; human; retina; eye; therapy; ophthalmological;  
XX KW antiinflammatory; rod dystrophy; rod-cone dystrophy;  
XX KW retinitis pigmentosa; macular degeneration; retinal detachment.  
XX OS Homo sapiens.  
XX PN WO200183516-A1.  
XX PD 08-NOV-2001.  
XX PF 01-MAY-2001; 2001WO-US013943.  
XX PR 01-MAY-2000; 2000US-0200863P.  
XX PA (WASS-) MASSACHUSETTS GEN HOSPITAL.  
XX PI Burgeson RE, Brunken W, Champliand M, Hunter D;  
XX WPI; 2002-041478/05.  
XX DR N-PSDB; AAI70817.  
XX

Query Match 24.9%; Score 5002; DB 5; Length 953;  
Best Local Similarity 100.0%; Pred. No. 3.5e-276;  
Matches 953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2743 SGVQLRTPRDLADLAAYTALKFYLGQPEPEPGGTEDRFVYMGSSQATGDMVSLRDK 2802  
Db 1 SGVQLRTPRDLADLAAYTALKFYLGQPEPEPGGTEDRFVYMGSSQATGDMVSLRDK 60  
QY 2803 KVHWYQLGGEAGPAVLSDIDSGEOPAAVSLDRTLQFGHMSVTVVERQMIOETKGDVAPG 2862  
Db 61 KVHWYQLGGEAGPAVLSDIDSGEOPAAVSLDRTLQFGHMSVTVVERQMIOETKGDVAPG 120  
QY 2863 AEGLLNLRPDDFVYVGGYSPSTFTPLLPFGVRCIEMDTNNEVSVLYNFERFOLD 2922  
Db 121 AEGLLNLRPDDFVYVGGYSPSTFTPLLPFGVRCIEMDTNNEVSVLYNFERFOLD 180  
QY 2923 TAVDRPCARSKSTGDPWLTDGSLDGTGFPARISFDSQISTTKRFBELRLVSYGVLFFL 2982  
Db 181 TAVDRPCARSKSTGDPWLTDGSLDGTGFPARISFDSQISTTKRFBELRLVSYGVLFFL 240  
QY 2983 KQSQFICLAVQEGSLVLLDFGAGLKKAVLPLOPPPLPTSASKAIQVFLLGSRKRLVLR 3042  
Db 241 KQSQFICLAVQEGSLVLLDFGAGLKKAVLPLOPPPLPTSASKAIQVFLLGSRKRLVLR 300  
QY 3043 VERATVYSVEQDNDELDADAYLGGVPPDOLPPLSLRWLPFTGSGVRGCVKGIKALGYVD 3102  
Db 301 VERATVYSVEQDNDELDADAYLGGVPPDOLPPLSLRWLPFTGSGVRGCVKGIKALGYVD 360  
QY 3103 LKRLNTGVSAAGCTADLLVGRAMTFHGHGFLRLALNSVAPLTGNVYSGFGFSAQSALL 3162  
Db 361 LKRLNTGVSAAGCTADLLVGRAMTFHGHGFLRLALNSVAPLTGNVYSGFGFSAQSALL 420  
QY 3163 YYRASPDGLCQVSLQOQGRVSLQLLRTEVKTQAGFADGAPHYAFYFNATGWMLYVDQDLQ 3222  
Db 421 YYRASPDGLCQVSLQOQGRVSLQLLRTEVKTQAGFADGAPHYAFYFNATGWMLYVDQDLQ 480  
QY 3223 QMKPHRGPPPELQPEGPRLILGLPESGTYNFGCISNVFQRLGQPVFDLQCN 3282  
Db 481 QMKPHRGPPPELQPEGPRLILGLPESGTYNFGCISNVFQRLGQPVFDLQCN 540  
QY 3283 LGSVNVSTGCAPALCAQTFGLGPRGLQATARKASRRSQPARHPACWLPFHLTRTDSYQ 3342

PT Novel substantially pure preparation comprising laminin having laminin  
PT chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders  
PT such as retinitis pigmentosa, macular degeneration, retinal detachment.  
XX Disclosure; Fig 2A; 58pp; English.  
XX The present sequence is that of the alpha 5 chain of human laminin-15, a  
CC novel member of the laminin family that is produced in the retina. The  
CC retina produces 2 novel laminin trimers, laminin-14 (alpha 4, beta 2,  
CC gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed  
CC within the inter-photoreceptor matrix and in the outer plexiform layer,  
CC and may serve to stabilise retinal synapses. The invention provides  
CC laminin-15 preparations and cells comprising a nucleic acid encoding the  
CC laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of  
CC producing laminin-15. The laminin-15 preparation is used in claimed  
CC methods of: increasing retinal immunophotoreceptor matrix stability;  
CC increasing the stability of retinal photoreceptor compounds, especially an  
CC outer segment, inner segment or synapse; increasing retinal adhesion; rod  
CC treating a disorder associated with retinal degeneration, especially rod  
CC dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration  
CC and retinal detachment; increasing the stability of synapses of the  
CC central nervous system or peripheral nervous system; stimulating an  
CC neuroregeneration, axon outgrowth or synapse formation; preparing an  
CC implant, e.g. a catheter, artificial joint, retinal implant, timed  
CC releasing device, neural cell growth guide or artificial tissue, by  
CC coating with the laminin-15 preparation; and increasing photosensitivity  
CC by implanting a tip coated with the laminin-15 preparation into an eye.  
CC The laminin may be recombinant, and the 3 chains co-expressed in the same  
CC cell or expressed in different cells  
XX Sequence 953 AA;

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DB 541 LGSVNVSTGCPALQACTPGFGLQATARKASRSRQPARPCACMLPPHLETTDSQ 600
QY 3343 FGGSLSHLEFVGLIARHNWPSLMVLPSSRGGLLLFTARLRPGSPSLAFLNSGHFV 3402
DB 601 FGGSLSHLEFVGLIARHNWPSLSMHLPPSSRGGLLLFTARLRPGSPSLAFLNSGHFV 660
QY 3403 AQMEGLGTRLRQAQRQRSPGRHKVSVRWEKNRILLVTDGARAWQEGPHRQHQAEHP 3462
DB 661 AQMEGLGTRLRQAQRQRSPGRHKVSVRWEKNRILLVTDGARAWQEGPHRQHQAEHP 720
QY 3463 QPHILFVGLGLPASGSHSKLPVTGFCSCVRLRLHGRPLCAPTRMAGVTPCILGPLAEGL 3522
DB 721 QPHILFVGLGLPASGSHSKLPVTGFCSCVRLRLHGRPLCAPTRMAGVTPCILGPLAEGL 780
QY 3523 FPGSGGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQIQVTEKQVLLR 3582
DB 781 FPGSGGGVITLDPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQIQVTEKQVLLR 840
QY 3593 ADDGAGBFSTVTPSPSVLDCQWHLAVMKSQVNLREVDQNSNHTVGPGLAAAGAPAP 3642
DB 841 ADDGAGBFSTVTPSPSVLDCQWHLAVMKSQVNLREVDQNSNHTVGPGLAAAGAPAP 900
QY 3643 LYLGLPEPMAVQWPWPAYCGCMRLAVNRSVPAMTRSVSVHGVAGASGCPAA 3695
DB 901 LYLGLPEPMAVQWPWPAYCGCMRLAVNRSVPAMTRSVSVHGVAGASGCPAA 953

RESULT 14
ID ABB09502
AC ABB09502;
XX ABB09502;
XX 01-NOV-2002 (first entry)
DE Human laminin alpha-5-like NOV1b protein, SEQ ID NO:4.
KW Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addition; tuberculous sclerosis; cancer; immune disorder; allergy;
KW autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW anti-inflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;
KW differentiation; proliferation; motility; haematopoiesis; wound healing;
KW angiogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV1b; laminin alpha-5-like; chromosome 20.
XX Homo sapiens.
XX WO200253742-A2.
XX 11-JUL-2002.
XX 07-JAN-2002; 2002WO-US0000375.
XX 05-JAN-2001; 2001US-0260018P.
XX 08-JAN-2001; 2001US-0260360P.
XX 28-FEB-2001; 2001US-0272411P.
XX 02-MAR-2001; 2001US-0272817P.
XX 05-JUL-2001; 2001US-0303231P.
XX 12-JUL-2001; 2001US-0305060P.
XX 10-SEP-2001; 2001US-0318405P.
XX 12-SEP-2001; 2001US-0318700P.
XX 04-JAN-2002; 2002US-00037417.
XX (CURA-) CURAGEN CORP.

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XX Ketuda R, Alsebrook JP, Tchernev VT, Liu X, Spytek KA;
PI Pattarajan M, Grosse WM, Jephley DM, Burgess CE, Vernet CAM, Li L;
PI Gorman L, Eisinger S, Schiore P, Ellerman K, Malyankar U;
PI Rothenberg M, Stone D, Boidog F, Guo X, Shency S, Anderson D;
PI Padigaru M, Taupier RJ, Miller CE, Eisen A;
XX WPI; 2002-583619/62.
DR N-PSDB; ABQ93880.
XX Novel polypeptides and nucleic acids homologous to transmembrane
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT treating cancer, atherosclerosis, neurological, skin and autoimmune
PT disorders.
XX Claim 1c; Page 17; 323pp; English.
XX The invention relates to 24 novel human proteins designated NOV1-NOV14
CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and
CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins, and
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-
CC associated disorders or in the manufacture of a medicament for treating
CC such disorders, with specific applications described for each of the 24
CC NOVX proteins, based on their homology to known proteins. Various
CC disorders are associated with NOVX proteins including neurological
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
CC pain, behavioural disorders, addition, tuberculous sclerosis, cancers
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
CC (e.g., hypertension), reproductive disorders, endometriosis,
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,
CC atherosclerosis, cell signal processing-related disorders and disorders
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
CC be used to identify cellular receptors or downstream effectors which
CC binds to a NOVX protein, and are also useful as targets for the
CC identification of small molecules that modulate or inhibit processes such
CC as neurogenesis, cell differentiation, cell motility, cellular
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC nucleic acid sequences can be used to identify a cell or tissue type and
CC are useful as a source of primers or probes for forensic biology and for
CC identifying and cloning NOVX homologues in other cell types. Cells
CC comprising NOVX nucleic acids are useful for producing non-human
CC transgenic animals which are useful for studying the function and
CC activity of NOVX proteins and for identifying and evaluating modulators
CC of NOVX activity. The present sequence represents the laminin alpha-5-
CC like protein NOV1b. The gene encoding NOV1b is located on chromosome 20
XX Sequence 908 AA;
SQ Query Match 23.6%; Score 4756.5; DB 5; Length 908;
Best Local Similarity 99.5%; Pred. No. 3.3e-262;
Matches 908; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
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QY 2963 TKRFEQELRLSVSYGVLPFLKQSQOFLCLAVQEGSLVLLYDFGAGLKKAVLPQPPPLTS 3022
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Qy 3263 SNVFORLLGPQRFVFLQNLGSLVNVSTGCAPALQATPGLGPRGLQATARKASRRSQP 3322  
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Qy 3503 APRTRMAGVPCILGPLEAGLFPFGSGGVITLDPGATLPDVGLLEVRPLAVTGLIHLG 3562  
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Qy 3623 AQSNHTVGPLLAAAGAPAPLYLGLLPEPMAVQPPWPAYCGCMRLAVNRSPVAMTSVE 3682  
Db 836 AQSNHTVGPLLAAAGAPAPLYLGLLPEPMAVQPPWPAYCGCMRLAVNRSPVAMTSVE 895  
Qy 3683 VHGAAGSAGCPAA 3695  
Db 896 VHGAAGSAGCPAA 906

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XX AC ADE09114;  
XX DT 29-JAN-2004 (first entry)  
XX DE Novel protein-related contig polypeptide sequence #180.  
XX KW novel gene; novel protein; tissue marker; molecular weight marker;  
XX KW chromosome marker; genetic disorder; contig.  
XX OS Unidentified.  
XX PN WO2003054152-A2.  
XX PD 03-JUL-2003.  
XX PF 10-DEC-2002; 2002WO-US039555.  
XX PR 10-DEC-2001; 2001US-0339739P.  
XX PR 11-DEC-2001; 2001US-0339453P.  
XX PR 14-MAR-2002; 2002US-0365091P.  
XX PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.  
PR 12-APR-2002; 2002US-0372615P.  
PR 22-APR-2002; 2002US-00128558.  
PR 24-APR-2002; 2002US-0376045P.  
XX (HYSE-) HYSEQ INC.  
XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
XX WPI; 2003-569235/53.  
XX PT New polynucleotides, useful for expressing recombinant proteins for  
PT analysis, characterization or therapeutic use, or as markers for tissues  
PT in which the corresponding protein is preferentially expressed.  
XX PS Disclosure; SEQ ID NO 2658; 1177bp; English.  
XX CC The invention comprises the amino acid and coding sequences of novel  
CC proteins. The DNA and protein sequences of the invention are useful as:  
CC markers for tissues in which the corresponding protein is preferentially  
CC expressed; as molecular weight markers on gels; as chromosome markers or  
CC tags; to identify chromosomes or to map related gene positions; and to  
CC compare with endogenous DNA sequences in patients to identify potential  
CC genetic disorders. The present amino acid sequence was used in the  
CC exemplification of the invention.  
XX Sequence 1486 AA;  
Qy Query Match 20.2%; Score 4058; DB 7; Length 1486;  
Db Best Local Similarity 45.5%; Pred. No. 4.4e-222;  
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Db 12 LHPTYFNLAE-AEDLATATCGERGPGRPQ--ELYCKLVGGTAPGS-GHTIQGQFCD 67  
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Job time : 140.335 secs

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816 FGLDQADYFGCRSCRDIGGALGQSCPRVTGCRCPNTQGTCTCEPARDHYLPDLHLR 875  
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1174 RLTAEQARFELHGVTLVPTTEPSEPEVEPRVSCISHGAFGPSAACLPSRFPKPPQPII 1233  
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1234 LRDCQVPLPPGLPLTHAODLTATSPAGRPRTAVDPDABP-TLLREPOATVVFYTH 1292  
1044 L-----DVLSGRFFPH---LPQSSSPS-----VDVLPGVTLKAPQNVTLRGR 1083  
1293 VPTLGRYAFLLHGYQFAHPTFPVEVLINAGRVWQGHANASFCPHGYGCRTLVVCBQALL 1352  
1084 VPHLGRYVFIHGYQAAHPTFPFAQSVGCGWPRAGSFHASFCHVVLGCRDQVIVXGQIEF 1143  
1353 DVTHSELTVTVRVEGRWMLDYVLVVPENYVSFGYLREEPLDKSYDFISHCAAQYHIS 1412  
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1444 LGWHELETADRVDIPVSENPFGSNWADLQELPATIHS-----SWVAP 1486

GenCore version 5.1.6  
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(without alignments)  
6824.493 Million cell updates/sec

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Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/2/1aa/5B-COMB.pep:\*  
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6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15839	78.7	3635	US-09-845-583A-2	Sequence 2, Appli
2	5002	24.9	953	US-09-845-583A-4	Sequence 4, Appli
3	3141.5	15.6	3106	US-09-562-702A-10	Sequence 10, Appl
4	3133.5	15.6	3084	US-09-562-702A-12	Sequence 12, Appl
5	3104	15.4	3111	US-08-460-309-4	Sequence 4, Appli
6	3104	15.4	3111	US-08-125-077-4	Sequence 4, Appli
7	3103.5	15.4	3110	US-09-562-702A-6	Sequence 6, Appli
8	3103.5	15.4	3110	US-09-561-709B-7	Sequence 7, Appli
9	3101.5	15.4	3110	US-09-562-702A-2	Sequence 2, Appli
10	3099.5	15.4	3088	US-09-562-702A-8	Sequence 8, Appli
11	3097.5	15.4	3089	US-09-562-702A-4	Sequence 4, Appli
12	2854	14.2	3075	US-08-460-309-5	Sequence 5, Appli
13	2854	14.2	3075	US-08-125-077-5	Sequence 5, Appli
14	2260.5	11.2	1713	PCT-US94-10261A-24	Sequence 24, Appl
15	2260.5	11.2	1713	US-08-600-982-24	Sequence 24, Appl
16	2136.5	10.6	1792	US-09-561-818A-4	Sequence 4, Appli
17	2136.5	10.6	1800	US-09-561-818A-8	Sequence 8, Appli
18	2136.5	10.6	1816	US-09-561-818A-2	Sequence 2, Appli
19	2136.5	10.6	1824	US-09-561-818A-6	Sequence 6, Appli
20	2111.5	10.5	1792	US-09-561-818A-12	Sequence 12, Appl
21	2111.5	10.5	1816	US-09-561-818A-10	Sequence 10, Appl
22	1604	8.0	1799	US-09-845-583A-6	Sequence 6, Appli
23	1573.5	7.8	1786	US-09-562-702A-14	Sequence 14, Appl
24	1573.5	7.8	1786	US-09-561-818A-14	Sequence 14, Appl
25	1573.5	7.8	1786	US-09-561-709B-9	Sequence 9, Appli
26	1572.5	7.8	1786	US-09-562-702A-18	Sequence 18, Appl
27	1572.5	7.8	1786	US-09-561-818A-18	Sequence 18, Appl

28	1564.5	7.8	1765	4	US-09-562-702A-16	Sequence 16, Appl
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30	1558	7.7	1725	4	US-09-562-702A-20	Sequence 20, Appl
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33	1535	7.6	1798	4	US-09-561-709B-11	Sequence 11, Appl
34	1524	7.6	1798	4	US-09-845-583A-8	Sequence 8, Appli
35	1460	7.3	1587	4	US-09-561-709B-3	Sequence 3, Appli
36	1460	7.3	1587	4	US-09-562-702A-3	Sequence 3, Appli
37	1355.5	6.7	1605	4	US-09-561-818A-26	Sequence 26, Appl
38	1355.5	6.7	1605	4	US-09-562-702A-32	Sequence 32, Appl
40	1329.5	6.6	1572	4	US-09-561-818A-28	Sequence 28, Appl
41	1317	6.5	1609	4	US-09-562-702A-22	Sequence 22, Appl
42	1317	6.5	1609	4	US-09-561-818A-22	Sequence 22, Appl
43	1317	6.5	1617	4	US-09-562-702A-26	Sequence 26, Appl
44	1295.5	6.4	1576	4	US-09-562-702A-24	Sequence 24, Appl
45	1295.5	6.4	1576	4	US-09-561-818A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champiaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 3635  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-2

Query Match	78.7%;	Score	15839;	DB	4;	Length	3635;
Best Local Similarity	79.4%;	Pred. No.	0;				
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Gaps	8;						
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Qy	259	VRLEFRLENTLLGLHMGKALRDPVTTRYYYSIKDISIGRCVCHGADACADKDPDPF	318				
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Db 721 QPHTLFVUGLPLASSHSSKLPVTVGPGCVKELRLHGRPLGAPTRMAGVTPCIIIGLEAGL 780  
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RESULT 3  
US-09-562-702A-10  
; Sequence 10, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 3106  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-562-702A-10

Query Match 15.6%; Score 3141.5; DB 4; Length 3106;  
Best Local Similarity 23.8%; Pred. No. 1.3e-185;  
Matches 975; Conservative 471; Mismatches 1161; Indels 1485; Gaps 131;

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Db 336 ECEACNCHGKABECYDDETVASRNLNLNKHGKIGGVCLNCHTNTAGINCETCVDPGFR 395  
QY 415 ----SPNHPDLSHVRCRNCESDFTDGTCEDL-----TGRCYCRPNFSGR 457  
Db 396 PKGVSPNY-----PRPCQCHCD---PTGSLSEYCVKDEKYAQRGLKPGSCHCKTGFEGYN 448  
QY 458 CDVCAEGFTGPPSCYPTPSSNDTRQVLPAGQIVNCDSCSAAGTQGNACRKPVRVGRCLC 517  
Db 449 CDCRVGVHGVPCQP-----CNCGLG-----STNEDPCVGPCSC 484  
QY 518 KPNFQCTHCLCAPFVG-----PGCQPCQSSPGVADDCDDPDTCQCRVRGFEATC 571  
Db 485 KENVEGSDCRCKSGGFPNLOEDNQKCEBCFCB--GVS----- 520  
QY 572 DRCAPGYFHFPLQLCQCSGAGTLPBG-----CDEAGRCLCQEPFAGPHCDRCRPGYHGF 626  
Db 521 NRCQSSVMTY-----GNIQDMRGWYLTDLGRIRMAPQLDNP-----SPQIISI 565  
QY 627 PNCOA-----CTCDPRGALDQICGAG----- 648  
Db 566 SNSEARKSLDGYWWSAPPYLCNRLPAPVGGQLSFTISYDLBEEEDDTTEKLQLMIFEG 625  
QY 649 ----- 648  
Db 626 NDLRISTAYKEVLEPSEEHVREVSLEBAFTHTGNLPTVRKDFMIVLTNLGEILLQIT 685  
QY 649 -----LCRCRPGYGTACQBCSPG----- 667  
Db 686 YNLGMDAIFRLSSVNLSPVYPTDRRIATDVVEVCOCPGEGYSGSCETCWPHRRVNGTI 745  
QY 668 FHGFPSCVPCCHCSAEGSLHA-ACDPRSGQC-SCRPRVTGLRCDTCVPGAYNFPYCEAGSC 725  
Db 746 FGGI--CEPCQCPA-----HAACDDITGECNLKQHTGPGYCNELPGYGPDP--TRGS- 796  
QY 726 HPAGLAPVDPALPEAQVPCMHRAHV-----EGPSCDRCK 759  
Db 797 -----FEDCQPCACPLNIFSNFSPCHLDRSLGLICDECPITYGTPRCERCA 844  
QY 760 PGFWGLSPSPNEG-CTRCSCLRLGLGVAEQPGTGQC-FCKPHVCGQACASCDKGFPG 817  
Db 845 EGYFG-QPSVPGSGCQPCQNDNDLYSIPGSCDSLGSCLICKPGTTRGYCELCADGYFG 903  
QY 818 LDQADYFGCRSCRCIDIGGALGQSCBEPRTGVCRORNTQGTCTSEFAPRDHLYPLDLHLRL 877  
Db 904 -DAVNTKNCQPCRCIDINGSFSEDCHTRTQCCRCRPNVQGRHCD----- 946  
QY 878 LEEAATPEGHAVRFGFNPLEFENFWSRGYAQMAPVQPRIVARLNLTSPLDLEWLYVNR 937  
Db 947 ----- 946  
QY 938 GAMSVSGRVSVREGRSAACACTAQSQVAPPPSTEPAFITVPORGFGEPVLPNGTWA 997  
Db 947 ----- 946  
QY 998 LRVEAEGVLLDYVLLPAYSAYEALLQLRVTEACTYRPSAQSGDNCCLLYTHLPDGPFS 1057  
Db 947 ----- 946  
QY 1058 AAGLEALCRQDNLPRPCPTQELSPSHPLITCTGSDVDVQLQVAVPOPGRYALVVEYAN 1117  
Db 947 ----- 946  
QY 1118 EDARQEVGVAVHTPQAPQOGLLSLHPCLYSTLCRGARTQDHLAVFHLDSASRLTA 1177  
Db 947 ----- 946  
QY 1178 EQARFFHGVTLVPIEFPSEFVEPRVSCISSHGAFGPNSAACLPSRFPKPPQIILED 1237

Db 947 -----CKPETF----- 952  
Qy 1238 QVIBPLPGLPETHAODLTTPATSPAGPRPPTAVDPDAEPTILREPOATVFFTHVPTLG 1297  
Db 953 -----GLQ----- 956  
Qy 1298 RYAFLLHGYQAPHTFPVEVLINAGRVOGHANASFCPHGYGCRITLWCEGOALLDVTHS 1357  
Db 957 -----GRG----- 960  
Qy 1358 ELTVTVRVPGRWLWDVVLVVPNTVSFGYLBREPLDKSYDFISHCAAQGYHISPSSSS 1417  
Db 961 ----- 960  
Qy 1418 LFCRNAASLSFYNNGARPCGHEVGATGPTCEPFGGQCPCHAHVIGRDCRSCATGYWG 1477  
Db 961 -----LPCNCSFGSKSFDCEA-SGQCMQCPGVAGKKDRCAGYEN 1001  
Qy 1478 PP-NCRPCDGG-ARLCDELTGOCICPPRTIIPDCLLCOPTFGCHPLVGCBECCNSGP 1533  
Db 1002 FQEGGCTACDCHSLGNCCDPKTCQICPPNTGKCECLPNTWHSIVTGCKVCNCSTV 1061  
Qy 1534 GIOELTPTCDTSGQCKCPNVTGRRCDTCSGPHGYPRCPDCEAGTAPGVC----- 1590  
Db 1062 G---SLASQCNVNTGQSCCHPKFSGMKSCSRGHNNYPLCTICDCFLPTDATTCDLET 1118  
Qy 1591 -----PLTGQCYCKENVQPKCDQCSLGTFSIDAANKPKCTCFPCFEGATERCRSSSYTR 1644  
Db 1119 KRCSCDQTCGCKVNVGCHDCRCPGKFGLDKKNPLGSCSSCFGVTSCSEAKGL- 1177  
Qy 1645 QBFVMEGWLLSDRQVPHRPGTGMLEADLRHV-----PEAV---PEAFPEL 1692  
Db 1178 -----IRTWVLSDEQITLP-----LVDEALQHTTTKGIAQFPEIVAKMDEVQRJEL 1224  
Qy 1693 -----YQAPPSYLGDRVSSYGTILRYELHSEFQGVFVPMBSRDDVLOG---NQMSI 1744  
Db 1225 HLEPFYKLPQOPEGKMLAYGKLYAIYFEARDETGFATY--KPQVIIRGGTPTHARI 1282  
Qy 1745 TFLPAPVPTPGHVRGOLQVGNFRH---TETRNTVSREELMVLASLEOLQIRALFS 1800  
Db 1293 ITRHMAAPLQGLTEHIEEMTEKWKYGGDDPRISRTVREDFLDILYDIHILIKATYG 1342  
Qy 1801 QISSAVSLRRVALEASP---AQGALASNVELCLCPASYRGDSQCECAPGYR----- 1851  
Db 1343 NVVRQSRISSEISMEVAPFHVLAGSP- AHLIERCCPPGYSGLSCETCAPGYRLRSEP 1401  
Qy 1852 --DVKGLFLGRVPCQCHGSHDRCLPGSGVCDQHNTEGAHCERQAGFMSRDDPSAP 1909  
Db 1402 GGRTPGPTLGTVCPCQCNHSSQCDPETSVCQNCQHTAGDPCERCALGYGIVRGLPND 1461  
Qy 1910 CVSCPEPLVSPNNFASGVLRGRT--QC-LCKPGYAGASCERCAPGFPGNPLVLGSSCQ 1967  
Db 1462 COPCACPLIGSPNNFSPSCVLEGLDYRCTACPRGYEQYCERCAPGYTGPSSPGSSCQ 1521  
Qy 1968 PCDCSGNDPMLPSDDCDPLTGACRGCLRHTTGPRCEICAPGYGNALLPGNCTRCDCPT 2027  
Db 1522 EC-----ECDP-----YGLPVP----- 1534  
Qy 2028 CGTBACDPSHCHLCKAGVGTGRCRDRQEGHFGFNGCGGCRPCACGPAEGECHECHPQSQ 2087  
Db 1535 -----CDRVTLGCTCRPGATGRKDCGCHWH-----AREGAE----- 1567  
Qy 2088 CHCRPGTMGPQCRBCAPGYMGLPQGCRRQCPCGRCDPHTGRCNCPGGLSBERCDTCSQ 2147  
Db 1568 ----- 1567  
Qy 2148 QHQPVPVGGPVGHSIHCEVCHDCVLLLDLERAGAL-----LPAIHQOLRGINAS 2198  
Db 1568 -----VFCG--DECTGLLGLDLALEQMTNMINTGLPAPYKILYGLENT 1611  
Qy 2199 SMAWARLRLNASIADLQSOILSRPLGPRHETAQOLEVLEQOSTL----- 2243  
Db 1612 T-----QELKHLSPQAPERLIQLAEGNVNLTWNETNELLTRATKYT 1654

Qy 2244 -----QDARRLLGGAVGTRDQASOLLAGTEA-----TLGHAKTLLAAIRAVDR 2287  
Db 1655 ADGEQTCQDAERTNSRAESLEEFKGLVQDAEAINKEKAVKLNELTGNQD-----KTAER 1708  
Qy 2288 TSELMSQTHGLGLANASAPSGEQLLRTLAVERLLWEMARDLGAPOAAAELAAAR 2347  
Db 1709 NLEBLOK-----EIDRMLKELRSKDLQTOKEVAEDELVAABG 1745  
Qy 2348 LLARVQQLSSLWEEQALATQTRDRLAQHEAGLMDLREALNRAVDATREAOELNSRNOE 2407  
Db 1746 LLKRVNKLFGEPRAQNEDEKOLQOKLAETYNKLDLWLLREATTXTKTDANRLSANOK 1805  
Qy 2408 RLEALQKQBELSRDNATLOATLHAARDTLASVFRLLSHLDQAKBELERLAASLDGARTP 2467  
Db 1806 NMTILETKKEAIEGSKFOIENTLKEGNDILDEANQLLGEINSVIDVDDIKTKLPWMSBE 1865  
Qy 2468 LLQEMQTFSPAGSKLRLAVE---AAEBAHQOLGOLALNLSIILDVNQD---RLTORAIEA 2521  
Db 1866 LSDKIDDLAQEIKDURRAEKVFOAESHAAQ-----LNDSSAVLDGILDRAKNSIFNATAA 1920  
Qy 2522 SNAYSRILOAVQAAEDAAQOA--LOQADHTWATVVRQGLVDRAQQLLANSTALEAMLOE 2579  
Db 1921 FRAYSNIKDVIDEAEKVAREKELAQCATKLATSPQGLLKEDAKGSLQKSFRI---LNE 1976  
Qy 2580 QORLGLVWAALQGAROTLRDVRRAKQOLEAH-----IQAAQAMLAMOTDETCKIAHA 2632  
Db 1977 AKULA---NDVGNHNDLNDKTRLETADLRNSGLLGALNDTMDKLSAITNDTAQLOAV 2033  
Qy 2633 KAVAAEACDTATRYQSOLOQAMQENVERWQOYBGL-----RGDLOQOAVLDAGH 2681  
Db 2034 KEKAREANDTAKAVALQVKDLHQNLQKQNYNKLADSVAKTNVAVKOPSRKXKIADACT 2093  
Qy 2682 SVSTLEKTLQOLLAKSILENRGVHNASLASISGRVRELIQAARGAASKVKVPMKFG 2741  
Db 2094 SVRNLEQEARLDLQK-----KPIKELENLKXNISEIKELINOARKQANGIKVSVSSG 2148  
Qy 2742 RSGVQLRTPRLADLAAYTALKFYLOPEPEPQOQTEDFVVMYMSGRQATGYMGVSLRD 2801  
Db 2149 DC---VRTYFETIKKGSYNNIVVHVK-----TAVADNLLFYLGSAKFI-DFLAEMRK 2197  
Qy 2802 KKHVWY---QJEGAGPAVLSTIDEDIGSOPAAVSLDRTLOFHMSTV---ERQMIQE 2853  
Db 2198 GKVSFLMVGSGVGRVGPDLTIDD---SYWRIEASRTGRNGSISVRALDGPKASWPS 2254  
Qy 2854 TKGDTVAPGAEGLNLRLPDDFVYVGGYPTFTFPLLPFGYRGCIEMDTLINEEVSLSY 2913  
Db 2255 TY-HSVSPPGVTILDVANAMLF-VGSLTGKIKKADAVRITFTGCMGETYFDNKPGLW 2312  
Qy 2914 NFERTFOLDTAVDRPCARSKSTGDPMLTDS-YLOGTGFEARIS---PDSQISTTKRPEQ 2968  
Db 2313 NF-REKEGDC---KGCTVSPQVED---SEGTIQDGBEGYALVSRPIRWTPNISTVM---F 2362  
Qy 2969 ELRLVSYSGVLFFL--KQSQFLCLAVQBSGLVLLYDFGAGLKAVLPLOPPPLTSASKA 3026  
Db 2363 KFRFFSSALLMYLATRDLDKDFMSVELSDGHVKVSYDLGSGMTSVVSNQ---NHNDRK 2417  
Qy 3027 IQVFLGGSBRVLRVVRERATVYSVEQDN-----DLELADAYVLOGVPPDQLP 3074  
Db 2418 WKAFITLSRIQOKANISI--VDIDSNOEENWATSSGNNFGLDLKADCKITFYGGL----- 2469  
Qy 3075 PSRLWLPFTGGSVR-----GCVRGKIK-ALGKYVDLKLRLNTTGVSACTADLLVG 3122  
Db 2470 PTLRNL-----SMKARPEVNVKYSGLCKDIEISRTFPYNLSSPDYGVVTKGSLENV-- 2522  
Qy 3123 RAMTFHGHGFLRLALSNAPLTGNVYSGFPHSAQDSALLY-----RASPD 3169  
Db 2523 NTVSFPKPEGVEVLAASVIDGT---BINLSFSTRNESGILLGSGGTLTPPRKRQTTQ 2579  
Qy 3170 GLCOVSLQOQRVSLQL-----LRTEVKTQAG-FADGAPHYVAFYSNATGVW-LYVDD- 3219  
Db 2580 AYYAIFLANKRLEVHLSSGTRTWKIVIKPEPNLPHDGRHSV-HVERTRGIFTVQIDED 2638





QY 1021 ALLQLRVTEACTYRPSAQOQSDNCLLYTHLPDGFPSAAGLEALCRQDNLSPRCPTEQL 1080  
Db 925  
QY 1081 SPSHPLITCTGSDVDVQLQVAVPQGRYALWVEYANEDARQEVGVAVHTPPQAPQOGLL 1140  
Db 925  
QY 1141 SLHPCLYSTLCRGSTAROTQDHLAVPHLDSEASVRLTAEOARFPLHGVTLVPPIEPPSEFV 1200  
Db 925  
QY 1201 EPRVSCISSHGAFGPNGAALPSPFPKPPPIILRDCQVLPPLPGLPLTHAQDLTPATSP 1260  
Db 925  
QY 1261 AGPRPPTAYDPAEPILLREPQAVVTHVPTLGRYAFLLHGVQPAHPTFPVPEVLIN 1320  
Db 935  
QY 1321 AGRVMOGHANASFCPHGYGCRTLVVCBQALLDVTHSELTVTVRVPEGRWMLDYVLVVP 1380  
Db 935  
QY 1381 ENVISFYLREPELDKSYDFISHCAAGYHISPSSSLFCRNAASLSFYNNARPQOC 1440  
Db 939  
QY 1441 HEVATGPTCPFFGQCPCHAHVGRDCSRCATGYWGP--NCRPCDCG--ARLDCDELGT 1496  
Db 944  
QY 1497 QCICPPRTIPDCLLCOPOFGCHPLVGBECNCSGPGIOELTDPCTDSDGCKCRPNV 1556  
Db 1003  
QY 1557 TGRCDTCSPGFHGYRCRCPDCHCACTAPGVC--PLGQCYCYCKENVQCPKC 1607  
Db 1060  
QY 1608 DCSLGTFSLDANPKGCTRCFCGATERCRSSYTRQEFVDMGVHVLSTDRQVPHR 1667  
Db 1120  
QY 1668 QPCTEMLRADLRHV-----PEAV-----PEAFPEL-----YWOAPPVSLGRVSSYGG 1710  
Db 1171  
QY 1711 TLRYELHSETORGDFVPMESRDPVLOG--NOMSIITFLEPAYPTPGHVHRGQLQVREG 1767  
Db 1226  
QY 1768 NFRH-----TETRNVTSRRELMVVLASLEQLQIBALFSQISSAVSLRRVALEVASP-----A 1819  
Db 1284  
QY 1820 QGQALANVELCLCPASVYRGSQECNAPGYR-----DVKGLFLGRVCVPCQCHGSDR 1872  
Db 1344  
QY 1873 CLPGSGVCDQHNTEGAHCERCOAGFMSRDEDFSPACVSCPCPLSVSPNNFAEGCVLRG 1932  
Db 1403  
QY 1933 GRT--QC--LCKPGYAGASCERCAPFNGNPLVLSSCPDCSNGDNPMLLFSDDCDPLTA 1990  
Db 1463  
QY 1991 CRGLRHTTGPBICAPGYGNALLPGNCTRCDCPTCGTEACDPSHGHLCKAGVTGRR 2050  
Db 1506

QY 2051 CDRQEGHGFNGGGCRPCACGPAAGSECHPQSQCHCRPOTMTGPOCRECAPGYWGLP 2110  
Db 1531  
QY 2111 EQGRCRCQCPGRCRDPHTGRCNCPGLSGRCDTCSQHQHVPVPGPVGSHSICVCDHC 2170  
Db 1546  
QY 2171 VTLLDDLRAGAL-----LPATHEQLGINASSMAWARHLRLNASIADLQSLRS 2221  
Db 1553  
QY 2222 PLGPRHETAQOQLEVLQOOSTSL-----QDARRLGGQAVTRDO 2260  
Db 1596  
QY 2261 ASQLLAGTEA-----TLGHAKTLAAIRAVDRTISELMSQTHGLGLANASAPSGE 2310  
Db 1656  
QY 2311 QLETLAEVERLLWEMRARDLGAPOAAAEALAAQORLLARVOEQSSWEENQALATQT 2370  
Db 1694  
QY 2371 RDLAOCHEAGLMDLREALNPAVDATREAOELASRQERLEALQKQELSRONATLQATL 2430  
Db 1747  
QY 2431 HAARDTLASVRLHSLDQAKSELERLAASLDGARTPLLQRMOTFSPAGSKLRLVE--A 2487  
Db 1807  
QY 2488 AEAHAQQLGQLANLASIILDVNQD--RLTORAIEASNAVSRILQAVQAAADAQOA-- 2542  
Db 1867  
QY 2543 LQOQADHTWTVRQGLVDRAQQLLANSTALEEAMLOEQORQLGLVMAALQAGARTQLRDVRA 2602  
Db 1922  
QY 2603 KKDQLEAH-----IQAAQAMLANDTDETSKIAHAKAVAAEAODTATRVOSQLQAMQE 2655  
Db 1975  
QY 2656 NVERWQOQYEGE-----RGQDLQAVLDAGHSVSTLEKTLPLQLLAKLSILENRG 2704  
Db 2035  
QY 2705 VHNASLALSASIGRVELTAOARGAASKVYPMKFNRSRGVQLRTPRDLADLAAYTALKE 2764  
Db 2090  
QY 2765 YLQGPPEPQCGTDEDFVMYMGSRQATGDYMGVSLRDKKVHVY-----QLGEAGPAVLIS 2820  
Db 2147  
QY 2821 DEBIGQPAVSLDRTLQGHMSVTV-----EQMQTQETKGDVAPGAEGLLNLRDDFVF 2876  
Db 2199  
QY 2877 YVGYPSTFPPLFPFGYRGCIEMDTLNEBWSLYNPFERTFQDITAVDRPCARSKSTG 2936  
Db 2255  
QY 2937 DPWLTDGS--YLDGTGEARIS-----PDSQISTTKRFEQELRLVSYSGVLEFL--KQOSFL 2989  
Db 2310  
QY 2990 CLAVQEGSLVLLYDFGAGLKKAVLPQPPPLTSASKAIQVFLGGSRKRVLRVERATVY 3049  
Db 2364  
QY 3050 SVEQDN-----DLELADAYLGGVFPDQLPPSLRWLFTTGGSVR----- 3088

Db 2417 SNQENVATSSGNFGLDKADDKYFGGL-----PTLRNL-----SMKARPEVNVYK 2465  
Qy 3089 --GCVKGIK-ALGKYVDLKEINTTYSAGCTADLLVGRAMTFHGHLRLALSNNVAPLTG 3145  
Db 2466 YSGCLKDIETSRTPYNTLSSPDVGVTKGSLNV--NTVSPKSGFVELAAVSDVCT- 2522  
Qy 3146 NVYSGFGFHAQDSALLY-----RSPDGLCQVSLQOGRVSLQ----- 3185  
Db 2523 --EINLSFVSNSEIILGGGTLTPPRKRQITQAYYAFNLKGRLEVHLSGGTTRM 2580  
Qy 3186 LRTEVKTOAG-FADGAPHYVAFYATGVM-LYVDD-----QLOQMKPHR-----GP 3230  
Db 2581 RKVIVKEPNLPHDGRHSV-HVERTGRTFTQIDEDRRHQNLTTEQPIEVKXLFVUGA 2639  
Qy 3231 PPELOPOPEPRLLLGGPESTIYNTFSGCISNVFQELLPQVDFLQNLQSLNVNST 3290  
Db 2640 PPEQPSF-----LNTIPA-----FQCVNVLVINSI-----FMDPAQPIAFKNADI 2661  
Qy 3291 G-----CAPALQAOPTGPGREGLOATARKASRRSQPARHPACMLPPLHRTT 3337  
Db 2682 GRCTYQKPREDESEAVAEVIVQ-----QSVETPAFPFVPTMWHGPCVAESEPAL 2734  
Qy 3338 RDSYQFGGSLSSHLEFVGILARRHNWPSLSMHVLPSSRGLLF-----TABLRP 3387  
Db 2735 TGSQFGLSRSNIAIVFDDTKVKNLTIIEVTRTEASGLLFYGRINHADFTVQLRN 2794  
Qy 3388 GSPSLALFLNSHFVAMQEGLTRUAQQRSRGRWHKVS-VWREKRRILLVTDGARA 3446  
Db 2795 GFPPFSYDLGSG-----STRMTIPTKINDGOWHKIKIVKQEGILYVDDAS-- 2841  
Qy 3447 WSQEGPHRQGAHEHPQH-----TLFVGGLPASSHSKL-PVTGFSGCVKRLRL 3496  
Db 2842 -----SQTSPKKAIDLVDGGLYVGGIPINVTYTRIGPVTYSLDGCVRNLM 2889  
Qy 3497 HGRP--LGAPTRMAGVTPCILGLPAGLFPFGS-----GGVITLPLGATLPDVGLEL 3547  
Db 2890 EQAPVLDQPTSSFFHGTCTFAN-AESGTYFDGTGFKAVGGFIVGLDIL-----VEF 2940  
Qy 3548 EVRPLAVTGILFHLGQARTFPYLOQVTEKQVLLRADDGAGEFST--SVTRPSVLCDCQW 3605  
Db 2941 EPRTTPTGVLGIGSSOKMDG-WGIEMIDKLMFHDVNGAGRFTAIYDAEIPGHCNGQW 2999  
Qy 3606 HRLAVKSGNVRL-----EVDASQNHVTGPIILAAAGAPALYLGILP 3649  
Db 3000 YKVTAKKIKRNLVVDGNQVDAQSPNSA-----STSADTNDPVPVGGFP 3044

RESULT 5

US-08-460-309-4  
Sequence 4, Application US/08460309  
Patent No. 5837495  
GENERAL INFORMATION:  
APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo  
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
TITLE OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
City: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460.309  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 08/125,077  
FILING DATE: 22-SEP-1993  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
TELEPHONE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-460-309-4  
Query Match 15.4%, Score 3104, DB 2, Length 3111;  
Best Local Similarity 23.8%, Pred. No. 2.8e-183;  
Matches 974; Conservative 479; Mismatches 1223; Indels 1418; Gaps 137;  
Qy 15 GPRGAPPLVGLLALGA-----ARAREAGGSPFLHPPYENLAEGARIAASATC 64  
Db 3 GAAGVLLLLLGGGQVQARFQQQRQSQAHQQRG-----LFPVAVNLASNALITTNATC 58  
Qy 65 GEEAPARGSPRTEDLYCKLVGGFVAGGDPNQTIRQYQYCDIC--TAANSNKAHPASNAID 122  
Db 59 GEGP-----EMYCKLVEHV-----PGQPVNPOCRICNQNSSNPQNHPITNAID 104  
Qy 123 GTERWQSPPLSRGLENEVNVTLDLQGVFHVAYVLIKEANSRPRDLVWLRSMDFGRY 182  
Db 105 GKNTWQSPSKNGIEHYVTIILDLQGVFQIAYVIVKAANSRPRGNWLLERSLD-DVEY 163  
Qy 183 QPWQFFASSRDL-----ERGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVN 236  
Db 164 KPWHYHVTDTTECLTLVNIYPTGPPS---YAKDDEVICTSPYKIHLENGEIHISLIN 220  
Qy 237 GRGAMNFSYPLIREFTKATNVRLRNLTLGLHLMGKALR-----DPTVTRYYSI 291  
Db 221 GRPSADD--PSPELLEFTSARYIRLAFQIRTLNADLMVFAHKDPREIDPIVTRYYSV 278  
Qy 292 KDISIGRCYCHGADAKADPTDPF--RLQCTCHNTCCGTCDCGCGFNQCPKAT 349  
Db 279 KDISVGMGCICYGHARAC-----PLDPATNKRCEHEHNTCGDCSCDCCGPGHQPWRAGT 334  
Qy 350 ANSANEQSCNCGHATDCYDPEVDRRERASQSLDTYQGGGVCIDCQHTAGVNCERCL 409  
Db 335 FLTKTEACNCHGKABECYDENVARNLSLNRKVIYGGVVCINCNTQNTAGINCETCT 394  
Qy 410 PGFVR-----SPNPLDSPHVCRCNCE--SDFTDGTCD-----LTGRCYCPNFSG 455  
Db 395 DGFPRKGVSNFY-----PRPCQCHCDPIGSLNEVCVKDEKHARGLAPGSCHTGFGG 450  
Qy 456 ERCDVCAEGFTGPPSCYPTPSSNDTRBQVLPAGIVNCDSCSAAGTQGNACKRCPVRGR 515  
Db 451 VSCDRCARGTYGPDCKA-----CNCGLGSK-----NEDPCFGPC 486  
Qy 516 LCKENFQTHCELCAFGYV-----PGCQPCQCSS----- 545  
Db 487 ICKENVEGGDCSKSGFPNQLDKNWKGDCDEFCSGVNSRCOSSVWTYGTQDMSGWILT 546  
Qy 546 --PG---VADDRCDPTGQCRKRVFEGATCDRCAPG--YHFFPLCQJCGCSPA--GTLF 596  
Db 547 DLFGRIARVPOQDLDSPQ---QISISNAEARQALPHSYWSAPAPYLGKLPVAGGOLT 603

QY 597 -----EGCD-----EAGRCLOQEFAGPH 615  
 Db 604 FTISYDLBEEBDETRVQLMILEGNDLSISTAQDEVILHPSBEHTVLLKKESTFIH 663  
 QY 616 CDRCPGVHGF-----NCQACTCDPRGAL 640  
 Db 664 -----GTH-FPVRRKEFTVLANKRVLLQITYSFGMDAIFRLSSVNLSEASVPTDG- 715  
 QY 641 DOLGAGGLCRCPGYTGTACQECSPG-----FHGFPSCVPCHCSAEGSLHA-ACDP 691  
 Db 716 -SIAAAVEVCOPPGYTGSSCSWPRHRRVNGTIFGGI--CEPCQCFG-----HAESDOD 768  
 QY 692 RSGQC-SRCPRTVGLRCDTCVFGAYNFPY-----CEAGSCHPAGLAPVDPALEAQP- 743  
 Db 769 VTGECLNKDHTGGYCKLPGFGEPTKGTSEDCQPCAC-PLNI-PSNNFSPCHLDR 826  
 QY 744 -----C-MCRHVEGSCDRCPGFWGLSPSNPEG-CTRCSDLRGTGGVABCPGTGQ 796  
 Db 827 SLGLICDGCPCVGTGPRCERCAEGYFG-QPSVFGSCQPCQCNLDNDFSIPGSCDLSGS 885  
 QY 797 C-FCRPHVCGQACSKDGFGLDQADYFGCRSCDCDGGALGQSCPEPTGVCRCRNPQT 855  
 Db 886 CLICRPGTTRGYCELADGIFG-DAVDKNCOPCRNAGGSEVCHSQTGOCECRANVO 944  
 QY 856 GPTCSEFARDHYLPDLHLRLLEBEAATPEGHAVRFGFNPLEFENFWSRWGYAQAAPVQPR 915  
 Db 945 GQRC----- 948  
 QY 916 IVARLNTSPDLFWLVRVYVNRGMSVSRVSRVBEGRSAACANCAQSQPVAFPPSTEP 975  
 Db 949 ----- 948  
 QY 976 AFTVPQGFGBFFVLNPGTWNALRVEAEGVLDVYVLLPSAYYEAALLQLRVTEACTYRP 1035  
 Db 949 ----- 948  
 QY 1036 SAQSQSDNCLLYTHLPDGFPAAGLEALCRQDNLSIPREPTQELSPSPHPLITCTGSDV 1095  
 Db 949 -----DKC----- 951  
 QY 1096 DVQLQAVPQGRYALVWEYANEDARQEVGVAHTPQAPQOGLSLHPLCYSTLCRGT 1155  
 Db 952 ----- 951  
 QY 1156 RDTQDHLAVFLDSEASVRLTAQARFFLHGVTLPVIEBSEFVEPRVSCISSHGARGP 1215  
 Db 952 -----KAGTFGL 958  
 QY 1216 NSAACLPSPRPQPPIILRDCQVPLPPGLPLTHAQDLTPATSPAGPRPRPTAVDPDA 1275  
 Db 959 QSA----- 961  
 QY 1276 EPTLLRPOATVVTTHVPTLGRYAFLLHGYQPAHPTFPVVLINAGRVMOGHANASFCP 1335  
 Db 962 ----- 961  
 QY 1336 HGYGCTLVVCEGOALLDVTHSELTVTVRVPBGRWLMDVYLVVPENVYSFGYLRPEPLD 1395  
 Db 962 ----- 961  
 QY 1396 KSYDFISHCAAQGYHISPPSSSLFCRMAAASLSFYNNGARPCGCGHEVGATGPTCEPFG 1455  
 Db 962 -----RGVPCNCSFGSKSFCDEE-SG 983  
 QY 1456 QCPCHAVIRGDCSRCATGWGFP--NCRPCDGG--ARLCEBLTGOCICPPPTIPDCLL 1511  
 Db 984 QWCQPGVTGKCDRAAGYFNFQEGGTACBCHLGNNDPKTKGICPPNTIIEKCSK 1043  
 QY 1512 QPQTFGCHPLVCEBNCSPGIGBELTPTCDTDSGCKRPNVTGRCDCSCSPGFHY 1571  
 Db 1044 CAPNTWHSITTCGKACNCSVG---SLDFQCNVNTGQCNCHPKPSGAKCTECSRHWNY 1100

QY 1572 PRCPDCDCEAGTAGPVC-----DPLTGCQCYKENVOGPKDCQCSLGTFFSLDAAN 1621  
 Db 1101 PRNLCDCLPLPGTDAITTCDSSETKKCSQDTTQCTCKVNVGHIHCDRCRPGKFGDLAKN 1160  
 QY 1622 PKGCTRCFCGATERCRSSSYTRQEFVDMEGVLLSTDRQVVP-----HERQPG- 1670  
 Db 1161 PLOCSCYCGTTCQSEAKGL-----IRTWTLKAEQITLLPLVDEALQHTTKGIVPQ 1214  
 QY 1671 -----TEMLRADLRHVEAPEAFPELYWQAPPYSYLDGVSSYGGTLYRLEHLSSTQRG 1723  
 Db 1215 HPIVAHMDLMDREDLHLEP-----FWKLPEQFEGKLMAYGGKLYAIYFEAREE 1265  
 QY 1724 DVFPMBESRPDVVLQ-----NQMSITLEPAYFPFHVRHQQLQOLVEGNFRH-----TETRN 1776  
 Db 1266 TGP--STYNPQVIRGGTPTHARIIVRMAAPLIGOLTREHEIEMTEKWAYGDDPRVHR 1323  
 QY 1777 TVSREELMVLASLEOLOIRALFESQISSAVSLRVALEVASPAGQAL-----ASNVELCL 1832  
 Db 1324 TVTREDFLDLYDIHVLILKATYGNFMRQSRISSEISWEVAE-QGRGTWTPPADLLEKCD 1382  
 QY 1833 CPASRYGDSQCECAPFYR-----DVKGLFGRVCVPCQCHGHSRCLPGSGVCDCCQH 1885  
 Db 1383 CPLGYSGLSCEACLPGFYRLRSQPGRTPTGLTCTVPCQCNHSLCDPETSICONCOH 1442  
 QY 1886 NTEGAHCRCQAGFMSRDDPSAPCVSCPPLSPNNFAEGCVLRG-GRTOC-LCKPGY 1943  
 Db 1443 HTAGDPCERCALGYIGIVKGLPNDCCQACPLISSNNFSPSCVABGLDDYRTACTCPGY 1502  
 QY 1944 AGASCRCAPGFTGNPLVLGSSCQPCDCSNGNDPLNLLFSDCDPLTGACRCLRHHTGPRC 2003  
 Db 1503 EGQYCERCAPYTGSPGNPGSQEC-----ECDF----- 1532  
 QY 2004 EICAPGVGNALLPGNCTRCDCPTCGTEACDPHSGHCLCKAGVTGRRRCDCRQCGHFGFNG 2063  
 Db 1533 -----YGLSLVP-----CDPVTGCTCRPGATGRKCDCKKWH----- 1565  
 QY 2064 CGGCRPCACPAEGSECHPQSQCHCRPGTMGPQCRECAPGYWGLPEQCRRCQCPGGR 2123  
 Db 1566 -----AREGWEC----- 1572  
 QY 2124 CDPTGRCNCPGLSBERCDTCSQHQVYPVPGPVGHSIHCEVCDHCVLLLDLBRAGA 2183  
 Db 1573 -----VFCG--DECTGLLLGDLEARLEQ 1592  
 QY 2184 L-----LPATHEQLRGINASS-----MAWARHLNASTADLQ 2216  
 Db 1593 MVMNSINTGLPAPYKMYLGLNNTQELKHLSPQAPERLIQLAEGNLNTLVTEMNELL 1652  
 QY 2217 SQRSPGPRHETAQOILEVLEQOSTSLGQDARLGGQAVGTRQOASOLLAGTEATLGHAK 2276  
 Db 1653 TRATKVTADGEOTGQDAERTNTRAKSLGEFIKELARDAEAVNEKAIKL-----NE 1702  
 QY 2277 TLLAAIRAVDRTLSLMSQTHGLANASAPSGEQLRLTLAEVERLIWEMRARDLGAPOA 2336  
 Db 1703 TLGTRDEAFERNLEGLQK-----EIDQMIKELRRKNLETKQE 1739  
 QY 2337 AAAEALAAQRLARVOEQLSSLWENQALATQTRRLAQHEAGLMDRLREALRNVADTR 2396  
 Db 1740 IAEDELVAABALLKKVKKLFESRGENEEMKDLREKLADYKNKVDADLLREATDKIR 1799  
 QY 2397 BAQELNSRQERLEBALQRKQELSRDNATLQATLHAARDTLASVFRLLHSLDQAKELER 2456  
 Db 1800 EANKLFVQCNKMTALEKKKEAVESGKRQENTILKEGNDILDEANRLADINSIIDVED 1859  
 QY 2457 LAASLDGARTPLLMOTTFSPAGSKRLVE---AAEAHAQQLGQLALNLSIILDVNQD- 2512  
 Db 1860 IQTKLPMSSEBNDKIDDLSEIKDKRLAEKVSQAESHAQA-----LNDSSAVLDGILDE 1914  
 QY 2513 ---RUTQRAIENASNYRILQAVQAAEDAGALQOQADHT--WATVVR-----QGLVDR 2561  
 Db 1915 AKNISFNATRAFKYNSIKDYIDEAEKVAEKDLAHEATKLATGPPGLLKEDAKGCLQK 1974  
 QY 2562 AQQLLANSTALEAWLQEQORGLGLVWAAALQARTQLRDVRAKKQDLBEAHTQAAQAMLAND 2621

Db 1975 SFRLNEAKKLANDVXENEDH-----LNGLKTRIENADARNGDLLRLNDLTKLSAI 2027  
Qy 2622 TDTSKXIAHAKAAEAQDTRVOSQOAMQENVERMQGVEGL-----RCQ 2670  
Db 2028 PNDTAAKLOAVKQKQANDAKDVAQITELHQNLDGLKQNKYKLAQSVAKTNAVVDK 2087  
Qy 2671 DLGQAVLDAGHSVSTLEKLPOLLAKLSILENGVGNASLALSASIGRVRELIQAARGAA 2730  
Db 2088 SKNKIADADATVNNLEQADRLDKL-----XPIKELEDNLKKNISEIKELINQARKQA 2142  
Qy 2731 SKYVPMKFNKRGVQLTRPRDLADLAAYTALKFYLOGPPEPGQGTQDRFVMWMSRQA 2790  
Db 2143 NSIKVSVSGGDC---IRTKYPEIKGGSYNNIVNVK-----TAVADNLLFYLGSAPF 2192  
Qy 2791 TGDYMGVSLDKKVHVYQVGEAGPAV---LSIDEDIGEQFAVSLDRITLOFGHMSVTV 2846  
Db 2193 I-DPLATEMRKGVSFVWDVGVSGVGRVEYDPLIDDSYWRIVA---SRTGRNGTISVRA 2248  
Qy 2847 -----ERQMIOETKGDTVAPAGELNLRDPDFVYVGVGPSTPTPPPLRFPFGYRCIEM 2902  
Db 2249 LDGPKASIVPSTHSTSPPGVT-ILVDANAMLF-VGGLTGKLDKADAVRVTFTGCMGE 2306  
Qy 2903 DTLNEEVSVLYNFBRTQLDTAVDRPCARSKSTGDPWLTGDS-YLDGTGTFARIS-----FD 2957  
Db 2307 TYFDNKPIGLWNF-REKEGDC---KGCTVSPQVED---SEGTFQDGEGLVSRPIRWY 2359  
Qy 2958 SQSTTRKFEQELRLVSVSGVLPFL--KQSQFLCLAVQEGSLVLLYDFGAGLKKAVP-LQ 3015  
Db 2360 ENISTVM---FKFTFSSALLMYLATRLDRDFMSVELTDGHKVSVDLGSWMASVVSQ 2416  
Qy 3016 PPPPLTSASKAIQVFLGGGRKRVLVRERATVYSV-----PODN-----DL 3057  
Db 2417 NHND-----GKWKSTLSIQOANISIVDITDQENIATSSGNNFGLDL 2463  
Qy 3058 ELADAYLVGGVPPDQLPSPRLWFLPFTGGSVR-----GCVKGIK-ALQKYVDLKR 3105  
Db 2464 KADDKIYFGL-----PTLNL-----SMKARPEVNLKYSGLKXIDIBSRFPYNLSS 2512  
Qy 3106 LNTTVSAGCTADLLVGRAMTFHGHFLRLALSNVAPLTGNVTSVGGFHSAQDSALLY- 3164  
Db 2513 PDYGVVTKGCSLENVY--TVSFPKGFVEL---SPVPIDVGTETNLSFSTKNESGILIG 2567  
Qy 3165 -----RASPDGLQVSLQOGRVSLQLRLTEVKTQAG-----PADGAPHY 3203  
Db 2568 SGGTPAPPRKRGRTQGAYYVILLNRGRLEVH-LSTGARTWKXIVTPEPNLPHDGRHS 2626  
Qy 3204 VAFYSNATGVW-LYVDDQLOQM-----KPHR-----GPPPELOPQDEGPRLLILGL 3249  
Db 2627 V-HVERTRGITVQVDENRNYQNLTVQEPTIEVKLFVGGAPPEFQPS-----LRNI 2678  
Qy 3250 PESGTIYNFSGCISNVFVORLLGQRVFDLQOGLSVNVSTG-CA----- 3293  
Db 2679 PP-----FEGCINLVINSV-----PMDFAPVSVFNADIGRCAHQKLEDEDDGAAPAE 2727  
Qy 3294 -----PALQQTPL--GPRGLQATARKASRRSQPARHPACMLPPLHRTTRDSY 3341  
Db 2728 IVIPEPVPTAFPTPTFVLTGHCAAES-----EPALLI-----GSK 2765  
Qy 3342 QFGGSLSHLEFVGILARHNPWSLMVLPSSRGILLF-----TARLPGPS 3391  
Db 2766 QFGLSRNSHIAIAFDTKVKRLTIELEVRTEASGLLFYMAAINHADPFTVQRNLGPF 2825  
Qy 3392 LALFLSNG--HFVAQMEGLGTRLAQRQRGRPRGRHVKSVVRWEKNRILLVTDGA--RAW 3447  
Db 2826 FSYDLGSDGTHM-----IPKI-----NDQWTKIKMRSQKQGLYVVDGASNRTI 2872  
Qy 3448 SQEGPHROHQAEHPQP-----HTLFVGLPASHSSKL-PYTVGFCGVKLELHGR 3499  
Db 2873 S-----BKKADILDVWGMVYVGLPYNITTRIGPVTYSIDGCVRNLMHAE 2919  
Qy 3500 P--LGAPTEMAGVTTCILGPLEAGLFFPGSG-----GVITLDLPGLATLPDVGLEVRPL 3552

Db 2920 PADLEQPTSPHVGTCTCFAN-AQRGTYPEDGTGFAKAVGFKVGL-----DLLVEFEFATT 2972  
Qy 3553 AVTGLIHLGQARTPEPYLOQVTEKQVLLRADDCGAGEFST--SVTRPSVLCDGQWHLAV 3610  
Db 2973 TTTGVILGISCKWDG-MGIEMIDEXLKFHVDNAGRFTAVYDAGVFGHLCDGQWHLVTA 3031  
Qy 3611 MKSNGVRLVDAQNSHTVGPFLAA--AAGAPAPLYLGLPEPMAVQWPPA--YCGCMWR 3667  
Db 3032 NKIXRIELTVQDNGVEAQSFPNPASTSDTNDPVFVGFPDDLKQFGLTTTIPRGCIRS 3091  
Qy 3668 LAVNRSPVAMTRSV 3681  
Db 3092 LKLTGKTASHWRLI 3105

RESULT 6  
US-08-125-077-4  
; Sequence 4, Application US/08125077  
; Patent No. 5872231  
; GENERAL INFORMATION:  
; APPLICANT: Engvall, Eva  
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
; TITLE OF INVENTION: Fragments and Uses Thereof  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/125,077  
; FILING DATE: 22-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/472,319  
; FILING DATE: 30-JAN-1990  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/919,951  
; FILING DATE: 27-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCES/DOCKET NUMBER: P-LA 9721  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-125-077-4

Query Match 15.4%; Score 3104; DB 2; Length 3111;  
Best Local Similarity 23.8%; Pred. No. 2.8e-183;  
Matches 974; Conservative 479; Mismatches 1223; Indels 1418; Gaps 137;

Qy 15 GPRGPAPLLVGLALIGA-----ARAREAGGGFSLHPPVFNLAEGARIAASATC 64  
Db 3 GAAGVILLLLLSGLGGLGVQVQARPPQQRQSQARQGRG-----LFFAVNLASALITTNATC 58



Db 1533 -----YGLPVP-----CDFVTGCTCPGATGRKCDGCKHH-----1565  
Qy 2064 CGGRFCACGAAEGSECHPQSQCHCRPTMTGPOCRECAPGWMGPEQGRRCQPGGR 2123  
Db 1566 -----AREGWEC-----1572  
Qy 2124 CDPHTRCNCPPGLSBERCDTCSQHQHVPVPGGPGVGHSHCEVCDHCVVLLDLDLERAGA 2183  
Db 1573 -----VPCG-----DECTGLLDGLARLBO 1592  
Qy 2184 L-----LPATHEQLRGINASS-----MAWARLRLNASADLO 2216  
Db 1593 MVMISINTGLPAPYKMYGLENNWTELXLLSPORAPERLQLAEGNLTNTVMENELL 1652  
Qy 2217 SQRLSPGPHETAQOLEVLEEQSTSLGQDARBLGGQAVTRDOASQOLLAGTEATLGHAK 2276  
Db 1653 TRATKYADGEOGQDAERTNTAKSLGETIKELARDAEAVNEKATL-----NE 1702  
Qy 2277 TLLAARAVRTISLMSQTHGLANASAPSGEQLLRTLAVERLWEMRADLGAPOA 2336  
Db 1703 TLGTRDAFERNLEGLQ-----EIDQMIKELRRKNLETOKE 1739  
Qy 2337 AAEELAAARLLARVOEQSSWEENQALATQTRDLAQHEAGLMDLREALNRADATR 2396  
Db 1740 IAEDELVAEALLKVKLFESGRGENEEMKOLREKLADYKKNYDDAMDLLREATDKIR 1799  
Qy 2397 EAQELNSRORLEALQRKQELSRDNATLOATHAARDTLASVRLHLSLDOAKEELER 2456  
Db 1800 EANKLFVQKMTALKEKKEAVESGRQENTILKEGNDILDEANRLADEINSIIDVED 1859  
Qy 2457 LAASLDGARTPLQRMOTFPAGSKRLVE---AAEHAQOQLALNLSIIIDVNDQ- 2512  
Db 1860 IQTKLPMSBELNDKIDLSQEIQRKLAEKVSAESHAQA-----LNDSSAVLDGLIDE 1914  
Qy 2513 ---RLTORAIEASNAYSRTLOAQAEADAAGALQOQADHT---WATVVS-----QGLVDR 2561  
Db 1915 AKNISFNATAAFKAYSNIKYIDBAEKVAKEADLAHEATKLATGPRGLLKEDAKGCLQ 1974  
Qy 2562 AQOLLANSTALEEAMLEQOORGLVMAALQARTQOLRDVRAKKQDLQEAHTQAQAMLMD 2621  
Db 1975 SFRILNEAKKLANDVKNEDH-----LNGLKTRIENADARNGLDRLTLNDTLGLKLSAI 2027  
Qy 2622 TDETSKTAHAKAABAQAQDATRVSQLOAQVQENVERWQOQEBGL-----RGQ 2670  
Db 2028 FNDTAALKQAVKDKARQANDAKOVLAQITELHQLDGLKKNYKKNLADSVAKTNVAVKDP 2087  
Qy 2671 DLGOAVLDAGHSVSTLEKTLQALLAKLSILENRGVHNASLASISIGRVELLIAQARGAA 2730  
Db 2088 SKNKIADADATVKNLEQADRLDKL-----KPIKELEDNKKNISEIKELINQARKQA 2142  
Qy 2731 SKVKVPMKFNRSVQLTRPDLADLAAYTALKFYLOGPEPEPQOQTEDEFRVYMGRQA 2790  
Db 2143 NSIKVSVSSGGDC---INTYKPEIKKGSYNNIVNVK-----TAVADNLLFYLGSAKF 2192  
Qy 2791 TGDYMGVSLRDKVHWYQLEAGPAPV---LSIDEDIGEQAFAVSLDRTLQFGHMSVTV 2846  
Db 2193 I-DFAIEMRKGVSLFMDVSGVGRVEYPLDITDSSVYRIVA---SRTRNGTISVRA 2248  
Qy 2847 ---EROMIQETKGTAVAGAEGLNLNRPDPFVYGVGPSTFTPPPLLRPPGVRGCIEM 2302  
Db 2249 LDGPKASIVPSTHSTSPPGYT-ILDDANAMLF-VGGLTGKLLKADAVRVTFTGCMGE 2306  
Qy 2903 DTLNEEVSVLYNFERTFOLDTAVDRPCARSKSTGDPWLTGDS-YLDGTGPARIS----FD 2957  
Db 2307 TYFDNKPGLWNF-REKGGDC---KGCTVSPQVED---SEGTIQFDGEGVALVSRPRWY 2359  
Qy 2958 SQISTTKRFEQELRVSVSGVLFLL--KQSQOFLCLAVQEGSLVLLYDFGAGLKVAPLQ 3015  
Db 2360 PNISTVM---FKERTFSSALLMYLARDLDRDFMSVELTDGHIKVSYDLGSGMASVSNQ 2416  
Qy 3016 PPPPLTSASKAIOVELLGGSKRVLVRERATVVSV-----EODN-----DL 3057  
Db 2417 NHND-----GKWSFTLSRIQKQANISIVDIDTNQENIATSSSGNNFGGLD 2463

Qy 3058 ELADAYILGGVPPDQLBPSLRNLWLPFTGGSVR-----GCVKGIG-ALGYKVDLKR 3105  
Db 2464 KADDKIYFGL-----PTLRNL-----SMKARPEVNLKKYSGCLKIDIESRTYNILSS 2512  
Qy 3106 LNTTGVSAQADTLVGRAMTFHGHFLRLALSNAVPLTGNVYSGFGFHSQAQDSALLYY- 3164  
Db 2513 PDYGVVTKGCSLENY-TVSPFKPGFVEL---SPVFDVGTGTEINLSFSTKNESGIILG 2567  
Qy 3165 -----RASPDGLCOVSLQCGRSVLQLLRTEVKTOAG-----PADGAPHY 3203  
Db 2568 SGGTPAPPRKRRTOGAYVYVILLNRGRLEVH-LSTGARTWKRKIVIRPEPNLFDGREHS 2626  
Qy 3204 VAFYSNATGW-LYVDQLOQM-----KPHR-----GPPPELOQPEGFPPLLLGL 3249  
Db 2627 V-HVERTGIFTVQVDENRRYMQNLTVEQPTIEVKKLFGVGGAPPEFQPS- -LRNI 2678  
Qy 3250 PESGTIYNFSCISNVFORLLGQRFVFDLOONLGSVNVSTG-CA----- 3293  
Db 2679 PP-----FECIWNLVINSV-----PMDFARVPSFKNADIGRCAHOKLREDEGAAPAE 2727  
Qy 3294 -----PALOQATPGL--GPRGLQATARKASRRSRQPARHPACMLPPLHRTTRDSY 3341  
Db 2728 IVIOPEPVPTAFPTPTFVLTHGPCAAS-----EPALLI-----GSK 2765  
Qy 3342 OFGGLSLHLEFVGLIARHNWPSLSMEVLPSSRGILLP-----TARLRPGSPS 3391  
Db 2766 OFGLSRNSHIAFDDTKVKVRLTIELEVRTEAESGLLFYMAAINHADFAVQLRNGLPY 2825  
Qy 3392 LALFLSNG--HFVAQMEGLGTRLRAQSRQRSGRHWKVSVRWEKNRILLVTGCA--RAW 3447  
Db 2826 FSYDLGSGDTHM-----IPTKI-----NDGWHKIKIMRSKQEGILYVDGASNRTI 2872  
Qy 3448 SOEGPHRQOHAHPQP-----HTLPVGLPASHSSSKL-PVTVGSQGVKRLRLHGR 3499  
Db 2873 S-----PKADILDVWVGMVYVGLPINYTRRIGPVYTSIDGCVRNLMHMAE 2919  
Qy 3500 P--LCAPTEMAGVTPCILGLEAGLFFPGSG-----GVITLDLPGATLPDVGLELEVRPL 3552  
Db 2920 PADLQPTSSHVGTCPAN-AQRGTYFDGTGFAKAVGGFKVGL-----DLLEVEFPATT 2972  
Qy 3553 AVTGIHFHGLQARTPPYLOLQVTEKQVLLRADDGAGEST--SVTRPSVLCGQWHRLAV 3610  
Db 2973 TTTGVLGLISSOKMDG-MGIEIMDEKLMFHVNDGAGREFAVYDAGVPGHLCGQWHKVTVA 3031  
Qy 3611 MESGNVLRLEVDQAQSNHTVGPILLAA-AAGAPAPLYLGLPBPMAVQPPPPA--YCGCMRR 3667  
Db 3032 NKIKRIELUTVDGNOVEAQSPNPASTADTNDPVFVGFFDDLKQFGLTTSIPFGCIRS 3091  
Qy 3668 LAVNRSPVAMTRSV 3681  
Db 3092 LXLTKGTASHWELI 3105

RESULT 7  
US-09-562-702A-6  
; Sequence 6, Application US/09562702A  
; Patent No. 6632790  
; GENERAL INFORMATION:  
; APPLICANT: Yurchenco, Peter  
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
; FILE REFERENCE: 99-274-B  
; CURRENT APPLICATION NUMBER: US/09/562,702A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/155,945  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: 60/143,289  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/139,198  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 60/131,720  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 3110

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-562-702A-6

Query Match 15.4%; Score 3103.5; DB 4; Length 3110;

Best Local Similarity 23.8%; Pred. No. 3.1e-183;

Matches 974; Conservative 479; Mismatches 1223; Indels 1417; Gaps 137;

QY 15 GPRGAPILLVGLLGA-----ARAREAGGGSLLHPFVNLAEARIAASATC 64  
DB 3 GAAGVLLLLSGGLGGVQARPOOROSQAHQRG-----LPPAVNLASNALLTTNATC 58  
QY 65 GEEAPARGSPRTELYCKLVGGPVAGDPNQITRGQYCDIC--TAANSKKAHPASNAID 122  
DB 59 GEKGP-----EMYCKLVEHV-----PGQPVNPOCRICNQNSNPNQRHPITNAID 104  
QY 123 GTERWQPPPLSRGLYEVNVTLDGVFHVAYVLIKFANSPPDLWVLSRWDGRTY 182  
DB 105 GKNTWQSPSIKNGIEHYVITLDOVFQIAYVIVKAA NSPPGNWILERSLD-DVEY 163  
QY 183 QWQPFASKRDL-----ERFGQTLERITRDDAAICTTEYSRIVPLENGEIVWSLVN 236  
DB 164 KPQWTHAVTDECLTYNYIFRTGPPS---YAKDEVICTSYFKHLENGEIHISLIN 220  
QY 237 GRPGANFSYSLREFTKATNVRIRLRTNTLLGHLMGKALR-----DPIVTRRYYSI 291  
DB 221 GRPSADD--PSPELLEFYSARYIRLRFIRTLNADLAWFAHKPREIDPIVTRYYYSV 278  
QY 292 KDISIGRCVCHGHADACDADPTDPF--RLQCTCOHNTCGOTCDRCPCGFNQOPWKAT 349  
DB 279 KDISVGMCMICIGHARAC-----PLDPATNKSCECHNTCGDSCDQCPCFPHQWRAGT 334  
QY 350 ANSANEQSCNCGYHATDCYYDVRRRASOSLDGTYQGGVCIIDCOHHTAGVNCERCL 409  
DB 335 FLTKTECEACNCHGAECYDENVARNLNLNIRGKYIGGVGVINCINQNTAGINCETCT 394  
QY 410 PGFYR-----SPNHLDSHVRCRNC--SDFTDGTCD-----LTGRYCRPNFSG 455  
DB 395 DGFPRPKGVSPNY-----PRCPQCHDPIGSNEVCVDEKARRGLAPGSCHTKGTGG 450  
QY 456 ERCDVCAEGTFFPSYPTPSSNDTREQVLPAGQIVMDCSAAGTQGNACKRDPVGR 515  
DB 451 VSCDRARGYTPDCKA-----CNCGLGSK-----NEDPCFGPC 486  
QY 516 LCKPNFQTHCELCAPIGV-----PGQPCQCS----- 545  
DB 487 ICKENVEGGDCSRCKSGFFNLOEDNWKGBDECFCSGVNRCCSSYWTYKIQDMSGWYLT 546  
QY 546 --PG---VADDRCDPTGQCRVGPFGATCDRCAPG--YFHFPLCQCGCSA--GTLF 596  
DB 547 DLPGRIRVAPQDDLDSPQ--QISISNAEQAALPHSYWSAPAPYLGKLPVAGGLT 603  
QY 597 -----EGCD-----BGRCLQPFAGPH 615  
DB 604 FTISYDLBEEEDTERVLQMIILEGNLDSISTAQDEVYLPSEHTNVLKLESFTIH 663  
QY 616 CDRCPGYHGP----- 640  
DB 664 -----GTH--FVVRKEFTVLANLKVLLQITYSFGMDAIFRLSSVNLSEAVSYPTDG- 715  
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RESULT 8  
 US-09-561-709B-7  
 ; Sequence 7, Application US/09561709B  
 ; Patent No. 6682911





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Qy 3669 AVNRSPVAMTRSV 3681

Db 3092 KLTKGTASHWRLI 3104

RESULT 9

US-09-562-702A-2

Sequence 2, Application US/09562702A

Patent No. 6632790

GENERAL INFORMATION:

APPLICANT: Yurchenco, Peter

TITLE OF INVENTION: Laminin 2 and Methods for Its Use

FILE REFERENCE: 99-274-B

CURRENT APPLICATION NUMBER: US/09/562,702A

CURRENT FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/155,945

PRIOR FILING DATE: 1999-09-24

PRIOR APPLICATION NUMBER: 60/143,289

PRIOR FILING DATE: 1999-07-12

PRIOR APPLICATION NUMBER: 60/139,198

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 60/131,720

PRIOR FILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2

LENGTH: 3110

TYPE: PRT

ORGANISM: Homo sapiens

US-09-562-702A-2

Query Match 15.4%; Score 3101.5; DB 4; Length 3110;

Best Local Similarity 23.8%; Pred. No. 4.1e-183;

Matches 973; Conservative 477; Mismatches 1217; Indels 1417; Gaps 137;

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Db 59 GERGP-----EMYCKLVEHV-----PGQPVNRPQCRICQNQSSNPNRHPITNAID 104

Qy 123 GTERWQSPPLSGLEYNEVNTLDLGOVPHVAYVLIKEANSRPRDLWVLRSMDFGRTY 182

Db 105 GKNTWQSPSIRKGIYHYTITLDLQQVFQIAYVIVKANSRPRGNWILERSLD-DVEY 163

Qy 183 QPMQFPASSKRDCL-----ERFPQTLBRITRDDAAICTTYSRIVPLENGEIVVSLVN 236

Db 164 KPMQYHVAVTDECLTYLNIYVPTGPPS---YAKDDEVICTSFYSKIHPLENGEIHISLIN 220

Qy 237 GRGAMNFSYPLRREFTKATNVRIRPLRNTLLHLMGKALR-----DPTVTRVYYSI 291

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Qy 516 LKXPNQGHTELCAFGFYG-----PGCQPCOCSS----- 545

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Db 2193 -DFLAEMKRGKVSFLMDVSGVGRVYPTDITDSSYWRIVA--SRTGRNGTISVRL 2248  
QY 2847 --ERQMTQETKGTQVAPGAEGLNLRPDDFVFGVGYPTFTPPPLLRPPGVRGCIEMD 2903  
Db 2249 DGRKASIVPSTHSTSPGYT-ILVDVANALF-VGLTGLKAKADAVRVIITGCMGET 2306  
QY 2904 TLNBEVSLYNPFTFQDITAVDRPCARSXSTGDPWLTDOS-YLDGTGFPARIS----FDS 2958  
Db 2307 YFDNKPIGLWNF-REKSGDC--KGCTVSPQVED--SEGTIOFDGEGVALVSRIRWTP 2359  
QY 2959 QISTTKRPEQRLVSVSGVLFLL--KQOQFCLAVQEGSLVLLDFGAGLKAVPLOP 3016  
Db 2360 NISVW--FKFRFTSSALLMYLATELDRFMSVELTDGHIKVSVDLGSWASVSNQN 2416  
QY 3017 PPPLTSASKAIOVLLGSGSRKRVLRVERATVSV-----EODN-----DLE 3058  
Db 2417 HND-----GKWSFTLSRIQKQANISVIDITNOENIATSSGNNFGLDK 2463  
QY 3059 LADAVYLGQVPPDQLPPLSLRWLPFTGGSVR-----GCVKGIK-ALGYVDLKR 3106  
Db 2464 ADDKIYFGL-----FTLNL-----SMKARPEVNLKYSGLCKDIBISRTFYNLSSP 2512  
QY 3107 NTTGVSAGCTADLLVGRAMTFHGHGFLRLALSNAVLPTGNVYSGFGFHSQAQDSALLY-- 3164  
Db 2513 DYVGVTGKCSLENY--TVSPFKPGFVEL--SPFVIDVGTTEINLSFKTNSGIIILGS 2567  
QY 3165 -----RASPDGLCOVSLQOQGRVSLQLLRTVKTQAG-----FADGAPHYV 3204  
Db 2568 GGTAPAPRRKEROQGOAYVYVILLNRGLEVH-LSTGARTWRKIVIRPEPNLFDGHSV 2626  
QY 3205 AFYGNATGW-LYVDDOLOQM-----KPHR-----GPPPELOQPGPGLLGLP 3250  
Db 2627 -HVERTREGIFTQVDENRRYMNQNLTVQEPTIEVKKLFVGGAPPEFQSP-----LRNIP 2678  
QY 3251 ESGTIYFSGCISNVFORLLGPQRFVLDQONLGSVNVSTG-CA----- 3293  
Db 2679 P-----FEGCIWNLVINSV-----PNDPARPVSKNADIGRCAHQKLRDEDEGAAPAEI 2727  
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Db 2766 FGLSRNSHIAIFDDTKVKNRLTIELEVRTEASGGLFYMAAINHADFATVQLNGLPYF 2825

QY 3393 ALFLSNG--HFVAQMEGLTSLRAQSRGRPGKRWKSVVRWEKNRILLVTDGA--RAWS 3448  
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 QY 3449 QEGPHROHQAHPQP-----HTLVGGLPASSHSSKL-PVTVGFSGCVKFLRLHGRP 3500  
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 QY 3501 --LGAPTRMAGVTPCILLPLEAGLFFPGSG-----GVITLDPGATLPDVGLEVRPLA 3553  
 Db 2920 ADLEQPTSSSHVHGCFAN-AQRGYTFDGTGFAKAVGFKVGL-----DLLVEFEFATT 2972  
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 Db 3032 KIKRIELTVGNGQVEAQSPNASTSADTNDPFGVGGFDDLKQFGLTTSIPFGCIRSL 3091  
 QY 3669 AVNR 3672  
 Db 3092 KLTK 3095

## RESULT 10

US-09-562-702A-8  
 ; Sequence 8, Application US/09562702A  
 ; Patent No. 6632790

; GENERAL INFORMATION:  
 ; APPLICANT: Yurchenco, Peter

; TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
 ; FILE REFERENCE: 99-274-B

; CURRENT APPLICATION NUMBER: US/09/562,702A  
 ; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/155,945  
 ; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: 60/143,289  
 ; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/139,198  
 ; PRIOR FILING DATE: 1999-06-15

; PRIOR APPLICATION NUMBER: 60/131,720  
 ; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 8  
 ; LENGTH: 3088

; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-562-702A-8

Query Match 15.48; Score 3099.5; DB 4; Length 3088;  
 Best Local Similarity 23.84; Pred. No. 5.4e-183;  
 Matches 967; Conservative 478; Mismatches 1213; Indels 1407; Gaps 136;

QY 33 ARAREAGGGSFSLHPPYFNIAEGARIAAASATCGEAPARGSPRPTEDLYCKLVGGFVAGG 92  
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 QY 93 DPNQTRIGQYCDIC--TAANSKAKHAPASNAIDGTERWQSPPLSRGLEYNVNVTLDIQ 150  
 Db 52 -PGQVRNPQCRICNQSSNPQRHPTNAIDGNTWQSPSIKNGIEHYHVTITLDIQ 110  
 QY 151 VFHVAYVLIKFPANSPDLVWLSRDMFGRTYQPMQOFFFASRRDCL-----ERFQPOTL 204  
 Db 111 VFQIAYVIVKAANSPPRGNWILERSLD-DVEYKPMQYHVAVTDECLTLVNIYVPTGPPS- 168  
 QY 205 ERTTRDAAICTEYSRIVPLENGEIVVSLVNGRPGAMNFSYPLIREFTKATNRIEFL 264  
 Db 169 --YAKDDEVICTSFYSKIHPLENGEIHISLINGRPSADD--FSPELLEFTSARYIRLRFP 224  
 QY 265 RTNTLGLHLMGKALR-----DPTVTRRYYSINDISIGRCVCHGHADACDAKDTDPF- 318

Db 225 RIRTLNADLMMFAHKDPREIDPIVTRRYYSVKDISVGMWCICYGHARAC-----PLDPAT 280  
 QY 319 -RLQCTQHNTCCGTCDRCPCPGNQPPWPAATANSANEQSCNCCYGHATDCYVDDEVER 377  
 Db 281 NKSCBCEBHTNCGSDCCQCCFPHQKPRWAGTFLTTTECEACNCHGKABECCYDENVAR 340  
 QY 378 RASQSLDGTYGQGGVCTIDCOHHTAGVNCERCLPGFYR-----SPNHPLDSPHYVCRNCB- 432  
 Db 341 NLSLNRIGKYIGGVCLNCTONTAGINCETCTDGFPRPKGVSPNY-----PRFCQPCCHDP 396  
 QY 433 -SFTDGTCE-----LTGEYCPRPFSGERCDVCAEGTGFPPSCYPTSSSNDTRE 483  
 Db 397 IGSINEVCVDEKHARGALAPGCHCKTGFVGSVDCRCARGTYGPDCKA----- 446  
 QY 484 QVLPAQIIVNCDGSAAGTQGNACRKDPVRGRCLCKENFGQTHCELCAFGYF- 537  
 Db 447 -----CNCGLGSK-----NEDPCGPCLCKENVEGGDCSRCKSGFFNLQEDNWK 492  
 QY 538 CQPCQCSS-----PG-----VADRCDDPTGQCRCRVGFEG 568  
 Db 493 CDEFCGSGVNRCCSSYTWYTKIQDMGMYLTLPGRIIRVAPQDDLDSPQ-----QISIN 549  
 QY 569 ATCDRCAPG--YFHFPLCOLCGSPA--GTLP-----EGCD 600  
 Db 550 AEARQALPHSYYSWAPAPYLNKLPVGGQLTFTISYDLSEEBEDTERVLQMLILEGND 609  
 QY 601 -----EAGRCCLQEPFAGPHCDRCRPGYHGP----- 627  
 Db 610 LSISTAQDEVYLLHPSBEHTNVLLKEESTIH-----GTH-FPVRRKEFMTVLNLANLRV 662  
 QY 628 -----NQACTCDPRGALDQLCGAGLCRCRPGYGTGTACQCSFG- 667  
 Db 663 LLQITYSFGMDAIFRLSSVNLSEAVSYPTDG--SIAAAVEVCQCPGYGTSSCESCWPRH 720  
 QY 668 -----FHGFPSCVCHCSAEGSLHA-ACDRPSGOC-SCRPTVGLRCDTCVPCAYNFP 718  
 Db 721 RVNNTIFGGI--CEFCQCFG-----HABSCDDVTGECLNCKDHTGGPYCDKCLPGFYGE 774  
 QY 719 Y-----CEAGSCHPAGLAPVDPALPEAQP-----C-MCRAHVEGSCDRCKEFGWL 765  
 Db 775 TKGTSEDQPCAC-PLNI-PSNNFSPCTCHLDRSLGLICDGCPCVGTGPRCERCAEYFG- 831  
 QY 766 SPSPNPG-CTRCSCLRLGTLGVAECPQGTGOC-FCKPHVCQACASCKDGFGLDQADY 823  
 Db 832 QPSVFGSCQPCQCNLDNDFSIPGSCDSLGSCLICKPOTTGRCYCLCADGTFG-DAVDA 890  
 QY 824 FGCRSCRDIGGALGQSCPRGTGVCRCRENTQGTCTSEPARDHYLFDLHLELELEEAAT 883  
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 Db 927 ----- 926  
 QY 944 GRYSVREGRSAACNCTAQSQVAFPPSTEPAFITVPQGFGEFVLPNPGTWALRVEAE 1003  
 Db 927 ----- 926  
 QY 1004 GVLLDYVLLPSAYEALLQLRVTEACTYRPSAQSGDNCLLYTHLPDGFPSAGLEA 1063  
 Db 927 -----DKC----- 929  
 QY 1064 LCRQDNLPRPCPTQLSPSPHPLITCTGSDVDVQLQAVPQPGRYALVVEYANEDARQE 1123  
 Db 930 ----- 929  
 QY 1124 VGVAVHTPQAPQGLLSLHPLCYLSTLCRGTDARTQDHLAVPHLDSEASVRLTAEQARFF 1183  
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 QY 1184 LHGVTLPVIEFSPFEVPRVSCISSHGAFGNSAACLPSRFPKPPQPIILRDCQVILP 1243

Db 930 -----XAGTFGLQSA----- 939  
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 Db 940 ----- 939  
 QY 1304 HGVQPAHPTFPVEVLINAGRWQGHANASFCPHGVGCRTLVVCBQALLDVTHSELTVTV 1363  
 Db 940 ----- 939  
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 Db 940 -----RGVPCNCSFSGSKSFDCEE-SGQWCQPGVTGKKCDRCARAGYFNFQGGC 989  
 QY 1482 RPCDCG--ARLCBELTGOCICBPRTIPDCLLOQPQTFGCHPLVGCBECCSGPGIOBELT 1539  
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 QY 1540 DPTCDTDSQCKCRNVNTRRCDTCSPGFHGVPRCPCDCHEACTAPGVCD----- 1590  
 Db 1047 DQCQVNTQCNCHPFSGAKTECSRGHVNYPRCNLCDCPLDGTDTTCDSETKKCS 1106  
 QY 1591 PUTGCYCKENYQKPCQCSLGTFSLDAANPKGCTRCFCGATERCSRSSYTRQEFVDM 1650  
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 QY 1651 EGWLLSTDRQVVP-----HERQPG-----TEMLRADLRHVPEAVPEAPPEL 1692  
 Db 1161 RTWVLKABQTLPLVDLBAHQHTTKTGIVFOHPIVAMDLMDREDLHLEP-----F 1211  
 QY 1693 YWQAPPSYLGDRVSSYGTGLAYELHSETQRGDVFVPMESRDVYVLOG---NQMSITFLEP 1749  
 Db 1212 YWKLPEQFECKLMAYGKGLKAIYVFEAREETGF--STYNPQVIIRGTPTTHARIIVRHM 1269  
 QY 1750 AYPTEGHVHGOLOLVEGNFRH---TETRNVTGREELMVLASLEOLOLRALEFSQISSA 1805  
 Db 1270 AAPLGQLTRHEIEMTEWKYGGDDPRVHTVTRFEDFLDIYDIHILIKAYGHEMRQ 1329  
 QY 1806 VSLRVALEVASPAGOGAL---ASNVELCLCPASYGSDSCQECAPFYR-----DVK 1854  
 Db 1330 SRISBISMEVAB-QRGRTTMTTPADLIEKDCPLGYSGLSCEACLPFYRLRSPQGRTP 1388  
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 Db 1449 CPLISSNNFSPSCVAEGLDDYRCTACPRGYGQYCCERCAPGYTGSFNGPNSCQBC--- 1505  
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 QY 2033 CDPHGHCLCKAGVTGTRCDRCQEGHFGNCGGCRPCACGPAEGBSECHPQSGQCHCRP 2092  
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 QY 2093 GTWQGCRCAPGYWGLPEQGRCCQCPGRCRCDPHTGRCNCPGSLGRCDCSCQHQHP 2152  
 Db 1550 ----- 1549  
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 QY 2306 APSGEOLLRTLAEBERILLWMBARDLCAPQAAAEELAAARQILLARVQEQQLSSIMBENQA 2365  
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 QY 2366 LATOTDRDLAHEAGLMDREALNRAVDATREAEQLNSRNOERLEALORQKBLSDNAT 2425  
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 QY 2426 LQATLHAARDTLASVFFLLHSLDOAKEELERLAASLDGARTPLLRQMOTFSPAGSKLRIV 2485  
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 Db 2146 NNIVVNVK-----TAVADNLLFYLGSAKFI-DFLAIEVRKGVFLNDVSGVGRVEY 2197  
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 Db 2363 LRDEMSVELTDGHLKVSYDYLGSQMASVVSQNHND-----GKWKSFILSRIQ 2409  
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 QY 3087 VR-----GCVKGIK-ALGKVVDLKRNTTQVSAGCTADLLVGRAMTFPHGFLR 3134  
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3226	QY	PHR-----GPPPELOQPEGPPRLLGLGPSGTYNFSGICSNVFORLLGQORVFD	3278
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3279	QY	LQCNLGSVNVSTG-CA-----PALQAOTPGI--GPRGLOA	3310
2674	DB	FARPVSFNADIGRCANQKUREDEGGAPEIIVIQPEPVTFAPTTPVLTHGPCAAES	2733
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2734	DB	-----EPALLI-----GSKQFGLSRNSHIAIADFDTKYNRLTIELEV	2771
3371	QY	LPRSSRGILLP-----TARLRPGSPSLAFLSNG--HFAVQMEGLGTRLRAQSRQ	3418
2772	DB	RTAESGULLFMAAINHADPATVQLRNGLPYFSYDLGSGDTHM-----IPTXI-----	2820
3419	QY	RSRPRGHWKVSVRWEKNRILLVTDGA--RAWSQEGPRHQGAHPPO-----HTLFV	3469
2821	DB	--NDGQHWKIKIMRSKQEGILYVDGASNRTIS-----PKKADILDVGVMLYV	2865
3470	QY	GGLPASHSSKX-L-FVTVGFSQCVKRLRHGRP--LGAPTRMAGVTPCILGPLPAGLFPPG	3526
2866	DB	GGLFINYTTTIRIGPVTYSIDGCVNRLHWAEPADLEQTSFHHVGTCTCFAN-AQRGTVFDG	2924
3527	QY	SG-----GVITLDLPGATLPVQGLELEVRPLAVTGLIFHLGQARTPPYLOLVTEKOVLL	3581
2925	DB	-----DLLVEFEFATTTTGVLLGHSSQXMDG-MGEMIDEXLMF	2977
3582	QY	RADDGAGBFST--SVTRPSVLCDGQWHLRAVMKGNVRLRLEVDQAQSNHTVGPLLAA--AAG	3638
2978	DB	HYDNGAGFTAYDAGVPHCLCDQGWKVTANKIKHRIELTVDCNQVQEAQSPNFASISAD	3037
3639	QY	APAPLYLGLPEPMAVQWP2FA--YCGCMRRLAVNRSPVAMTRSV	3681
3038	DB	TNDPVFVGFPDDUKQFGLTTSIPFRGICRSKLTGKTASTHWRLI	3082

RESULT 11

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US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-4

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Query Match	15.4%	Score	3037.5	DB 4	Length	3089
Best Local Similarity	23.8%	Pred. NO.	7.1e-183			
Matches	966	Mismatches	1207			
Conservative	476	Indels	1407	Gaps	136	

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QY 93 DPNQTIRGYCYIC--TAANSKAHPASNAIDGTERTWQPPLSRGLYNEVNVTLDLGQ 150

52	Db	PGQPVNPOCRICNQNSNPNQRHPITNAIDGKNTWQSPSINKGIEYHYVITITLDLQ	110
151	Qy	VFHVAVYLKPFANSPPDLWLWLSRMDFGRTYQWQFFASSKEDCH	204
111	Db	VOIAYVIVKAAANSPPGNWILERSLD-DVEYKPMQYHATVDTTECTLNINYERTGPPS	168
205	Qy	ERITRDDAAICTEYSRIPLNENGEIWSLVNRPGMNFYSFLLREFTKATNRLRFL	264
169	Db	--YAKDDEVICTSPYSKIHPLENGEIHISLINGRPSADD--PSPELLEFTSARYIRLRFQ	224
265	Qy	RTNLLGHLMGKALR-----DPTVTRYYSIKDISIGGRVCVCHGADACADKDPDPF	318
225	Db	RIRTLANLAWFAHKDPREIDPIVTRYYSVKDISVGGMCICYGHARAC-----PDPFAT	280
319	Qy	RLQCTCOHNTCGTCDRCPCGPNQOPWKATANSANECOSCNCYGHATDCYDYDPEVDRR	377
281	Db	NKSCEBHTNCGSDCCQCPGHQKPRWAGTFLTKTECEACNCHGKAESCYDENVARR	340
378	Qy	RASQSLDGTYYGGGVCIIDCHHTAGVNCERCLSGFYR-----SPNHPLDSHVHCRCNCE	432
341	Db	NLSLNRGKYIGGVCINCTONTAGINCETCTDGFPRKGVSPNY-----PRPCQFCHCDP	396
433	Qy	SDFTDGTCD-----LTGRCYCEPNFSGERCDCVCAEGFTGFSPCYPTPSSSNDTRE	483
397	Db	IGSLNEVCVXDEKHARGLAPGSCCHKTFGGVSCDCRCARGYGYDCKA-----	446
484	Qy	QVLPAQGIIVNDCSAACTQGNACRKDPRVGRCLCKPNFQGTCHCLCAPGYG-----PG	537
447	Db	-----CNCSGLGSK-----NEDPCFGPCICKENVEGDCSRCKSGFNLQEDNWKG	492
538	Qy	QPOCQCSS-----PG--VADORDCDPTGOCRCRVGFEG	568
493	Db	CDEFCFSGVNRCOSSYWTYKGIQDMGWLTLDFGRIRVAPODDLDSPQ---QIISIN	549
569	Qy	ATCDRCAPG--YHPFLCQLCGCSPA--GTLF-----EGCD	600
550	Db	AEARQALPHSYWAPAPYLNKLPVAGGQLTFTISYDLSEEEEDTERVLQMLILEGND	609
601	Qy	-----EAGCLCQPFAGPHCDRCRPGTHGFP-----	627
610	Db	LSISTAQDEVYLPSEETHNVLLKESFTIH-----GTH-FPVRRKEPMTVLANKRV	662
628	Qy	-----NQACTDPRGALDOLCGAGGLCRCPGVGTATACECSPG--	667
663	Db	LLQITYSGMDAIFRLASVNLSEAVSYPTDG--SIAAAVEVCQCPGGYTGSSECSCHWRH	720
668	Qy	-----FHGPFSPVCHCSAEGSLHA--ACDPRSGQC--SCRPRVTJGRCDTCVPGANFP	718
721	Db	RVNGTIFGGI--CEPCQCFG--HAESCDVDTGECLNKDHTGGPYCDKCLPGFYGEP	774
719	Qy	Y-----CEAGSCHPAGLAPVDPALPRAQVP-----CMCAHVEGSPCDRCRPGWGL	765
775	Db	TKGTSEDQPCAC--PLNI--PSNNFSPCTHLDRSLGLICDGPVGYTGPRCRCAEGVFG--	831
766	Qy	SPSNPEG--CTRCSCDLRTGLGGVAECQGTQC--FCKPHVCGQACASCKDGFGLDQADY	823
832	Db	QPSVPGSCQPCQNDNLDFSI PGSCDSLGSCLICKPGTGTGYCELCAQGYFG--DAVDA	890
824	Qy	FGRCSCRCDIIGALQSCSEPTGVCRCRPNQGTCTCEPARDHYLPDLHLRLLEERAT	883
891	Db	KNCOPCRNAGGSFSEVCHSQTQCECRANVQGORC-----	926
884	Qy	PEGHVRFGFPLEFENPSNRGYAQPQPRIVARLNLTSPDLFWLVERYVNRGAMSVS	943
927	Db	-----	926
944	Qy	GRVSVREGRSAACANCTAQSOPVAFPPSTEPAFITVPQRFGEFFVLNPGTWARLVEAE	1003
927	Db	-----	926
1004	Qy	GVLIDYVLLPSAYEALLQLRVTEACTYRPSAQSGDNCLLYTHLPDLGFPSPAAGLEA	1063
927	Db	-----DKC-----	929

QY 1064 LCRQDNLSPRPCTEQLSPHPLITCTGSDVDVOLQVAVPQGRYALVVEYANEDARQE 1123  
Db 930 ----- 929  
QY 1124 VGVAVHTPORAPQOGLSLHPCLYSTLCRGRTARDQDHLAVFHLDSASVELTAEQARFF 1183  
Db 930 ----- 929  
QY 1184 LHGVTLVPIEFPSPFVPRVSCISSHGAFGNSAACLPSPRPKPQPIILRDCQVPLP 1243  
Db 930 ----- KAGTFLQSA----- 939  
QY 1244 PGLPLTHAODLTATSPAGPRPRPTAVDPAETLLREPOATVFTTHVTLGRYAFLL 1303  
Db 940 ----- 939  
QY 1304 HGYPAPHTFPVEVLINAGRVWQHANASFCPHGYGCTLLVVCBQALLDVTHSELTVTV 1363  
Db 940 ----- 939  
QY 1364 RVPEGRWLWDYLVVVPENVYSFGYLRBEPDKSYDFISHCAAQGYHISPSSSLFCRNA 1423  
Db 940 ----- 939  
QY 1424 AASLSLFYNGARPCGCHVGATGPTCEPFGGQCPCHAVVIGRDCSRCATGYNGFP--NC 1481  
Db 940 ----- RGCVCNCSNFGSKFDCCE--SGQWCQCPGVGTGRKCDRCARHYFNQEGGC 989  
QY 1482 RPCDCG--ARLCELTGOCICPPRTIPDCILCQFQTFGCHPLVGCBECCNCPGQIQLT 1539  
Db 990 TACECSHLGNCDPKTGRCICPPNTIGBKSKCAPNTWHSITTGCKACNCSTVG--SL 1046  
QY 1540 DPTCDTDSGCKCRNVTGRCDTCSQFPHGYPCRCPCDCEAGTAPGVC----- 1590  
Db 1047 DFCQNVNTGQCNCHPKFGAKCTECSRHWNYPNCNLCDFLPGTDATTCDSBTCKSCS 1106  
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QY 1651 EGWLLSDTROVP-----HERQPG-----TEMLRADLHYVPEAVPEAPFL 1692  
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QY 1693 YWQAPPSYLGDRVSSYGGTLYELHSETQRGDVFPVMESEPDVVLQO---NQMSITFLRP 1749  
Db 1212 YWKLPEQPEGKLMAYGKLYAYFEAREETGP--STYNPQVIIRGTPTHARIIVRH 1269  
QY 1750 AVPTPGHVRGQLQVGNFRH---TETNTYSREELMMVLASLQLOIRALFSQISSA 1805  
Db 1270 AAPLIGQUTRHEIEMTEKMYGDDPRVHRTVTRDFDILYDIHYILIKATYGNFMQ 1329  
QY 1806 VSLRRVALEVASPAGQAL----ASNVELCLCPASYRGDSQCEAPGFYR-----DYK 1854  
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QY 1855 GLFLGRVPCOCHGSHDRCLPGSGVCDVCOHNTGACHRCQAGFSSRDDSPAPCVSP 1914  
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QY 1973 NGNDBNLLFSDCDPLTGACRCLRHHTTGPCEICAGFYGNALLPNCNTRCDCTPCGTEA 2032  
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Db 1517 CDPVTGCTCRPGATGRKCDCKHWH-----AREGWEC----- 1549

QY 2093 GTMGPCRECAPGWGLPEQCCRRCQCGGRCDPHTGRCNCPPLSGERCDTCSQHQVP 2152  
Db 1550 ----- 1549  
QY 2153 VEGPVGHSIHCEVCHCWLILLDDLERAGAL-----LPAIHEQLRGINASS----- 2199  
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QY 2246 DARLGGQAVTRQOASQOLLAGTEATLGHAKTLAAIRAVDRTLSELMSQTHGLANAS 2305  
Db 1659 FIKELARDAEAVNEKAIKL-----NETLGRDEAFERNLEGLOK----- 1697  
QY 2306 APSGEQLLRTLAVERLILWEMRARDLGAPOAAAABELAAARLLARVQBOLSSLEWNOA 2365  
Db 1698 -----EIDQMIKELRRKNLTKETKEIAEDELVAABALLKVKKLFGBSNGENEE 1745  
QY 2366 LATOTRDLAQHEAGLMDLREALNRVADATREAEQELNSRQERLEALORQELSBDNAT 2425  
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QY 2426 LOATLHAARDTLASVFLHLSLQAKBELRLAASLDGARTPLLRMQTFSPAGSKRLRV 2485  
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QY 2486 E---AASAHAAQOLGOLALNLSIILDVNOD---RLTORAIEASNAYSRLIQAQVAAEDAA 2539  
Db 1866 EKVSQAESHAQ-----LNOSAVLGDILDEAKNISFNATAAFKAYSNIKDYIDAEKVA 1920  
QY 2540 GOALQOQADHT--WATVVR-----OGLVDRAOQLLANSTALEEAMLOQCORLGLVWAAL 2590  
Db 1921 KEAKDLAHEATKATGPRGLLKEDAKGCLQKSPRIINEAKKLANDVYKENEDH-----L 1973  
QY 2591 QGARTQLDRVRAKQDQLEAHIAQAQAMLANDTDETSKIAHAKAVAAEAQAQTATRVQSO 2650  
Db 1974 NGLXTRIENADARNDLRLTLNDTLGKLSAI PNDTAAKLAQVKDKARQANDTAKOVIAQI 2033  
QY 2651 QAMQENVERQOQYEG-----RGQDLQOAVLDAGHSVSTLEKTLQOLLAKLSI 2699  
Db 2034 TELHONLDGKKNYKNLADSVAKTNVWDPKKNIIADADATVKNLEQAEORLIDKL-- 2091  
QY 2700 LENRGVNASIALSASIGRVRELIAQARGAASAKVPMKFNCRSGVQLTRPTDLADLAAY 2759  
Db 2092 ---KPIKELEDNLKKNISEIKELINQARKQANSIKVSVSSGGDC---IRTYKPEIKKGSY 2145  
QY 2760 TALKFYLGPEPEPGOGTDRFVWYMGSRQATGDYMGVSLRDKKWHVYQLGEAPV-- 2817  
Db 2146 NNIVNVVK-----TAVADNLLFYLGSAKFI--DFLAIEMRKGVSVFLWDVSGVGVEY 2197  
QY 2818 --LSIDEDIGEOFAAVSLDRTLQFGHMSVTV---EROMIQETKGDVTAPGAEGLLNRP 2871  
Db 2198 PDLTIDDSWYRIVA--SRTGRNGTISVRALDGPKASIVPSTHSTSPGYT--ILDVDA 2253  
QY 2872 DDFVYVGGYPSTFTPPILLRPPGYGCTEMDTLNEEVVSLNXPFTQLDTPAVDRPCAR 2931  
Db 2254 NAMLF-VGGUTGKLVKADAVRVTFTGCMGETYFONKPIGLWNF--REKEGDC---KGCTV 2308  
QY 2932 SKSTGDPMLTDS-YLDGTGFARIS---FDSQISTTRFEQELRLVSYSGVLFEL--KQ 2984  
Db 2309 SPOVED---SEGTIQFDGEGYALVSRPIRWYENISIVM---FKPRTFSSALLMYLATRD 2362  
QY 2985 QSQFLCLAVQBSGLVLLYDFGAGLKXAVLPQPPPLTSASKAIQVFLGSGSKRVLRVE 3044  
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QY 3045 RATVYSV-----EQDN-----DLBLADAYYLGVPVPPQLPPLPFWLFFPGS 3086  
Db 2410 KQANISIVDITNQEBENIATSSSGNNFGLDKADDKIVFGGL-----PTLNL-----S 2458  
QY 3087 VR-----GCYKGIK-ALGKYVDLKLRLNTTGVSAAGCTADLLVGRAMTFHGHGFLR 3134

Db 2459 MKARPEVNLKYSGLCKDIEISRPYNLLSPDVTGVTKGCSLENY--TVSPKPGFVE 2516  
QY 3135 LALSNAVPLTGNVSGFGFHSQAQSALLY--RASPDGLCQVSLQOGRV 3181  
Db 2517 L---SPVIDVGTENLSFSTKNSGIIILGSGGTAPPRKRQRTQGAQVYILLNRGL 2573  
QY 3182 SIQLARTEVKTAQ-----PADGAPHVAVFVSNAATGV--LYVDDQLQOM-----K 3225  
Db 2574 EVH-LSTGARTWKIVIRPEPNLPHDREHSV-HVERTRGIFTVQVDENRRYQNLTV EQ 2631  
QY 3226 PHR-----GPPPELOPQEPRLGLGGLPESGTINFGCSINVFQRLIGPORVFD 3278  
Db 2632 PTEVKLFVGGAPPEFQSP-----LRNIPP-----PEGCIWNLVINSV-----PMD 2673  
QY 3279 LQONIGSVNVSTG-CA-----PALQACTPGL--GPRGLQA 3310  
Db 2674 PARPVSNADIGRCAHCKLREDEDAAPAEIVQPEPVTPTPTPTVLTGHCABES 2733  
QY 3311 TARKASRRSOPARHPACMLPPLHRTTDSYQFGSLSSHLEFVGIILARHNWPSLSMHV 3370  
Db 2734 -----EPALLI-----GSKQFGLSRNSHIAIAFDDTKVKNRLTIELEV 2771  
QY 3371 LPRSSRGLLF-----TARLRGSPSLALFLSNG--HFVAQMEGLGTRLRASRQ 3418  
Db 2772 RTEASGLLFYMAINHADPATVQLRNLGFLPYFSYDLGSGDTHM-----IPTKI----- 2820  
QY 3419 RSRPORMHKSVRMEKRIILLVTDGA--RAWSQEGRHQHQAHPQP-----HTLFV 3469  
Db 2821 --NDQWMIKIMRSKQBGLIYVDGASNRITIS-----PKADILDVGVGMLYV 2865  
QY 3470 GGLPASSHSSKL-PYTVGFSQVCKRLRLHGRP--LGAPTRMAGVTPCIIPLGLEAGLFFPG 3526  
Db 2866 GGLPINYTRIGPVTYSDICVNLHMAEPADLEQTSFVHGTCFAN-AORGTYFDG 2924  
QY 3527 SG-----QVITLDLPGATLPDVGLLEVRPLAVTGLIFHLGQARTPPYLOLQVTEKQVLL 3581  
Db 2925 TGFKAAGVGFVGL-----DLLVEFFFAITTTTGVLLGSSQXMDG-MGIEMIDEKLMF 2977  
QY 3582 RADDGAGFST--SVTRPSVLCDQWHRLAVMKSQNVRLVLEDAQSNHTVGPLAA--AAG 3638  
Db 2978 HYDAGAGFTAVYDAGVPHGLCDQWHKVTANKIKHRIELTVQDNQVBAQSPNASTAD 3037  
QY 3639 APAFLYGLPEPMAVQWPPA--YCCMRRLAVNR 3672  
Db 3038 TNDPVFVGFPDDLKQGLATTSIPFRGICRSLKTK 3073

## RESULT 12

US-08-460-309-5

Sequence 5, Application US/08460309

Patent No. 5837496

GENERAL INFORMATION:

APPLICANT: Engvall, Eva

APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Fragments and Uses Thereof

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,309

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/125,077

FILING DATE: 22-SEP-1993

APPLICATION NUMBER: US PCT/US 94/10730

FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/472,319

FILING DATE: 30-JAN-1990

APPLICATION DATA:

APPLICATION NUMBER: US 07/919,951

FILING DATE: 27-JUL-1992

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INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3075 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-460-309-5

Query Match 14.2%; Score 2854; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 9.1e-168;

Matches 941; Conservative 513; Mismatches 1255; Indels 1320; Gaps 140;

QY 23 LLVGLALLGAARAREEAGGGFSLHPVFNLAEGARTAAAGATCGEAPARGSPRPTDLYC 82  
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QY 83 KLVGPGVAGDPMQITRGQYCDIC--TAANSNKAHPASNAIDGTERWQSPPLSRGLEYN 140  
Db 51 KLVEHV-----PGRPVNPQCRIKCDGNSANPRERHPI:SHAIDGTNNWQSPSQNGREYH 105  
QY 141 EVNVTLDLGOVHVAVYVLIKFNANPRPDLWVLEFERSMDFGRTYQPMOFFPASSKDCLEF- 199  
Db 106 WVTITLDRQVQVAVYVLIKFNANPRPDLWVLEFERSMDFGRTYQPMOFFPASSKDCLEF- 164  
QY 200 -----GQPTLERTDAAICTTEYSRIVPLENGEIVSVLNGRPGAMNFSVPLLEPT 254  
Db 165 ITPRRGPTVYR---ADDEVICTSVYSLVPLEHGEIHTSLINGRPSADL--SPKLEPT 219  
QY 255 KATNVRLRLRTNTLLGLHMGKALR-----DPTVTRRYVYSIKDISIGRCVCHGHADAC 309  
Db 220 SARVIRLRFERITLADLMTLSHREFKELDPM:LPRIYYSIKDISVGGWCICYGHASC 279  
QY 310 DAKDPTDFPLOCTCOHNTCGTCDRCPCGFNOQPMKATANSBECQSCNCGVHATDCY 369  
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QY 370 YDPRVDRRRASQSLDGTGTYGGVCIDCQHHTAGVNCERCLPGFYR---SPNHPLDSPHV 425  
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QY 426 CRRNCB-----SDFTDGTCEBLTGRCYCRPNFSGERCDCVCAEGTGFPS 470  
Db 394 CRPCNCDPVGSLSSVCIKDDLHSDLENG---XPGQCPCKEGYTGKCDRCOLGVKDYPT 450  
QY 471 CYPTPSSNDTRQVLPAGQIVNCDCAAGTQGNACRKPVRGCLCKENFGTHCELCA 530  
Db 451 C-----VSCGNPVGSAD-----EPCTGCPVCKENVSGKACDRCK 486  
QY 531 PGFVG-----PGCQPCQCSSPGVAD-----DRCDP-----D 556  
Db 487 PGFVNLKEKNPRGSCBFCF--GVSIVCSSLSWPLQGVNMSGWLVTLISPRKIPSOQD 544  
QY 557 TGQCRCEVGFEG-ATCDRCAPGVYEHFPLQLCG----- 588  
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665 NVTHLLIRATVNSAMALRYLESVSLDIASNALDLVVAADVEHCPCPGYGTGTSCSCL 724  
666 PGHGFPS-----CVPCHC-----SAEGSLHAACDPRSGQSCRRPVTVGLRCDTCVPGAYN 716  
725 SGYVRVDGILFGGICQPCCECHGAAECNVHVC-----IACAHTTGVHCEQCLPGFYG 778  
717 PP-YCEAGSCHPA-----GLAPVDPALPEAQVPC-MCRAHVGPSPCDCKPGFWGL 765  
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897 KNCRACECHVKGSHSAVCHLETGLCDCKPNVTGQC-----932  
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944 GRVSREGRSAACANCTAOSQVAFPPSTEPAFITVPQGFGEFPVFNPGTWNALRVEAE 1003  
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933 -----DQCL-----936  
1064 LCRQNSLPRPCPTQOLSPSPHPLITCTGSDVDVQLQVAVPQPGRYALVVEYANEDARQE 1123  
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949 -----948  
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949 -----RPNCSVAGSVSGCCTD--EQCHCVPGVAGKRCDCRCAHGFIAYQDGC 995  
1482 RPDCC--GARLQDELTCGICPPRTIPDCLLQCPQTFGCHPLVGCBECCSGPGIOBLT 1539  
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1694 HQAPSYLGDVRSSYGGTLRYELHSETQGDVFVPMBS-----RPDVVLOQNOW--SIT 1745  
1219 MFLPQOQDQUMAYGGKLYSV-----AFVSLDQVGTSTNPEPQVLIKGGRIRKQVI 1270  
1746 FLEAPYPTFGVHRQQLQVVEGNF---RHTBTRNTVSREELMMVLALEQIQIRALFSQI 1802  
1271 YMDAPAPENG--VRQOEAVAMRENFWKYSVSEKPVTRDEDFMSVLSDEYILIKASYQG 1329  
1803 SSAVERLRVALVYASPA---GQALASNVELCLCPASVYRGDSQOECAPGVR-----D 1852  
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1450 ALCACPHSPPA--SF8PTCVLEGDHDFRCDACLLGYEGKHCCERCSSYXGNPOTPGSCOK 1508  
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1548 ----LMTDCVSCD-----1557  
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2209 NASIADLOQLRSLPLGPRHETAQQLVLEEQSTS--QDARLGGQAVGT---RDCASOLL 2265  
1595 ENTLYQBSL-----LKENMOKDQK--IKLEGVAEBTDNLQKLTML 1637  
2266 A-----GTEATLGHAKTLIAAIRAVDRITLSELSOT-----GHIGLANASAPSGEQ 2311  
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2312 LRLTAEVERLLWEKARDLGAPOAAABELAAQALLARVOEQLSSLWEENQALATQTR 2371  
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1752 HVLSKNNEL--KAAEALVREAAKWOESNHLMLLVNANLREPSDKLHVQEBQNLTSLEI 1810  
2431 HAARDTLASVFRLLHSLDOAKSELE-----RLAASLDGARTPILQRMQTFSPAG 2479  
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2480 SKRLVEAAEAHAQQLGQALNLSIILDVNQDRLTQRAIEASNAYSRTLOVAOAEADA 2539  
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Db 1972 LRNKTFRQENAVEITROTNESSLILRAIPGIRDKGAKTKELATSAQSQAVSTLRDVAG 2031  
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Db 2032 LSQELLNTASLSRVNTLRETHQLLOQSTWATLLAGKVKVVEIQAKVLPDRKPKLWML 2091  
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Db 2092 EEN-----LSRNLSEIKLISQARKQASIKVAVSAD-RDCIRAYQPO--ISSTNYN 2140  
QY 2761 ALKFYLOPEPEPGGTEDRFVMTYMGSRQATGDMVGSRLDRKKVHVYQYOLGEAGPVLISI 2820  
Db 2141 TLTLNVKTQEP-----DNLFLVLSGSTAS-DPLAVEMRGVAFVFLNDLGSSTLEPP 2192  
QY 2821 DEDTGE-QFAVSLDRTLQGHMVTVEROMIQSTKGT---VAPGABGLLNLRPDDFVF 2876  
Db 2193 DFPIDDRNWHIHRVAFNGISLSV--KEMSSNQKSPTKTSKSPGTANVLDVNNSTLME 2249  
QY 2877 YVGGVPSFTFPPLRPBGVCGCTEMDTLNEEVSLSYNF-ERTFOLDTAVDRPCARSKST 2935  
Db 2250 -VGLGGGOKSPAVKVFHFGKCLGEAFNGKSLGWNVIERGKC-----RCFCSSQN 2303  
QY 2936 GPMWTDGSLDGTGFAFISFDSOISTKRFPEQLRVSYGVLFILKO--QSOPLCLAV 2993  
Db 2304 EDP-----SFHFDGSGYSVVE-KSLPATVQTILMFTFSPNGLLILVLSYGTDKDPLSIEL 2358  
QY 2994 QEGSLVLLYDFGAGLKXAVLPQPPPLTSASKAIQVFLGGSRKVLVRVERATVYSV-- 3051  
Db 2359 PRGRVKTMDLGSQ-----PILJLTD-----RYNGTWTXIAF 2392  
QY 3052 ---EODNLELADAY-----YLGVPDPQLPPSLRWLF 3081  
Db 2393 QNRNRKQGVLAVIDAYNTSNKTKOGETFGASSDLNRDKDPIYVGGILPRSRV---VRRGV 2449  
QY 3082 PTGGSVRCVKGKALGKYVDLKRNTTGVSAGCTADLLVGRAMTHGHGFLRLALSNA 3141  
Db 2450 TTKSFV-GCIKNLISRSTFLLR-NSYGVKRGCLLEPI--RVSFLKGGIIEILPKKSL 2505  
QY 3142 PLTNGVSGFGFHAQSDALLYRASPDGLCQVSLQGRV---SLQLL--RTEVKTQAG- 3195  
Db 2506 PESEWLVT---FATTNSSGIILAAALGGDEKRGDREAHVFFTSVMLGNIHVHVNPD 2562  
QY 3196 -----FADGAPHYVAFYSNATGVWLYVDQLOQMKEHGPPEL----- 3234  
Db 2563 GTGURKALLHAPTCTSDGQAHSLVNRNRITVQLDE-----NNFVEMKLGTLV 2613  
QY 3235 QPQEGPRLLLGLPE-SGTIY-----NFGSCISNVFQRLGQRPVFDLQNLGSNVV 3288  
Db 2614 ESRTINSVLYVGGIPEGETSLTMRSPHGCINKL-----IFNLE--LLDFNS 2661  
QY 3289 STGCAPALQAOTPGIGRGLQATARKASRESROPARHP-ACMLPPLHRTITRDSYQFGSL 3347  
Db 2662 AVG-HEQVDLDTCLWSEPKLAPDAEDSKLLRFPAPPEOCVVDAALEYVPGHAGHGLTQ 2720  
QY 3348 SSH--LEFVGILARHNPWLSMHVLPSPRSGLLFTARLPSPSLALFLSNG--HFVA 3403  
Db 2721 NSHFLPFPQSAVRKLSVELSIRTL--ASSGLIYMAHQNDADYAV-LQLHGRHLHMF 2777  
QY 3404 QMEGLGTRLAQSRQSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQ--HQBAB 3461  
Db 2778 DL-KGK-RTKVSHALLSDGKHTVTKDYKRGKFTVDG-----RESMVTVGDGTM 2830  
QY 3462 POPHTLVFVGLPASHSSKUL-PVTVGPSCGVKRLHGRPL--GAPTRMAGVTICLGLP 3518  
Db 2831 DVEGLYFGLGLPSQYQARKIGNITHSIPACIGDVTVNSKQDKDSVSAFTVNR- 2889  
QY 3519 EAGLFFPGSGVITLDPGATLDPVGLLEVRPLAVTGLIFHLGOARTPPYLOLOVTEKQ 3578  
Db 2890 QEGTYFGSGVYALVKEGYKVQSDVNITLFEFRYSSQNGVLLGISTAKVDA-IGLELVGDK 2948  
QY 3579 VLLRADPGAGEFSTVTRP---SVLDCGQWHRJAVNMKSGNVLRLEVD-----AQSNHTVG 3630

Db 2949 VLFHVNAGRI-TPAYEPTATVLCGKWHITLQANKSKHRIITLIVDGNVAGAESPT-- 3005  
QY 3631 PLLAAAGAPAPLYGLGLPEPMAVQ--PWPPAYCGQWRRLAVNRSP-----VAMTRSGVEVH 3684  
Db 3006 --QTSVDVTNNPIYVGGYPAGVKQKCLRSTQTSFRGCLRLALIKSPQVQSLDFSRFAELH 3063  
QY 3695 GAVGASGCP 3693  
Db 3064 G-VFLHSCP 3071

## RESULT 13

US-08-125-077-5  
; Sequence 5, Application US/08125077  
; Patent No. 5872231  
; Patent No. 5872231 5840863  
; GENERAL INFORMATION:  
; APPLICANT: Engvall, Eva  
; APPLICANT: Leivo, Ilmo  
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
; TITLE OF INVENTION: Fragments and Uses Thereof  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/125,077  
; FILING DATE: 22-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/472,319  
; FILING DATE: 30-JAN-1990  
; PRIOR APPLICATION DATA: US 07/919,951  
; APPLICATION NUMBER: US 07/919,951  
; FILING DATE: 27-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 9721  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-3001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3075 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-125-077-5

Query Match 14.2%; Score 2854; DB 2; Length 3075;  
Best Local Similarity 23.4%; Pred. No. 9.1e-168;  
Matches 941; Conservative 513; Mismatches 1255; Indels 1320; Gaps 140;  
QY 23 LLVGLALLGAARAREBAGGGSFLHPPYFNLAEGARIAASATCGEAPAPAGSPRPTEDLYC 82  
Db 5 VLVLLVLLCVAAQCR-----GLFPALLNLASNAHISTNATCGEKP-----EMFC 50  
QY 83 KLVGPGVAGDPPNQITRQGVCDIC--TAANSKNAHPASNAIDGTERWQSPPLSRGLEYN 140  
Db 51 KLVEHV-----PGRPVNPQCRICDGSANPRERPISHADGTNNWQSPSIQNGREYH 105



Db 1548 -----LMETDCVSCD----- 1557  
Qy 2149 HQVPVGGPVGHSIHCEVCHCVLLDDLEAGALLPAIHEOLRGINASSMAMARLHEL 2208  
Db 1558 -----DECVGVLNDLDBIGDAVLSN--LTGI--IPVPYGLSNL 1594  
Qy 2209 NASIADLOQLSRPLGRHETAAQLEVLBQOQSTSLGQDARRLGQAVGT---RDQASOLL 2265  
Db 1595 ENTTKYLOBSL-----LKENMOKDLGK--IKLEGVABEDTNLQKLTML 1637  
Qy 2266 A-----CTEATLGHAKTLLAIRAIVDRTLSLNASQT-----CHGLANASAPSGEO 2311  
Db 1638 ASTQKNRATERIFKESQDLAVAIERLQMSITTEIMEKTTLNOTDLBDFLPLNSTLQNMQQ 1697  
Qy 2312 LRTTAEVERLLWEMEARLDIGAPQAAAEALAAQELLARVQEOQLSSLWEEENQALATOTR 2371  
Db 1698 NGTSLLEI-----MQIRDFTQLHONATLELKAEDLLSQICENYCKPLEEVLKEAAS 1751  
Qy 2372 DRLAQHEAGLMDLREALNRAVDA--TREAQELNSRQERLEALQKQELSRDNATLQATL 2430  
Db 1752 HVLSKENNEL--KAAEALVREAEAKQMESNHLMLMNVANLREPSDKKLHVQEEQNLTSELI 1810  
Qy 2431 HAARDTASVFRLLHSLDQAKELE-----RLAASLDGARTPLLRMQTFSPAG 2479  
Db 1811 VQGRGLIDAAAGTDAVQDALEHLEDHQDKLLWSAKIRHHIDDLVMEHSQR----- 1862  
Qy 2480 SKRLVVEAFAHAQOIGOLALNLSIILVNDQRLTORAIEASNAVSRILQVQAAEDAA 2539  
Db 1863 NAVDLVYRAEDHATFQRLADVLSLENIR--NVSLNATSAAVYHYNISQILIESEELA 1920  
Qy 2540 GQALOQADHTWATVVRQGLVDRAQOQLANSTALEEAMLEOQOGLGLVAAALQCATQLRD 2599  
Db 1921 RDHRTVET--SLLSESLVNSGKAQVRS-----RFLKEGNLS-----RKLPGIALEISE 1971  
Qy 2600 VRAKXQDLRAHI-----QAAQAMLDWT--DETSKKIAHAKAVAAEAOQTATRVSOQLOA 2652  
Db 1972 LRNKTNRFOENAVEITRQTNESLLIRAIPEGTRDKGAKTELATASQASVSTLRDVAG 2031  
Qy 2653 MOENVERWQOYEGLRG-----ODLQAVLDAGHSVSTLE---KTLPLLAKLSIL 2700  
Db 2032 LSOELLNTSASLSRVNTTIRETHOLLQDSTMATLLAGRKVDVEIQAKVLFRLKFLKML 2091  
Qy 2701 ENRGVHNASLALSASIGRVELIAQARGAASKVKYPMKFNRSRGVQLRTPRDLADLAAYT 2760  
Db 2092 EEN-----LSRNLSEIKLLISQARKQAASIKVAVSAD--RDCIRAYQPO--ISSTNYN 2140  
Qy 2761 ALKFYLOGPEPEPGQGTEDRFVWYMGSRQATGDYMGVSLRDKKXVHVYOLGEGAVLSI 2820  
Db 2141 TLTANVKTQEP-----DNLFLYLGSTAS--DFLAVEMRRGRVAPFLWDLGSGSTRLEFP 2192  
Qy 2821 DEDIGE-QPAAVSLDRTOFGHMSVTVVEROMIQTETKGT---VAPGAEGLLNLRPDDFVF 2876  
Db 2193 DPFIDNRWHSIHVAFRFGNIGLSV---KEMSNQKSPKTSKSPGTANVLVDVNNSTLMF 2249  
Qy 2877 YGGYESTFTPPPLRFPYRGVRCIEMDTLNEEVSILYNF--ERTFQDLTAVDRPCARSKT 2935  
Db 2250 -VGGLGGQIKKSPAVVTHFKGCLGFAFLNGKSLGWNVIERGKC-----RGCFGSSQN 2303  
Qy 2936 GDPWLTDGSLDGTGARISFDSQISTTKRFECELELVSGVLPFLKQ--QSQFLCLAV 2993  
Db 2304 EDP-----SFHFDGSGYSVVE--KSLPATVTQITMLFNTFPGNLLLYLGSYTKDFLSIEL 2358  
Qy 2994 QEGSLVLLYDFGAGLKKAVPLOPPPLPPLTSASKAIQVFLGGRKRVLVRVERATYVS-- 3051  
Db 2359 FRGRVMTDLGG-----PITLLTDR-----RYNNGTWYKIAF 2392  
Qy 3052 ---EQNDLELADAY-----YLGGVPPDQLPPSLRWLF 3081  
Db 2393 QNRKQGVLAVIDAYNTSKETKQGTGPGASSDLNKLKDPYVGLPRSRV---VRGVG 2449  
Qy 3082 PTGGSVRGCVKIGKALGKYVDLKRNLNTGVSGAGCTADLLVGRAMTFHGHGFLRLALSNA 3141  
Db 2450 TTKSFV-GCIKNLETSRSTFDLLR--NSYGVKRGCLLEPI--RSVSFLKGGYELPPKSLIS 2505

Qy 3142 PLTGNVYSGCFHSAQSAALLYRRASPDGLCOVSLQQGRV---SLQLL--RTEYKTOAG- 3195  
Db 2506 PESEWLYT---FATNSSGIIILAALGQDVEKRGDBEABHVPFFSVMLIGNIEVHVNPGD 2562  
Qy 3196 -----PADGAPHYVAFYSNATGVWLYVDQLQOMKPHRGPPPEL----- 3234  
Db 2563 GTGLRKALLHAPTGTCTDGGQAHISILVNRRIITVQLDE-----NNPVENKLGTLV 2613  
Qy 3235 QPOPEGPPRLLLGLPE--SGTIY-----NFGSGISNVFVQRLLLQPQVFLDQNLGSLSVV 3288  
Db 2614 ESRITVNSLVNLYVGGIPGEGTSLTWERSPHGCIKNL-----IPNLE--LLDFNS 2661  
Qy 3289 STGCAPALQATQPGRLGRLQATARKASRRSRQPARHP--ACMLPPHLLTRTDSYQFGSSL 3347  
Db 2662 AVG--HEQVLDLTCVLSRPRKLPADPAEDSKLLREFAPEQCQVVDAALEYVFGAHQFGLTQ 2720  
Qy 3348 SSH--LEFVGILARHWNPSLSMHVLPSSRGLLFTARLRPGSPSLALFLSNG--HFVA 3403  
Db 2721 NSHFILPFGQSAVRKKLSVELSIRTL--ASSGLIYYMAHQNDYAV--LQHGGRLHFMF 2777  
Qy 3404 QMEGLGTRLRAQSRQRPRGRWVKVSVRWEKNRILLVTDGARAWSQEGPHRQ--HQGAEH 3461  
Db 2778 DL--GKG--RTKVSHPALSDGKWHVTKTDYVVRKGFITVDG-----RESPMVTYVGDGTML 2830  
Qy 3462 PQHTLVFGGLPASSHSSKL--PVTVGFSGCVKRLRLHGRPI--CAPTEMAGVTPEILGPL 3518  
Db 2831 DVEGLFYLGLPFSYQARKIGNITHSPACIGDVTVNSKQDKDQSPVSAFTVARC--YAVA 2889  
Qy 3519 EAGLFFPGSGVITLDPGATLPDVGLEVRPLAVTGLIFHLGQARTPYLOLQVTEKQ 3578  
Db 2890 QEGTYFDGSGVAAALVKEGYKVQSDVNITLFTSSQNGVLLGISTAKVDA--IGLELVDBGK 2948  
Qy 3579 VLLRADGAGEFSTSVTRP---SVLCDGOWHRLAVMKSQNVLEVD-----AQSNHTVG 3630  
Db 2949 VLFHVNNGAGRI--TPAYEPTATVLCGRKWHITLOANKSKHRITLIVDGNVAGAESPH-- 3005  
Qy 3631 PLLAAAAGAPAPLYLGLPEPMAVQ--PWPPAYCGCMRRLAVNRSP-----VAMTRSVVEH 3684  
Db 3006 --QSTSVDTNNPIVGGYPAGVKQKCLRSQTSFRGCLRLKALIKSPQVQSLDFSRAPFELH 3063  
Qy 3685 GAVGASGCP 3693  
Db 3064 G-VFLHSCP 3071

## RESULT 14

US-08-600-982-24  
; Sequence 24, Application US/08600982  
; Patent No. 6120991

## GENERAL INFORMATION:

; APPLICANT: Carter, William G.  
; APPLICANT: Gil, Susanna A.  
; APPLICANT: Ryan, Maureen C.  
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness  
; STREET: 1420 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-8100  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/600,982  
; FILING DATE: 02-SEP-1994  
; CLASSIFICATION: 435



[REDACTED]

[REDACTED]

Db 1632 IHLHLEDTSSVTAGIIPFPFPASTQEPHLHGAPANLTLRIPVWKSFPGLRNIHVNHI 1691  
Qy 3674 PVAMTRSVVHGAVGAGSCP 3693  
Db 1692 PVPVTEALEVQGPVSLNGCP 1711  
RESULT 15  
PCT-US94-10261A-24  
Sequence 24, Application PC/TUS9410261A  
GENERAL INFORMATION:  
APPLICANT: Carter, William G.  
APPLICANT: Gil, Susanna A.  
APPLICANT: Ryan, Maureen C.  
TITLE OF INVENTION: Epligrin, an Epithelial Ligand for  
TITLE OF INVENTION: Integrins  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESS: Christensen, O'Connor, Johnson, and Kindness  
STREET: 1420 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101-8100  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10261A  
FILING DATE: 02-SEP-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Shelton, Dennis K.  
REGISTRATION NUMBER: 26,997  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-8100  
TELEFAX: (206) 224-0779  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1713 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: E170 protein as translated from sequence of  
DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R  
PCT-US94-10261A-24  
Query Match 11.2%; Score 2260.5; DB 5; Length 1713;  
Best Local Similarity 31.5%; Pred. No. 2.6e-131;  
Matches 612; Conservative 296; Mismatches 711; Indels 321; Gaps 48;  
Qy 1818 PAQGGAL-ASNVELCLCPASRGDSQCECAPGYRDVKGFLGRCVPCQCHGHSRCLUPG 1876  
Db 29 PPGSQQLQASYVEF-----RPSQGCSPGYRDHKGFLGRCVPCNCNGHSNQCQDG 79  
Qy 1877 SGVUCQCHNTEGAHCERCAQPMSSRDPSPCVSCPCLSPVSPNFAEGCVLGGRTO 1936  
Db 80 SGICVNCQHNTEGAHCERCAQPMSSRDPSPCVSCPCLSPVSPNFAEGCVLGGRTO 134  
Qy 1937 CLCKPGVAGASCRCAPGFGNPLVLGSSCPQDCSGNPDNLLFSDCDPLTGACRGCLR 1996  
Db 135 CSCKAGYGTQCECAPGYFGNPKFGSGCQPCSCNSGQ-----LGSCHPLTGDCIN--- 187  
Qy 1997 HTTGPRCEICAPGYGNALLPGNCTCDCTPCGTEACDPHSGHCLCKAGVGTGRRCDROE 2056  
Db 188 -----QDSSPAEE----- 189  
Qy 2057 GHFGNGCGGRCPCACGPAAGSECHPQSQCHCRPGTGWGPGQRECAPGYWGLPQGCRR 2116  
Db 190 -----PKDSSPAEE----- 198

Qy 2117 CQCPGRCDEHTGRCNCPCPLSGERCDCITCSQHQHPVPGPGVGHSHCEYCDHCWVLLLD 2176  
Db 199 -----CDDCDSQVMTLLN 211  
Qy 2177 DLERAGALLPAIHQOLRGINASSMAMARHLRLNASTIADIOSQLRSLPGPHETAQOQLEVL 2236  
Db 212 DLATMGQLRLVKSQLQGLSASAGLLQMRHMETQAKDLRNLNLYRSALSHGSKTEGL 271  
Qy 2237 EQOSTSLGQDARRLGGQAVGTROQASOLLATGTEATLGHAKTLAAIRAVDRTILSEMSQ- 2295  
Db 272 EREUTDLNQEFTELQEKARQVNSKATQTLNNVNRATQSAKELDVKIKVIRNVHILLKQI 331  
Qy 2296 TGHGLANASAPSGEQLRLTAEVERLLWEMVARDLGAPOAAAEAAQRLARVQEQ 2355  
Db 332 SGTDGEGN-NVPSGD-FSREWAEARWRELRNFKHLREAEADKRESQLLNIRTW 389  
Qy 2356 LSSLWEENQALATOTRDLAQHEAGLMDIREALNRAVDATREACELNSRQERLEALOR 2415  
Db 390 QKTHQGENGLANSIRDSLSNEYAKUSDLRARQEAQAAQKQANGLNQEN-ERALGAIQR 448  
Qy 2416 K-QELSRDNATLQATLHAARDTLASVERLLHSLDQAKEELERLAASLDGARTPLQRMOT 2474  
Db 449 QVKEINSIQSDFTKYLTATDSSLLQTNIALQLEKSKQEKYKLAASLNEARQELSDKVE 508  
Qy 2475 PSPAGSKRLVWEABAHQAQOLGALNLSSILLVDNODRLTORAIBASNAYSRLQAVQA 2534  
Db 509 LRSAGKTSLEVEAEKEARSLQELAKQLEIKRNASGDELVRCAVDAATAYENILNAKA 568  
Qy 2535 AEDAAGQALQQAADHTWATVVRQGLVDRQAQOLLANS-TALBEAMLQEOORLGLVMAALQGA 2593  
Db 569 AEDANRAASASESALQTVKEDLPRAKTLSSNSDKLINEAKWTKKQKQEVSPALNNL 628  
Qy 2594 RTQLRDYRAKKDQLEAHQAAQ-AMLAMDTDETSTKTAHAKAVAAEAQDTATRVQSOLOA 2652  
Db 629 QOTLNIQVQKEVIDTNLTTRDGLHGIQGRDIDAMISSAKSMVRKANDITDEVLDGLNP 688  
Qy 2653 MQENVWRQOYEGRLGQDLGQAVLDAGHSVSTLEKTLPLLAKLSLLENRNVHNASLA- 2711  
Db 689 IQDVERIKDTYGTQNEDEPKALTADNSVKNLTKNLPDLNRKIESI-----NQQLLP 742  
Qy 2712 ---LSASIGRVRELIQAARGAASKVKVPMKFNRSRGVQLRTPRLADLAAYATKALFYLOG 2768  
Db 743 LGNISDNMDRIRELIQQAARDAASKVAVPMRFGKSGVEVRLPNDLEDLKGYTSLSLFLQR 802  
Qy 2769 PEPEPGQGTEDRFVWNGSRQATGYNGLRDKKVVHWYQIGEAGPAVLISIDEDIGE- 2827  
Db 803 PNRENGTEENMFVYLGKNDASRDYTGMAVVDGQLTCVYNLGR-EAELQVQILTKSE 861  
Qy 2828 ----FAAVSLDRTLQFGHMSVTVERQMIQ-ETKG--DTVAPGAEGLLNLRPDDFVFYVG 2879  
Db 862 TKEAVMDRVKFORIYQPARLNYTKGATSSKPETPGVYDMDGRNSNTLLNLDPENNVFVG 921  
Qy 2880 GYPSTFTFPPLLRPGVRCIEMDTINEEVSILYNPERTELOLDTAVDRPCARSKSGTGPV 2939  
Db 922 GYPDFKPLRSLSPPPYKGCIELDNLNVLNFKKTNLNTTEVEPCRRKKE-----977  
Qy 2940 LTDGSLDGTGFARI SFDSQISITTKREFQELRLVSVSGVLFFLKQSQOFLCLAVQEGSLV 2999  
Db 978 -SDKNYEGTGAYRVPQPH-APIPTGQTIQTVDRGLLFFAENGDRFISLNEIDGKLM 1035  
Qy 3000 LLYDFGAGLKX-----AVPLQPPPLTSASKAIQVFLGGSRRKRLVVRERATVYVEQ 3053  
Db 1036 VRYKLSNELPKERGVGDAIN-----NGRDHSITQI-KIGKLOKRMWINVD---VQNTII 1084  
Qy 3054 DNDLELADAYVLGGVPPDQLPPSLRMLFP-TGSGVRGVGKIGKALGVVLDKRLN-ITGV 3111  
Db 1085 DGEVDFSTYLLGI-----PIAIRERFNISTAFRCGMKNLK---KTSGVRLNDTVGV 1136  
Qy 3112 SAGCTADLLVGRAMTFHGHLFALNSVA-PLTGNVYSGFGFHSQAQDSALLYRASPDG 3170  
Db 1137 TKKCSDEWKLVSASFSGG-QLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQWTR 1194

Search completed: May 18, 2004, 14:59:57  
Job time : 117.952 secs